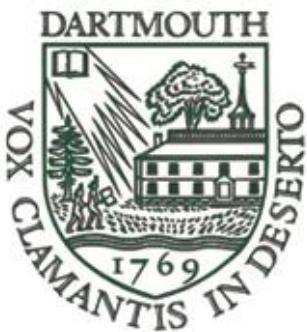


Computationally-driven deimmunization of therapeutic proteins

Chris Bailey-Kellogg



Disclosure

Chris Bailey-Kellogg and Karl E. Griswold are co-founders of Occulo Holdings LLC, Occulo Bio LLC, Stealth Biologics LLC, and Lyticon LLC. These biotechnology companies are pursuing design and development of deimmunized biotherapeutic agents and antibacterial biotherapies. Related research in the Griswold and Bailey-Kellogg Dartmouth academic labs is subject to a conflict of interest management plan, including public disclosure of financial interests in these companies.

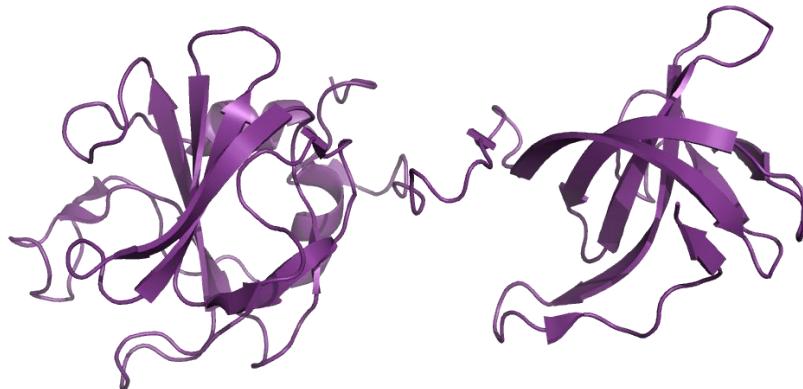
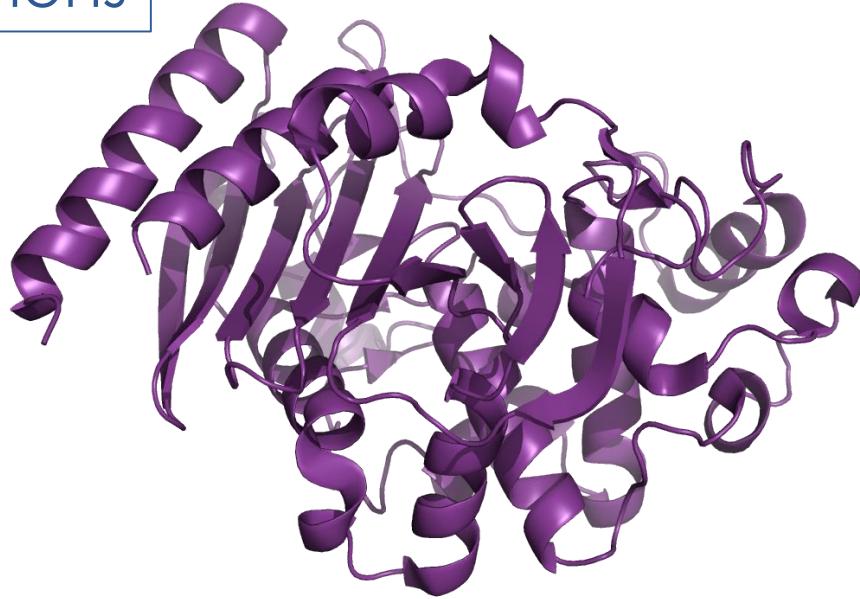


(Non-Ab) protein therapeutics

diverse structures, functions

β -Lactamase

- cleaves lactam ring
- antibody-directed anti-cancer therapies



lysostaphin

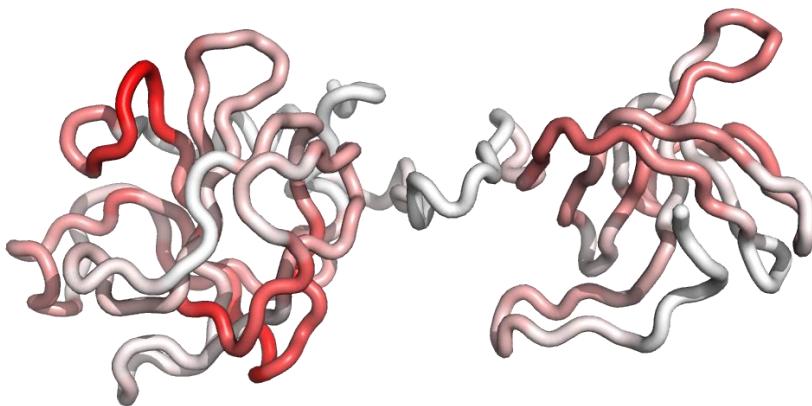
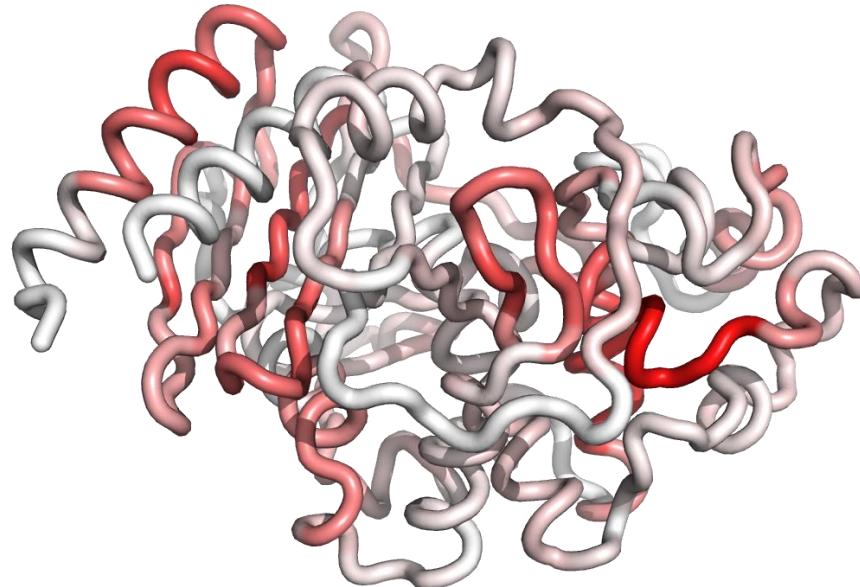
- degrades cell wall
- anti-staph

Protein therapeutics: immunogenicity

red: epitopes

β -Lactamase

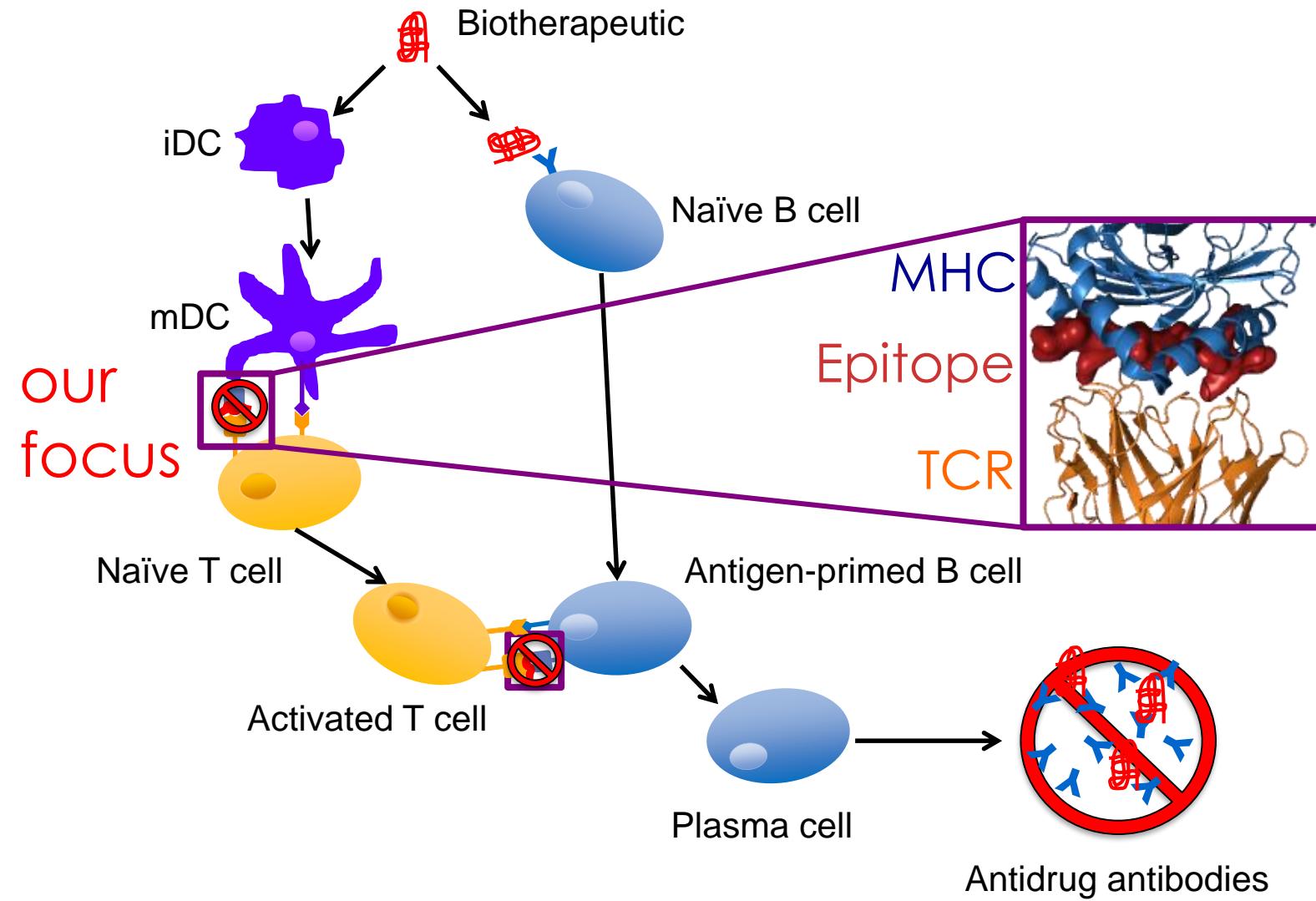
- cleaves lactam ring
- antibody-directed anti-cancer therapies



lysostaphin

- degrades cell wall
- anti-staph

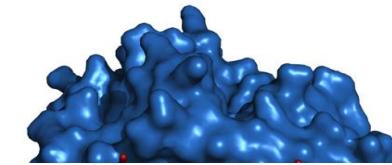
Anti-biotherapeutic immunogenicity



Deimmunization: competing objectives

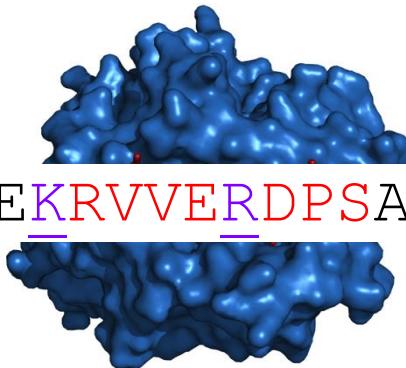
wild-type

...TAYKEFRVVELDPSAKI...



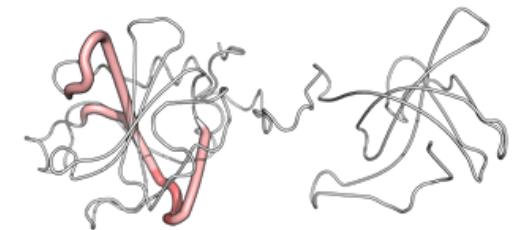
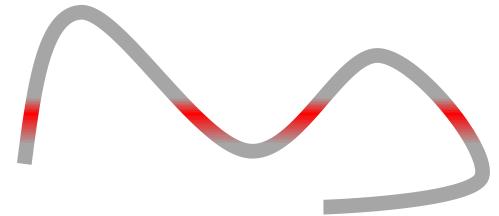
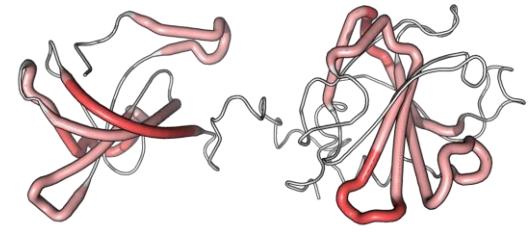
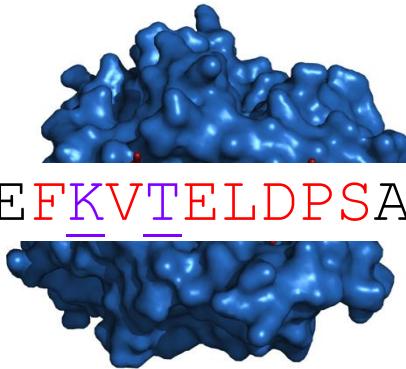
variant 1

...TAYKEKRVVERDPSAKI...



variant 2

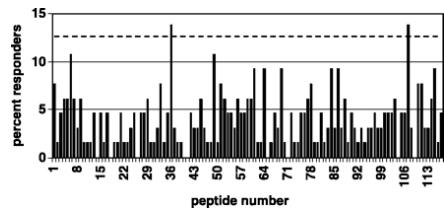
...TAYKEFKVTELDPSAKI...



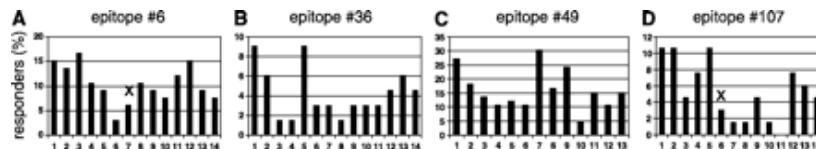
Experimentally-driven approaches

E.g., Genencor [Harding et al., Mol Cancer Ther 2005]

immunogenicity screening



alanine scanning



engineer into whole protein

Epitope	Mutation	Expression	Stability
6	M20A	0.05	ND*
6	K21A	1.73	0.53
6	S24A	2.23	1.11
6	V30A	0.12	7.6
36	L107A	0.10	ND*
36	D108A	0.09	ND*
36	T113A	0.21	ND*
36	P118A	0.16	ND*
49	T146A	0.47	0.42
49	T147A	0.43	0.38
49	L149A	0.73	0.2
49	I155A	0.19	ND*
107	S324A	0.80	0.65
107	V326A	0.53	0.50
107	I329A	0.05	ND*
107	P330A	0.06	ND*

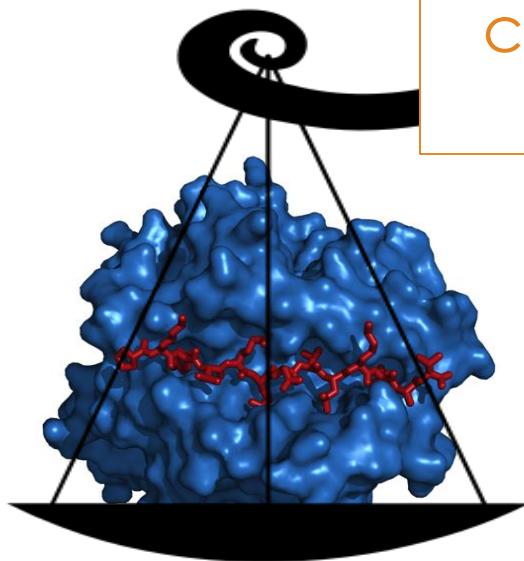
possible variants

lots of experimental time and expense
may not consider some good possibilities

K21A, S324A

Our approach: computationally-driven deimmunization

Delete T cell epitopes



Maintain function



computational protein
design algorithms

computational models

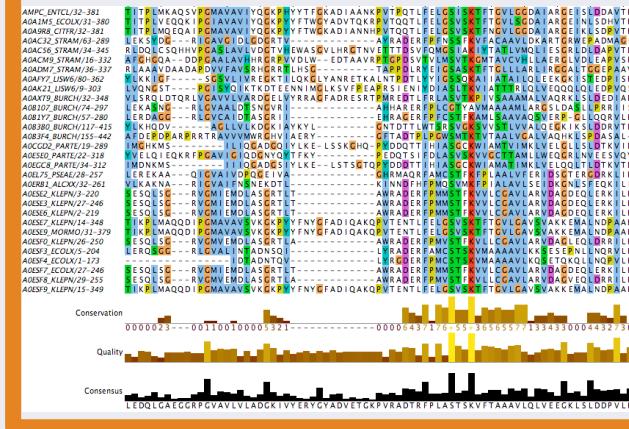
epitope content

stability, activity

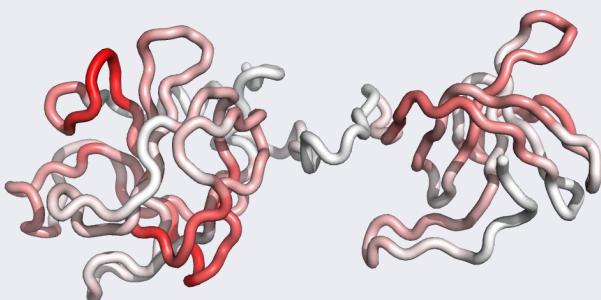
Landscape of approaches

Evolutionary

Individual variants

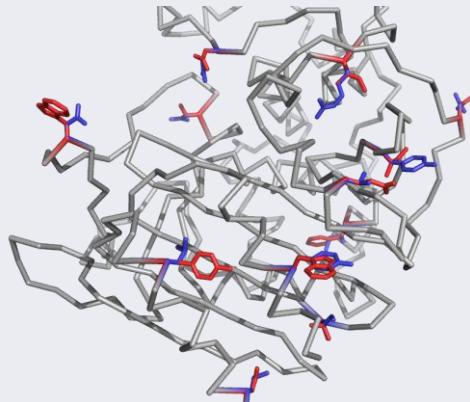


Structural

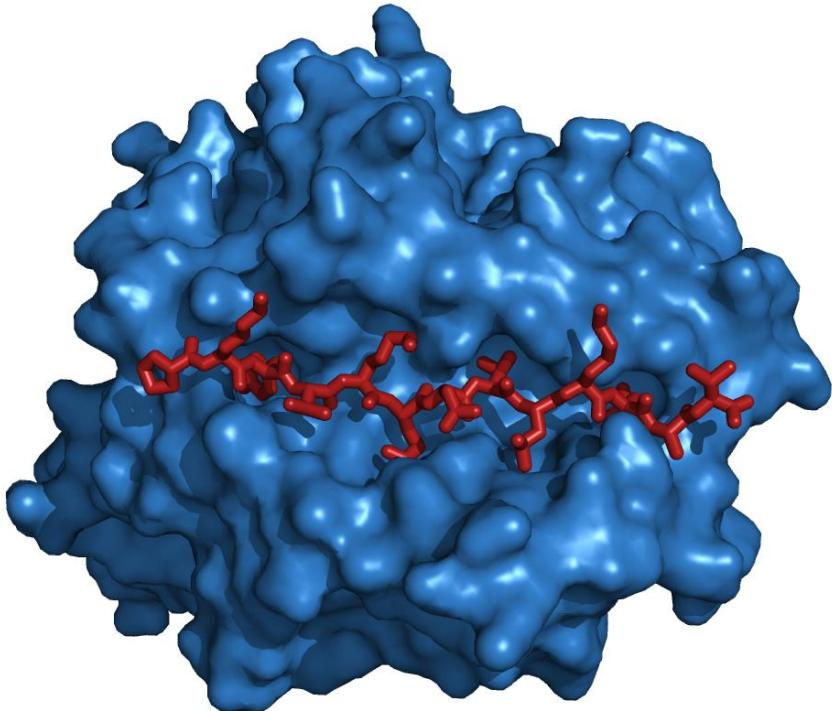


Combinatorial library

... TAYKE_EFRVVELDPSAKI ...
 | D | A |
 | E | S |
 | T |
 ↓
 ... TAYKD_DFRVVELDPAAKI ...
 ... TAYKE_EFRVVELDPSAKI ...
 ... TAYKD_FFRVVELDPTAKI ...
 ... TAYKE_EFRVVELDPAAKI ...
 ... TAYKD_FFRVVELDPSAKI ...
 ... TAYKE_FFRVVELDPTAKI ...



Epitope content



different “pocket” shapes

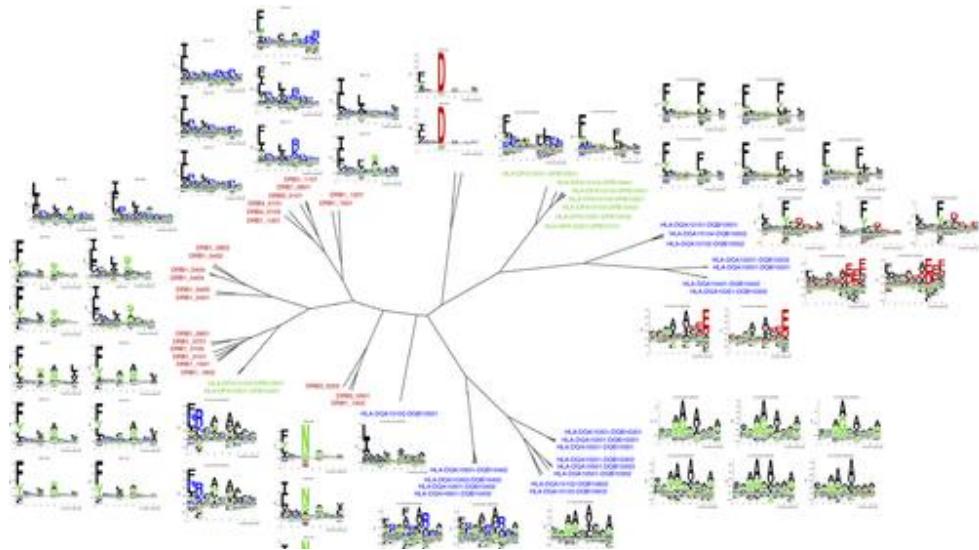


Sturniolo et al., Nat. Biotech. 1999

=> different side-chain preferences

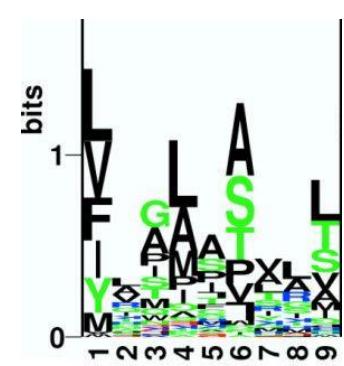
Nielsen et al.,
BMC Bioinformatics 2007

=> predictors for representative alleles



Jensen et al., *J. Immunology* 2018

DRB1*01:01



Function: evolutionary

Target

SAK_STAAU/71-87

1-body I, L, V

Relatives

Q54685_STRPY/58-73

- K H P D Y I I T K R D S S I V T

Q7X0T5_STRPY/58-73

- E H P D Y I I T K R D S S I V T

Q7X0Y3_STRPY/56-71

- A D L L K A I Q E R L I A N V H

Q53284_STREQ/56-71

- A D L L K A I Q E Q L I A N V H

STRP_STREQ/56-71

- A D L L K A I Q E Q L I A N V H

Q9RIL4_STRUB/56-68

- L Q L D Y S Y E L V D - - - F A

Q9ZFE3_STREQ/53-65

- T F E N K K L K A V D - - - F A

A2I7K2_STAAU/58-74

T A Y K E F R V V E L D P S A K I

Q2FFF5_STAA3/58-74

T A Y K E F R V V E L D P S A K I

Q70YZ7_STRDY/58-74

V T V D K Y R I V K I P E D A Q I

Q9ZFE2_STREQ/58-73

- S M E N F K V I D L H E V K L V

A0FJ59_9STRE/49-64

- R D K A K L L Y N N L D A F G I

Q7X0X4_STREQ/58-73

- T H P G Y T I Y E R D S S I V T

Q7X0T4_STRPY/58-73

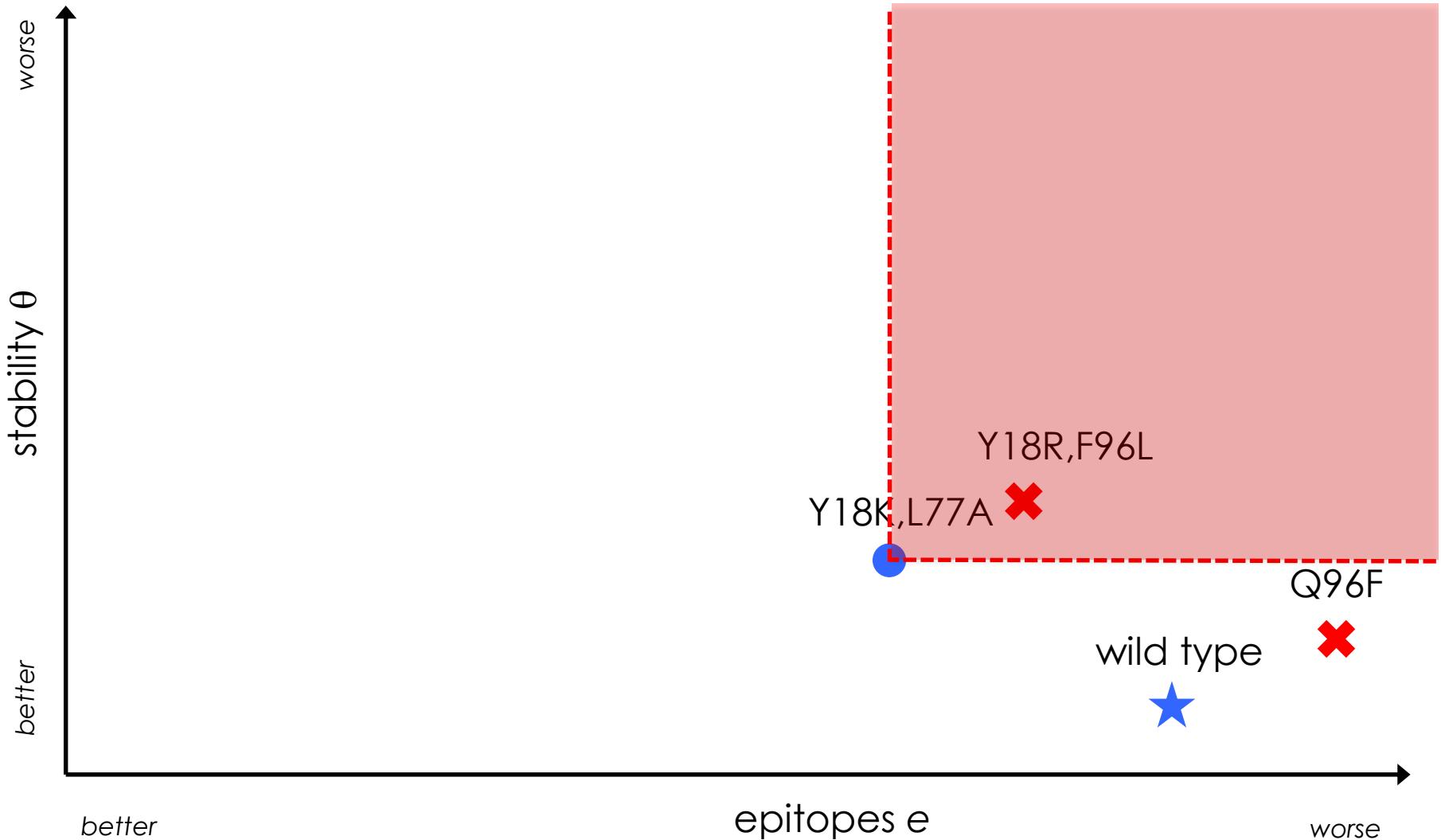
- S H P D Y T I Y E R D S S I V T

...

2-body YF, HY, DK

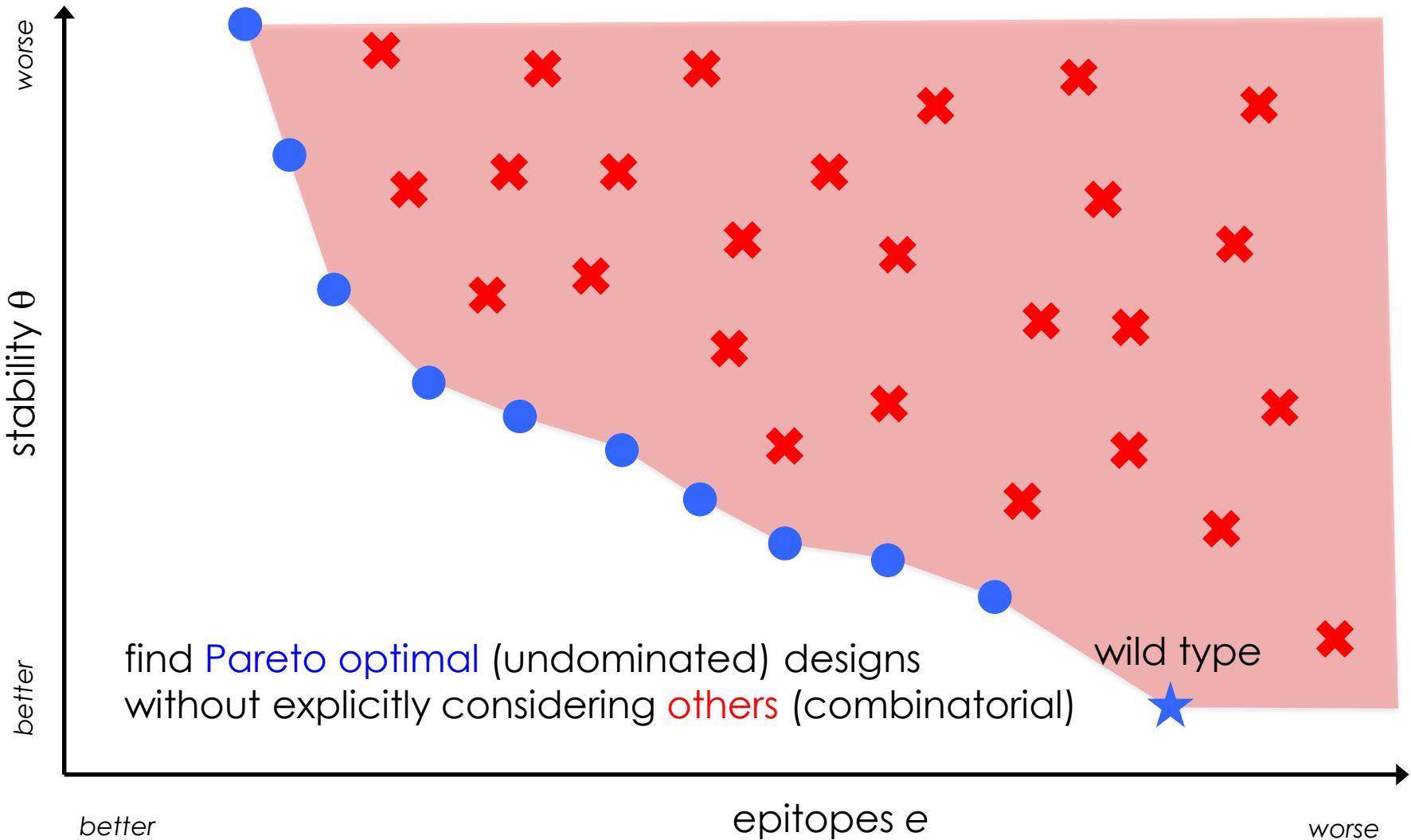
Trade-offs: EpiSweep

[He et al., *Proteins*, 2011]
[Parker et al., *J Comp Biol*, 2013]



Trade-offs: EpiSweep

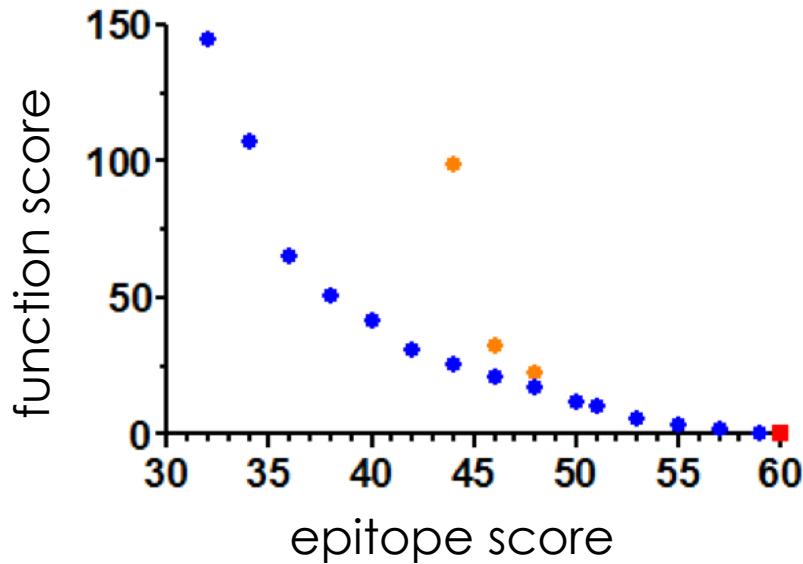
[He et al., *Proteins*, 2011]
[Parker et al., *J Comp Biol*, 2013]



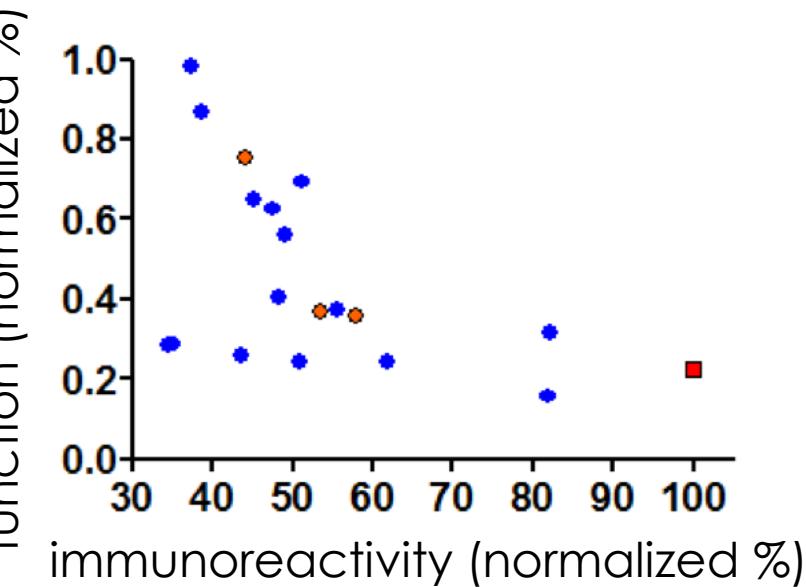
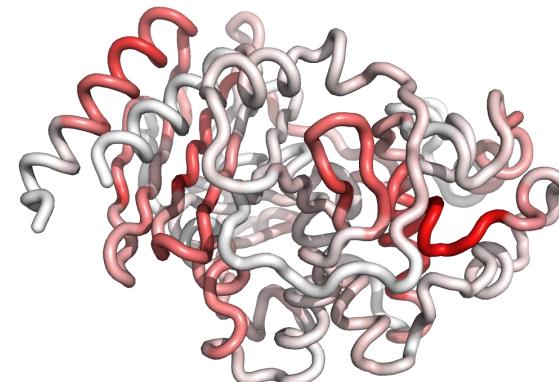
Trade-offs in theory vs. practice

[Salvat et al., PLOS Comp Biol, 2015]

p99 beta lactamase:
a component of ADEPT
anti-cancer therapy

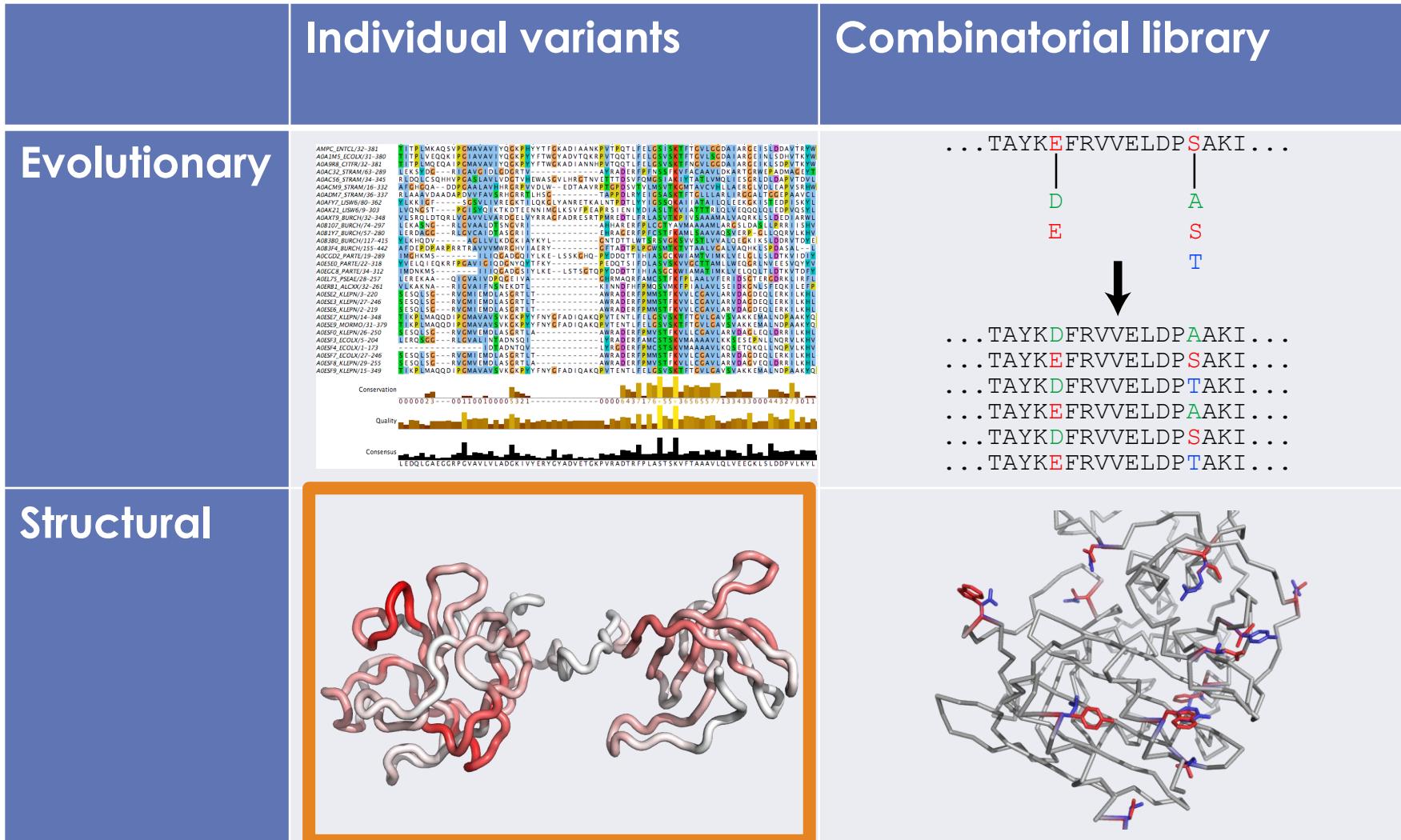


predicted/designed



experimental

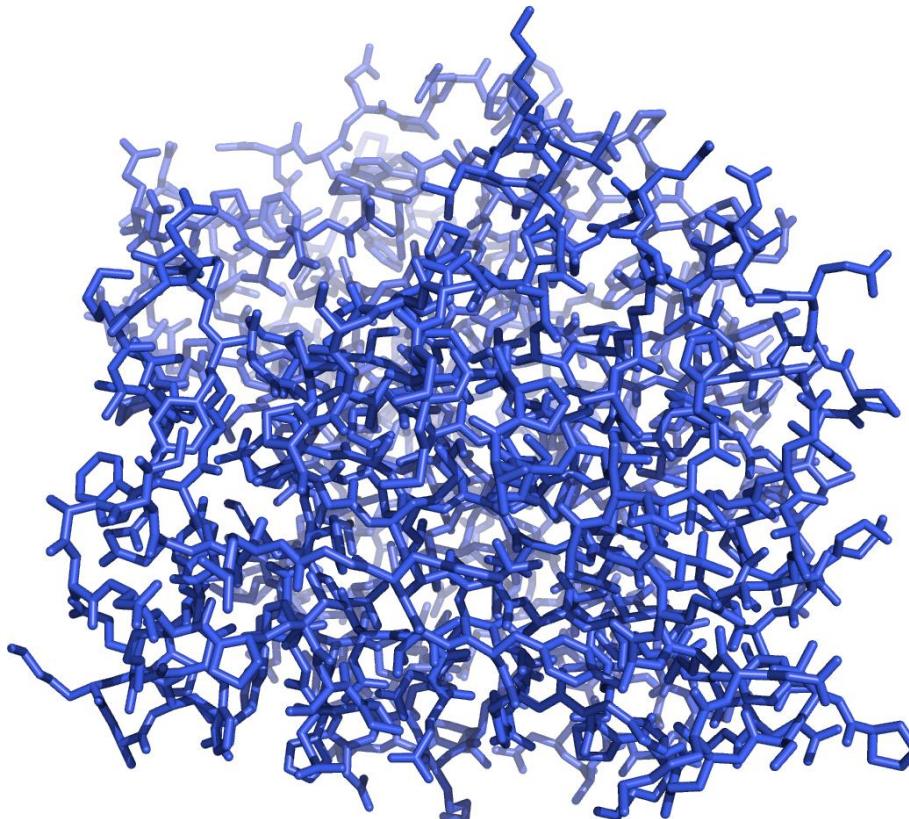
Landscape of approaches



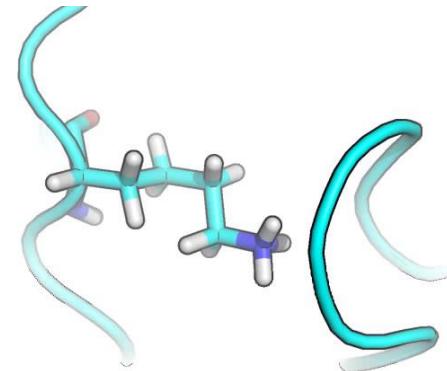
Function: side-chain packing

Given primary sequence; take backbone as fixed (target)

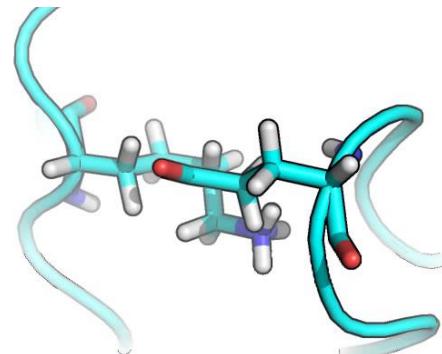
Select side-chain conformations to minimize energy



one-body
internal + vs. backbone



two-body
vs. each other



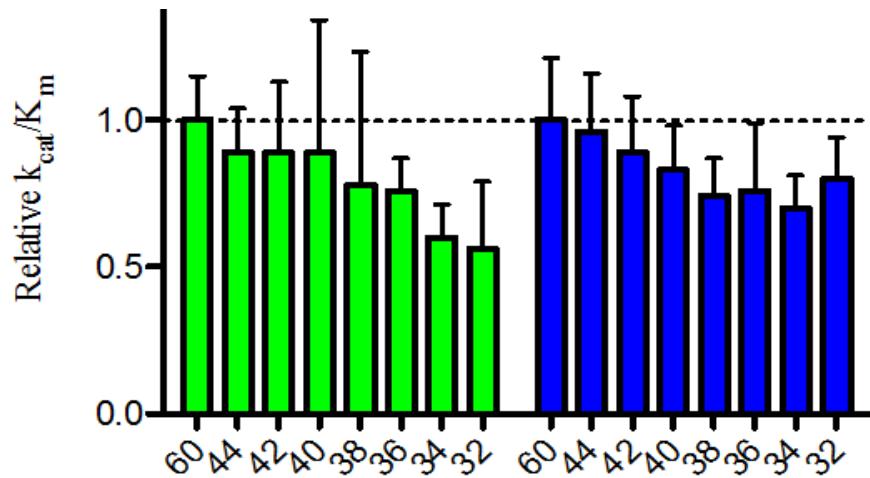
Function: β lactamase

[Salvat et al., Biotechnol Bioeng 2015]

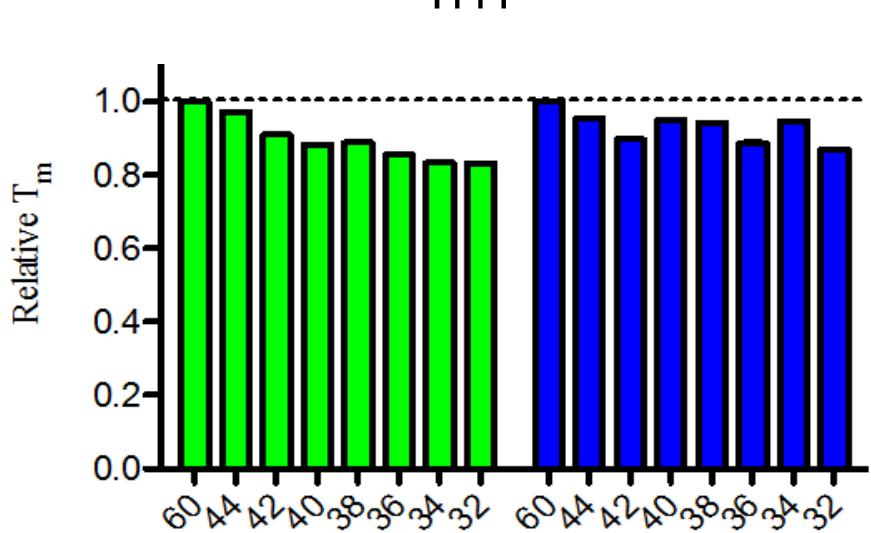
8-mutation variants

Evolutionary and structural function scores
Matched epitope scores

kcat/Km



Tm

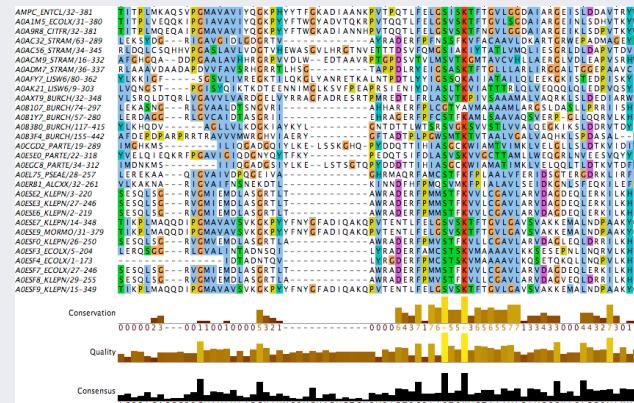


decreasing epitope content

Landscape of approaches

Evolutionary

Individual variants

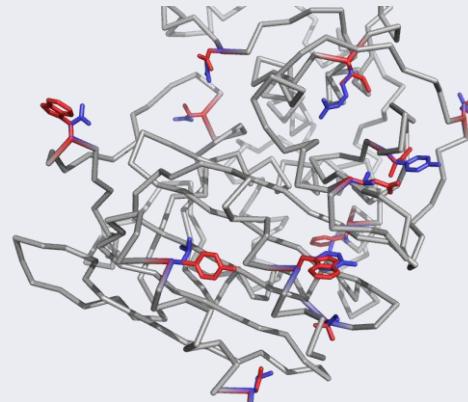
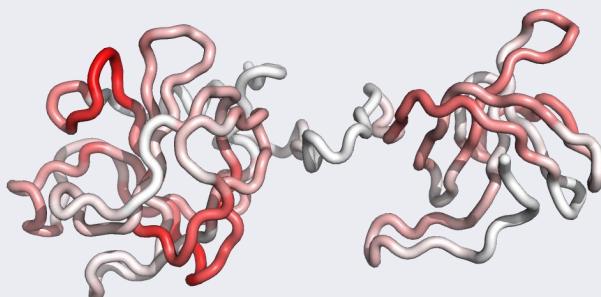


Combinatorial library

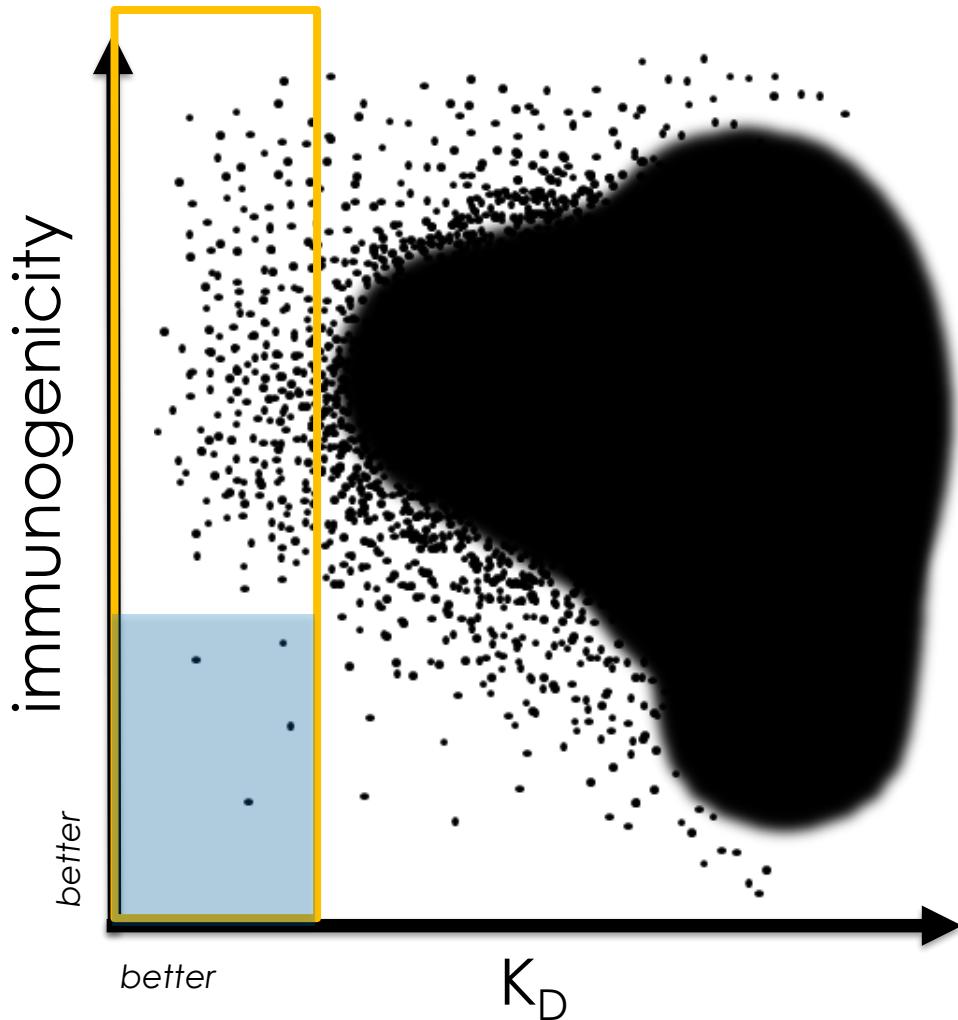
... TAYKE_EFRVVELDPSAKI ...
 ↓
 D A
 E S
 T

... TAYKD_FRVVELDPAAKI ...
 ... TAYKE_EFRVVELDPSAKI ...
 ... TAYKD_FRVVELDP_TAKI ...
 ... TAYKE_EFRVVELDPA_AKI ...
 ... TAYKD_FRVVELDPSAKI ...
 ... TAYKE_EFRVVELDPTAKI ...

Structural

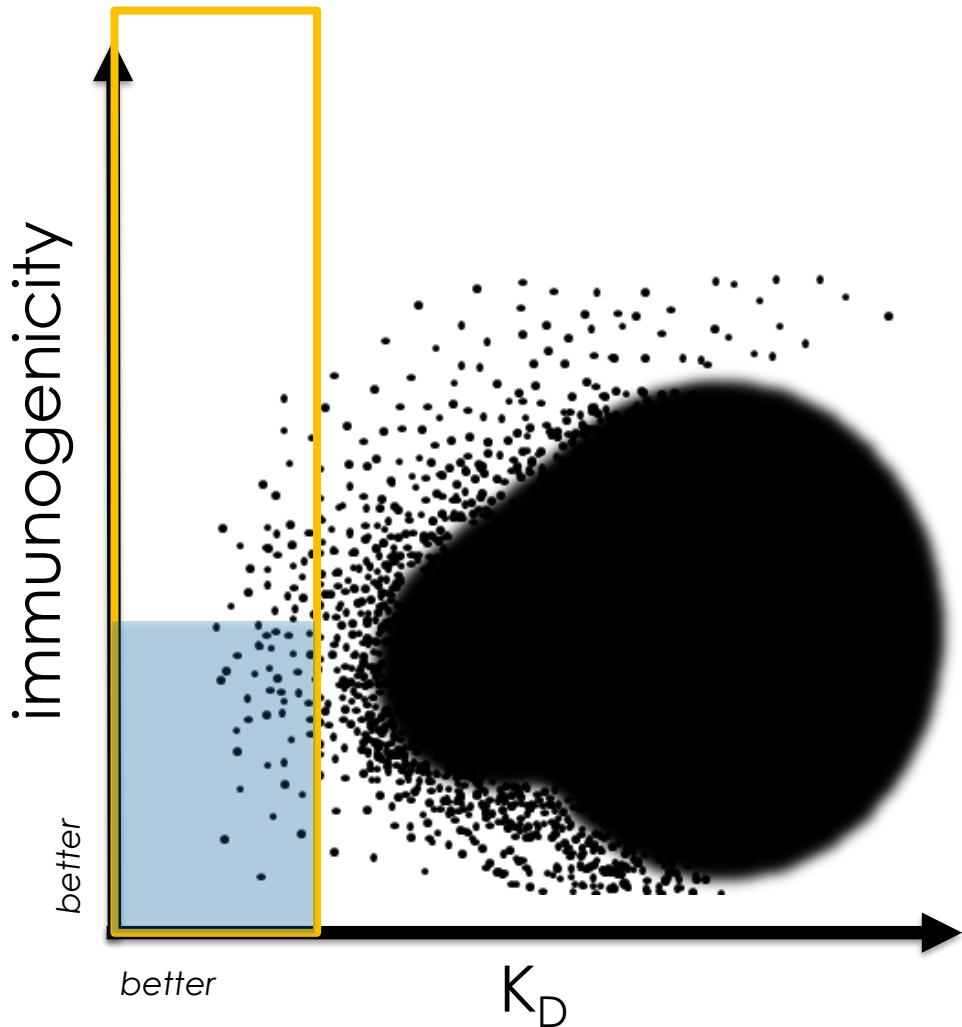


Library-based deimmunization



1. Naïve library
2. High-throughput functional screen
=> many high function clones
3. Detailed immunogenicity analysis
=> few low immunogenicity clones

Libraries optimized for deimmunization

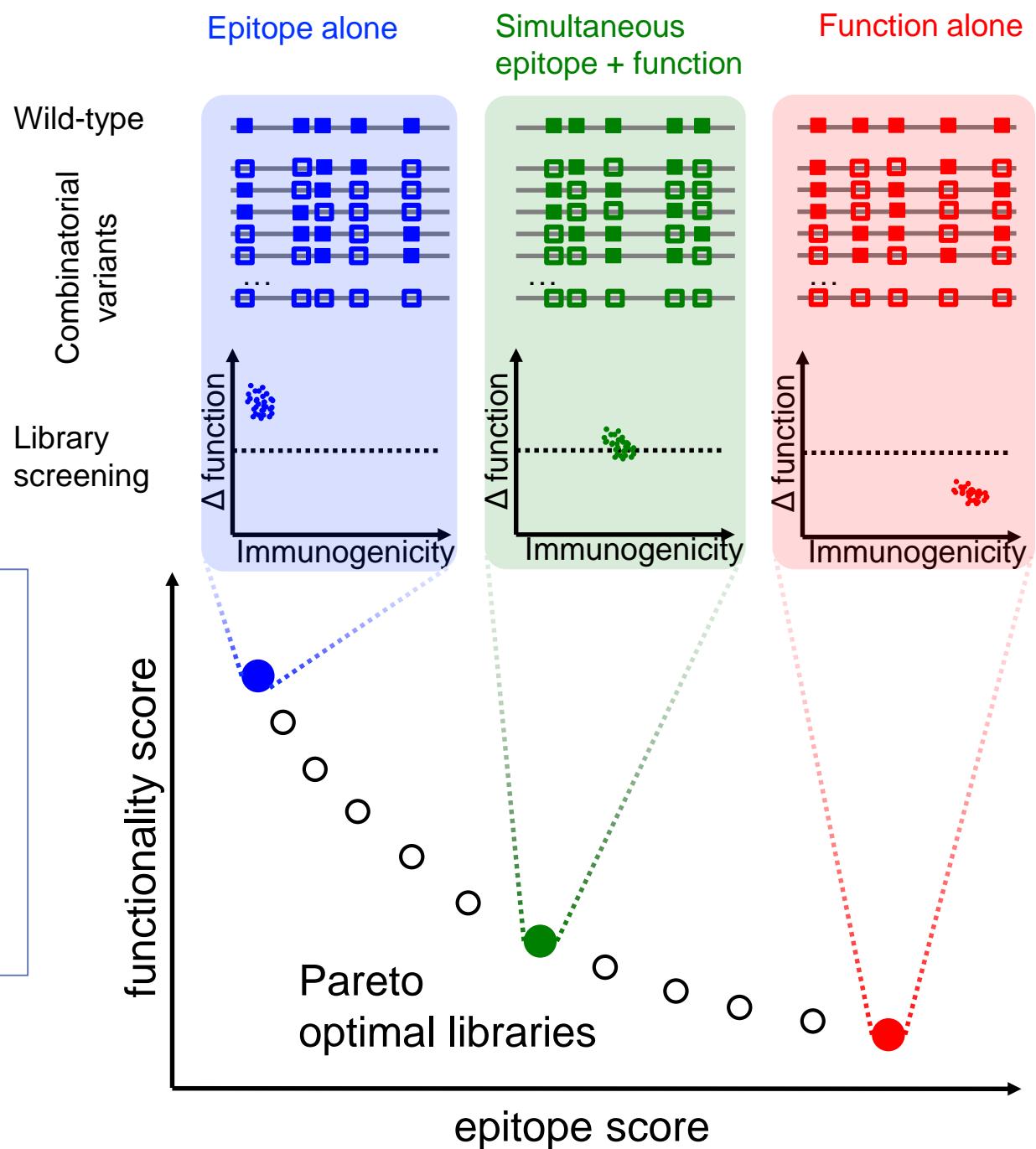


1. Design library to be enriched in low-immunogenicity variants
2. Naïve library
3. High-throughput functional screen
 - => many high function clones
 - => most also low immunogenicity

Library trade-offs

[Salvat et al.. PNAS, 2017]

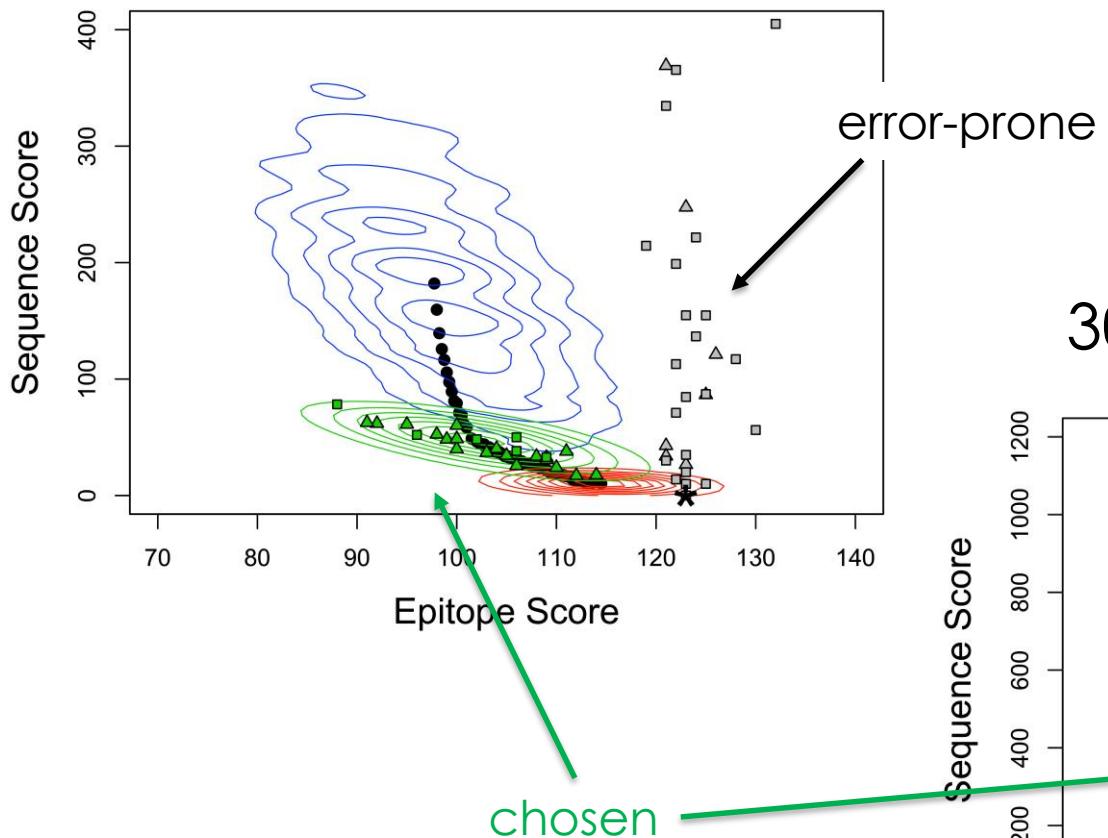
=> design for balance, enrichment of functionally deimmunized clones



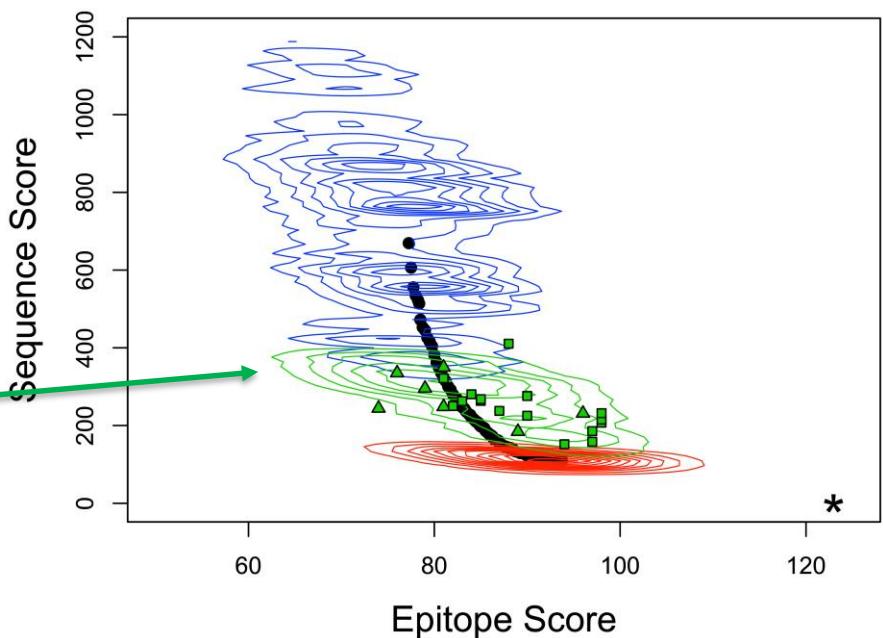
Application: β -lactamase

[Salvat et al.. PNAS, 2017]

10-site libraries



30-site libraries

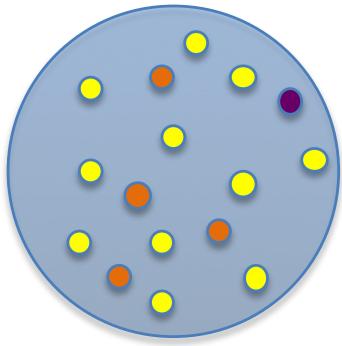


Libraries enriched in high-function variants

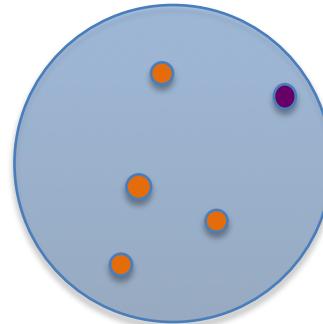
[Salvat et al.. PNAS, 2017]

β lactamase => growth selection based on cefazolin

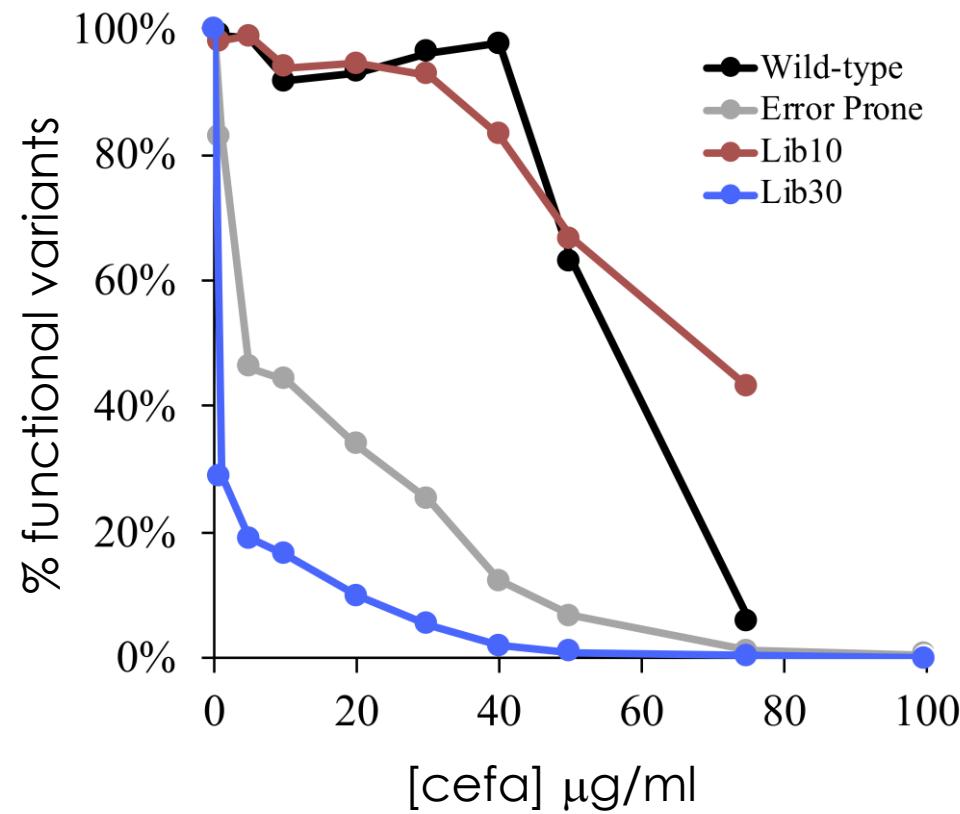
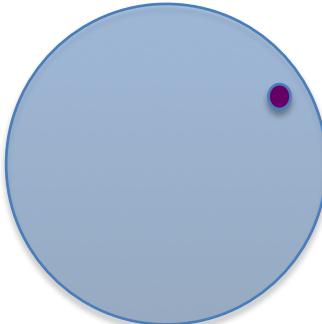
[cefa] = 0 $\mu\text{g/ml}$



[cefa] = 20 $\mu\text{g/ml}$

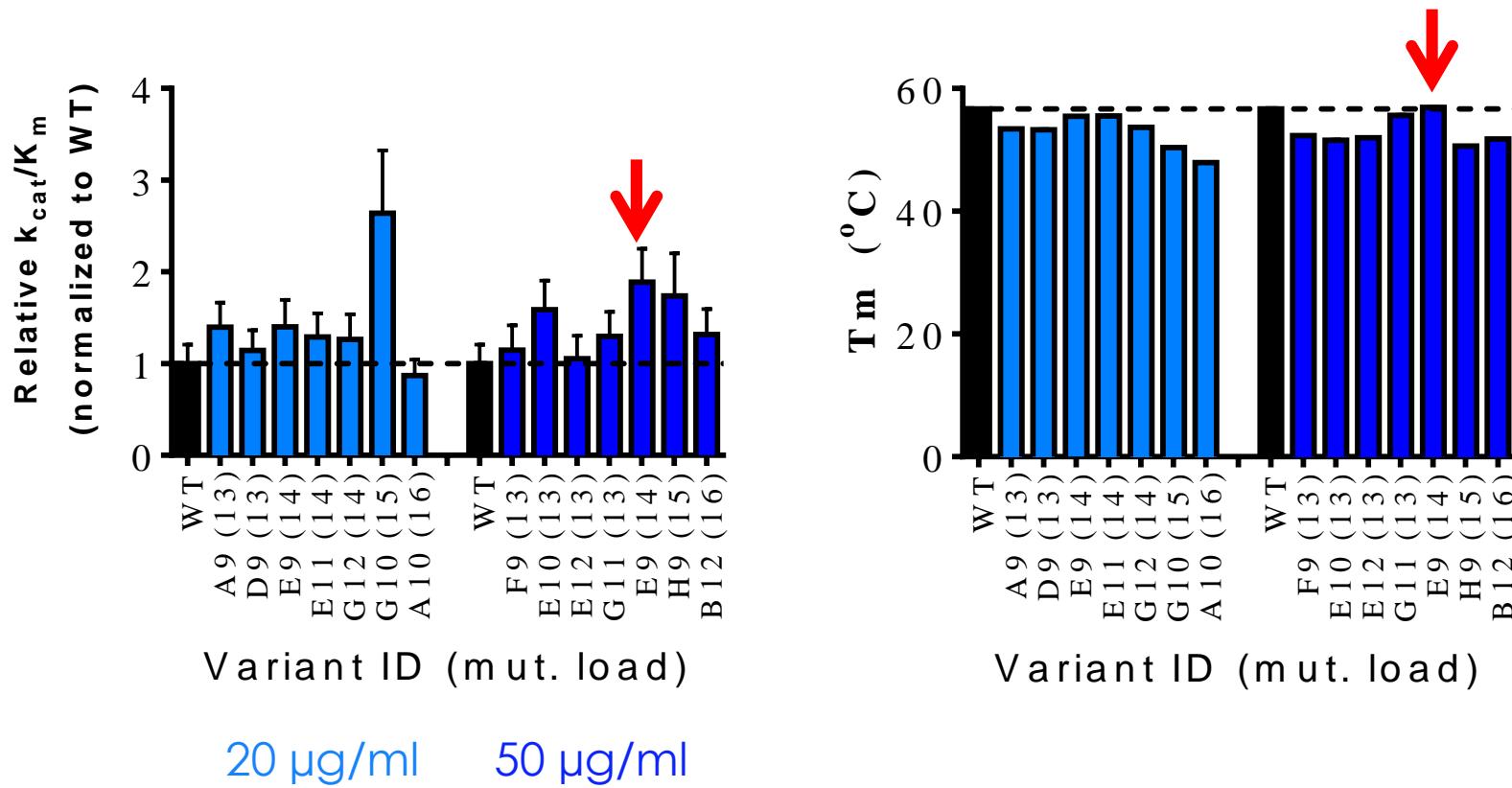


[cefa] = 75 $\mu\text{g/ml}$



Highly engineered clones -- high activity & stability

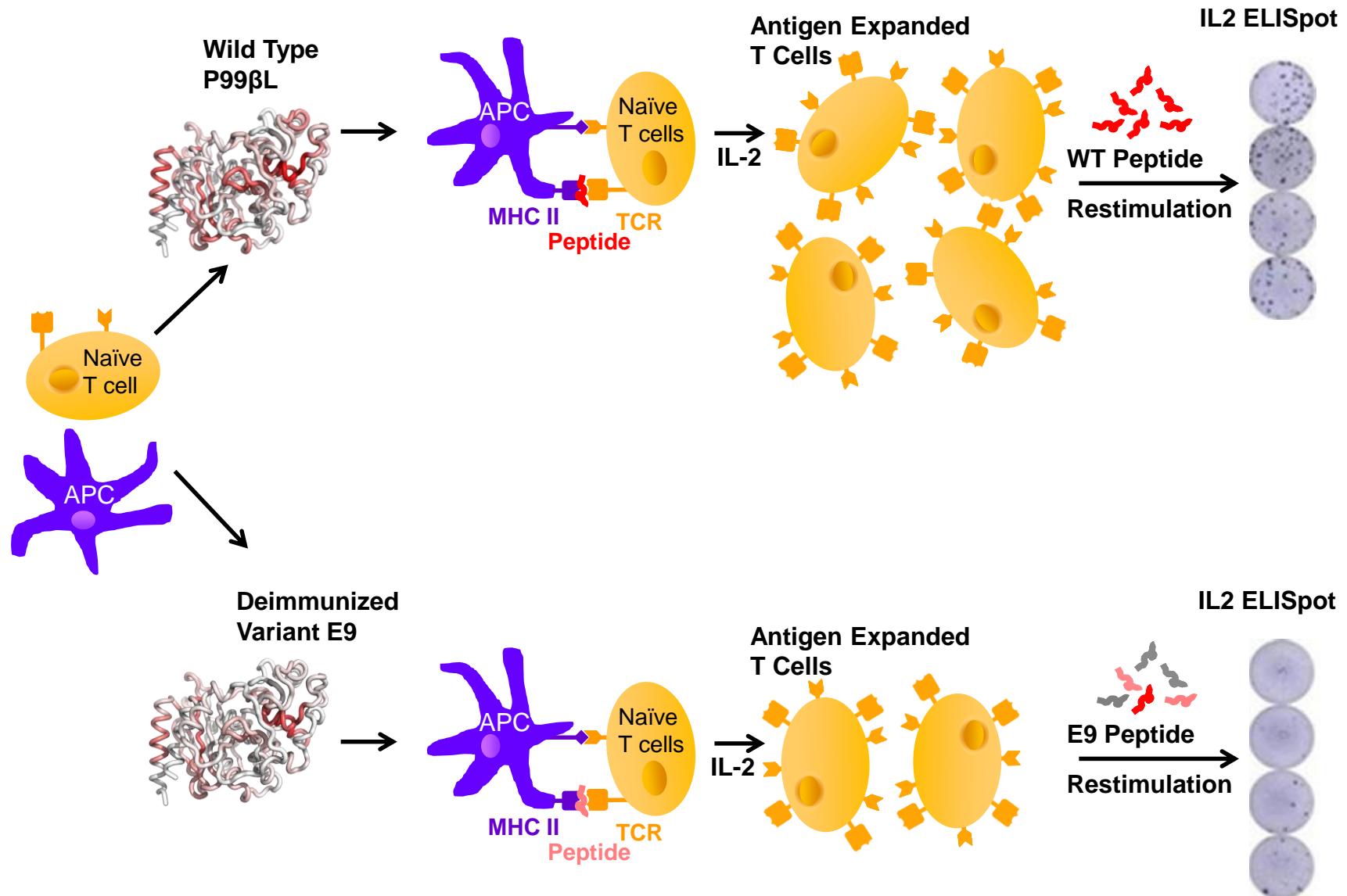
[Salvat et al.. PNAS, 2017]



Enzyme	# Mutations	K _m (µM)	k _{cat} (s ⁻¹)	k _{cat} /K _m (s ⁻¹ µM ⁻¹)	T _m (°C)
Wild Type	N/A	106 ± 7	200 ± 10	1.9 ± 0.2	56.66 ± 0.03
30:50:E9	14	90 ± 5	320 ± 10	3.6 ± 0.3	56.92 ± 0.06

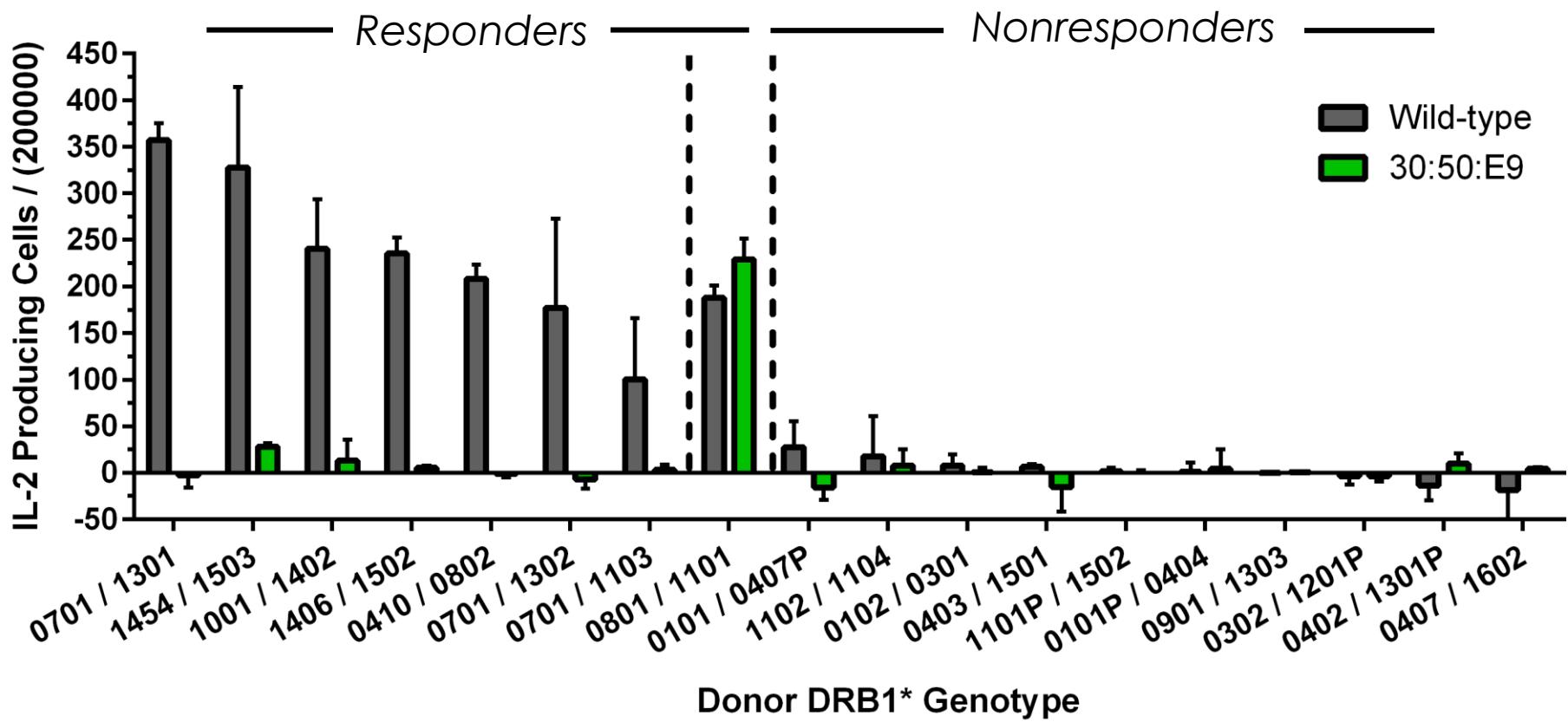


PMBC-based immunogenicity



Evades immune recognition

[Salvat et al.. PNAS, 2017]

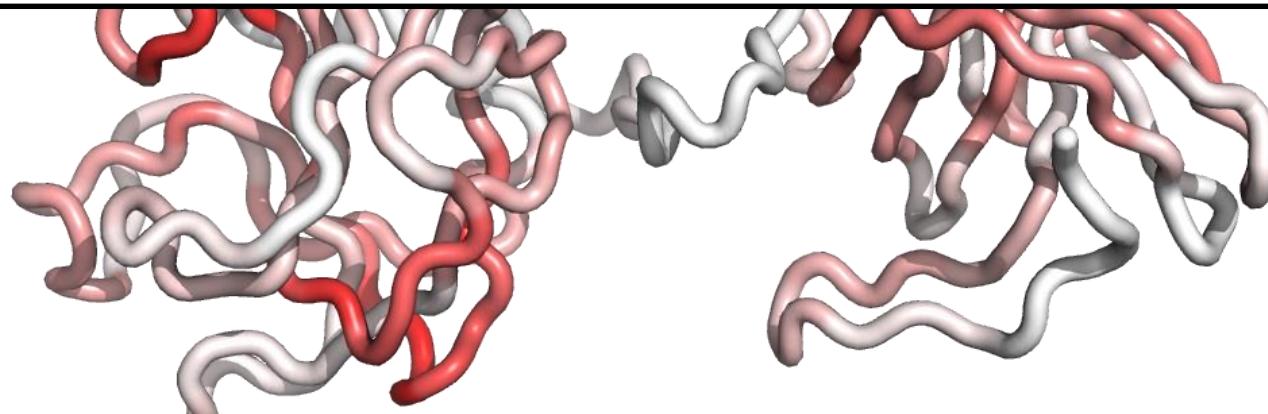


Lysostaphin

anti-staph treatment (incl. MRSA)

- + novel, potent, specific, biodegradable, renewable, less susceptible to resistance, ...
- known to be immunogenic

AATHEHSAQWLNNYKKGYGYGPYPLGINNMMHYGVDFFMNIGTPVKAISSGKIVEAGWSNYG
GGNQIGLIENDGVHRQWYMHL SKYNVKVDYVKAGQIIGWSGSTGY STAPHI HFQRMVNSFS
NSTAQDPM PFLKSAGYGKAGGTVTPTPNTGWKTNKYGTLYKSESASFTPNTDIITRTTGPFR
SMPQSGVLKAGQTIH YDEV MKQDG HVWVG YTGN SGQRIYLPVRTWNKSTNTLGVLWGTIK

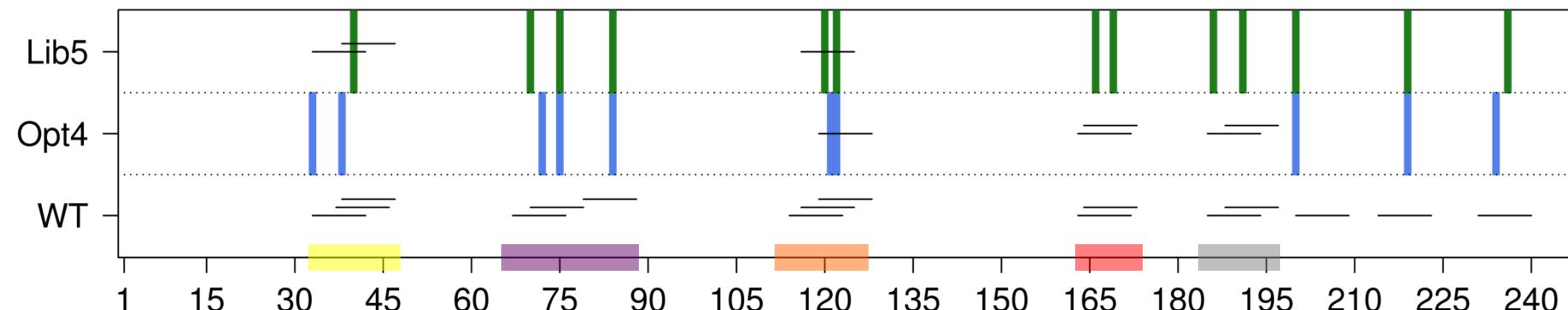


catalytic domain (endopeptidase)

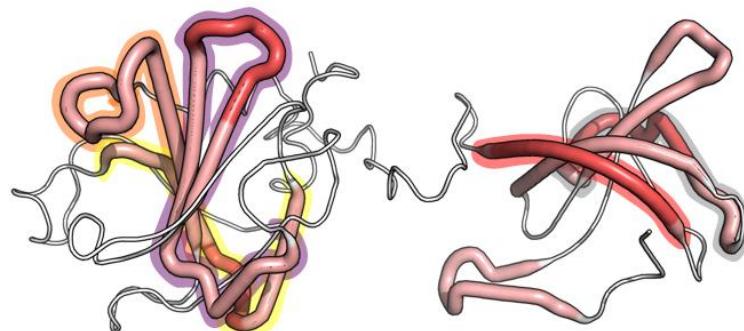
cell-wall binding domain (SH3b)

Variant summary

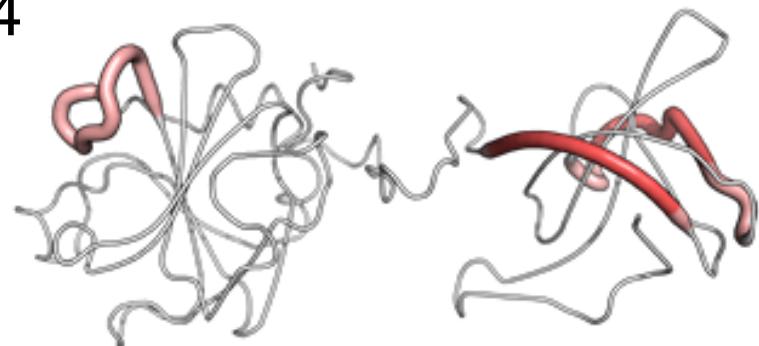
[Zhao et al.. *Chem. Biol.*, 2015]



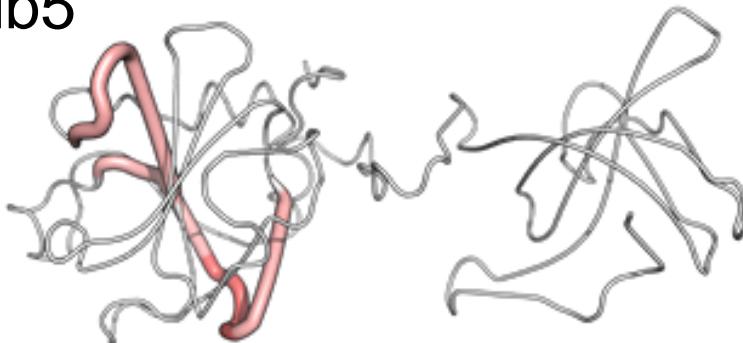
WT



Opt4



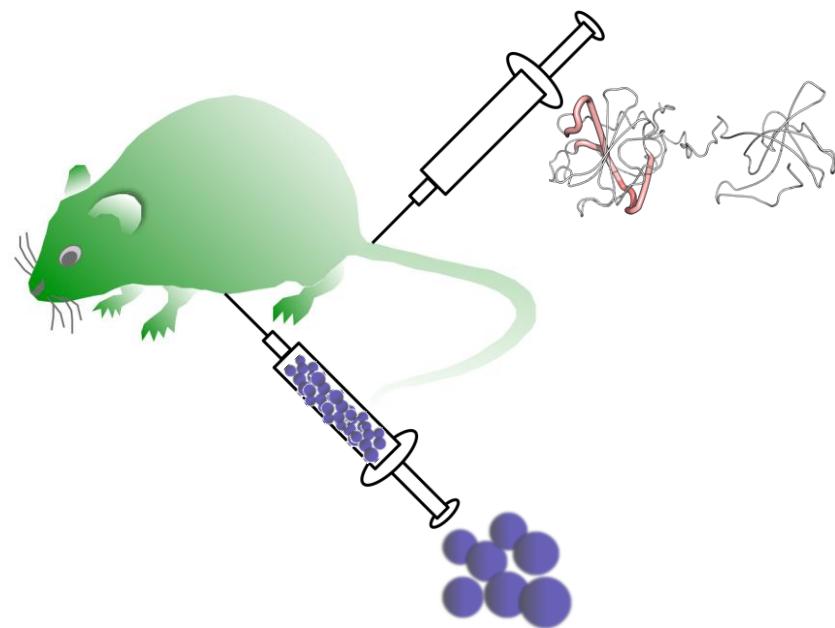
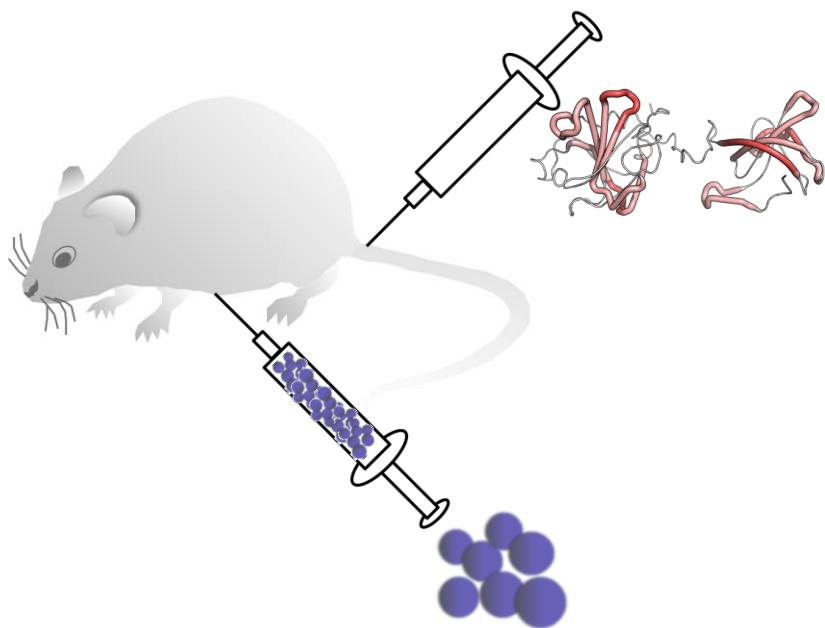
Lib5



In vivo immunogenicity & efficacy

DR4 transgenic mice (i.e., with human MHC)

Two arms: wild-type, Lib5



1. Immunized
2. Infected with MRSA
3. Treated according to arm

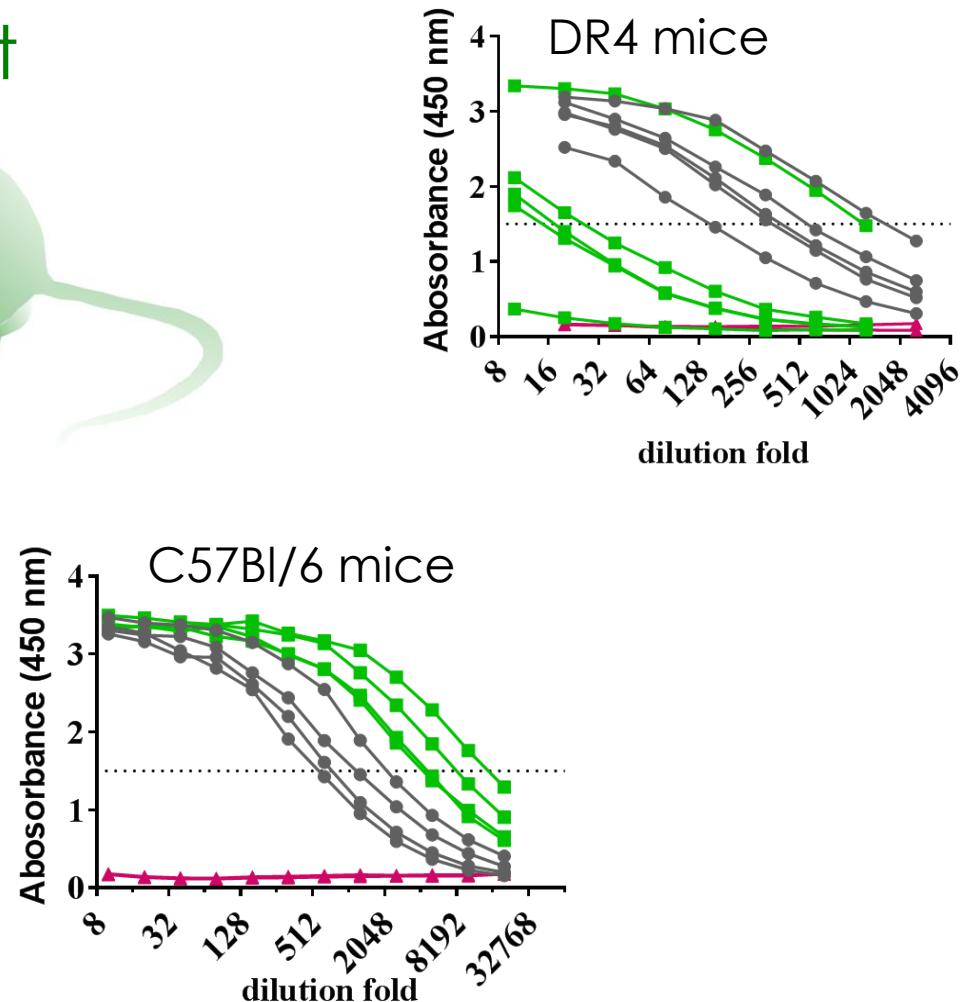
After 3x immunization

[Zhao et al.. *Chem. Biol.*, 2015]

Higher Ab titers in
wild-type arm vs. variant

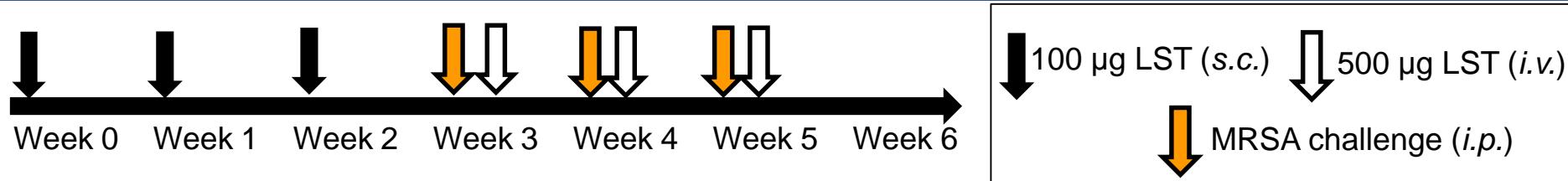


For targeted allele!



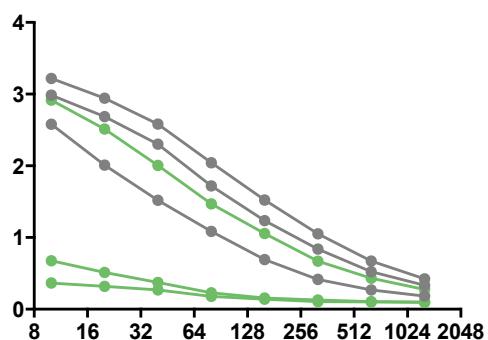
Infection & treatment

[Zhao et al.. Chem. Biol., 2015]



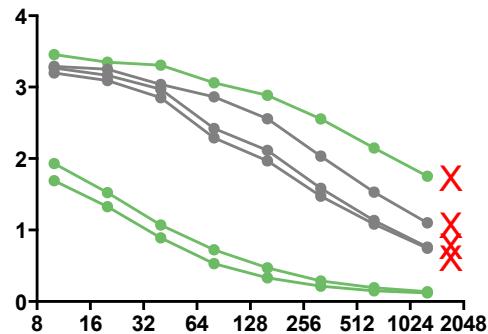
Week 3

All mice recued
from initial infection



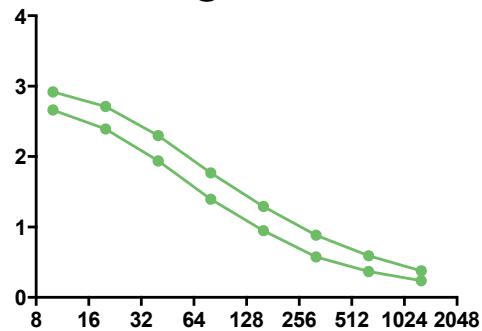
Week 4

Avg Ab titers increased
rapidly for wild-type,
and mice exhibiting
high titers succumbed
to MRSA challenge



Week 5

Variant mice maintained
low Ab titers and were
rescued from a third MRSA
challenge

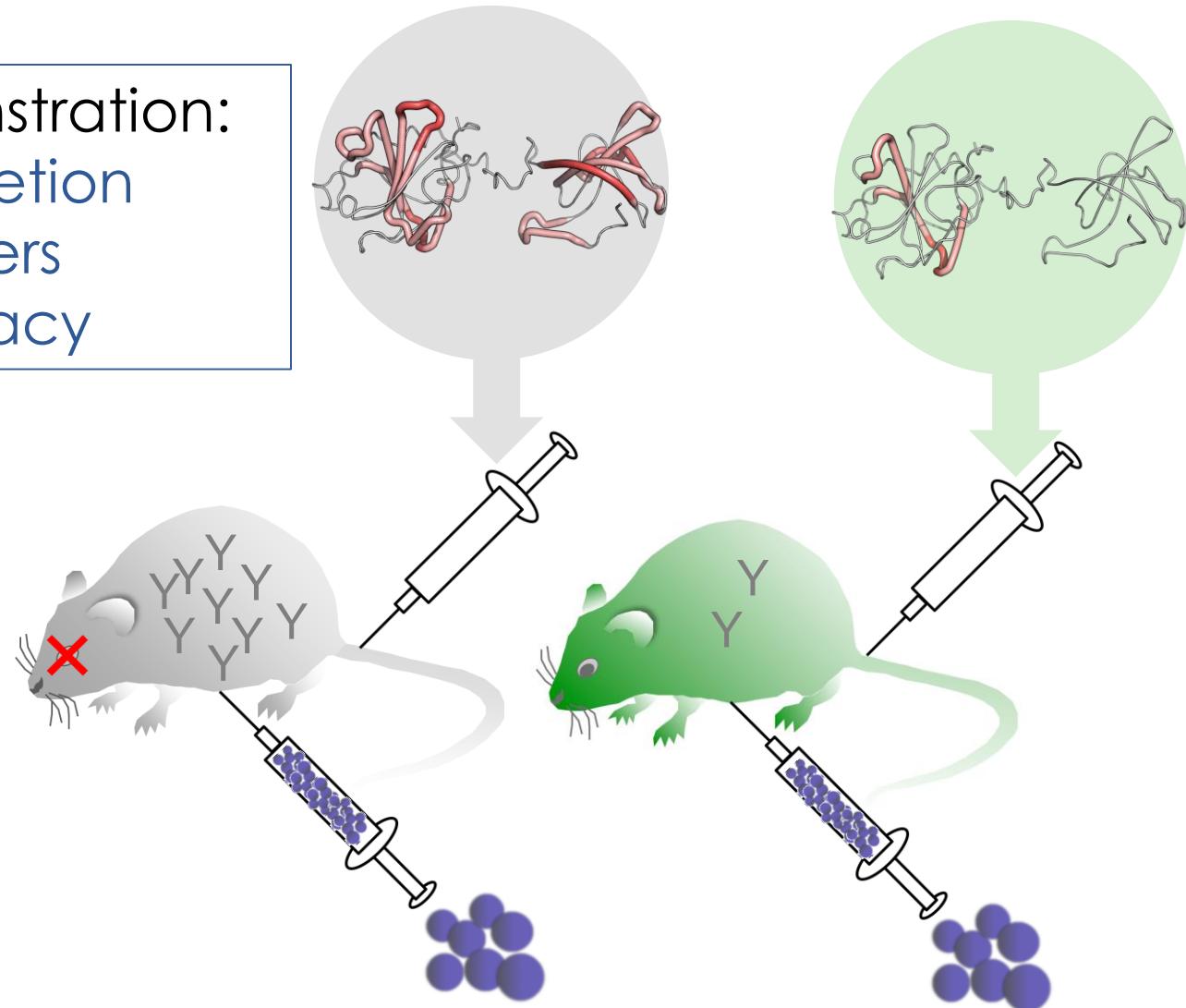


x: serum dilution
y: ELISA absorbance
for wild-type and variant

Epitope depletion summary

[Zhao et al.. Chem. Biol., 2015]

First direct demonstration:
T cell epitope deletion
⇒ reduced Ab titers
⇒ improved efficacy



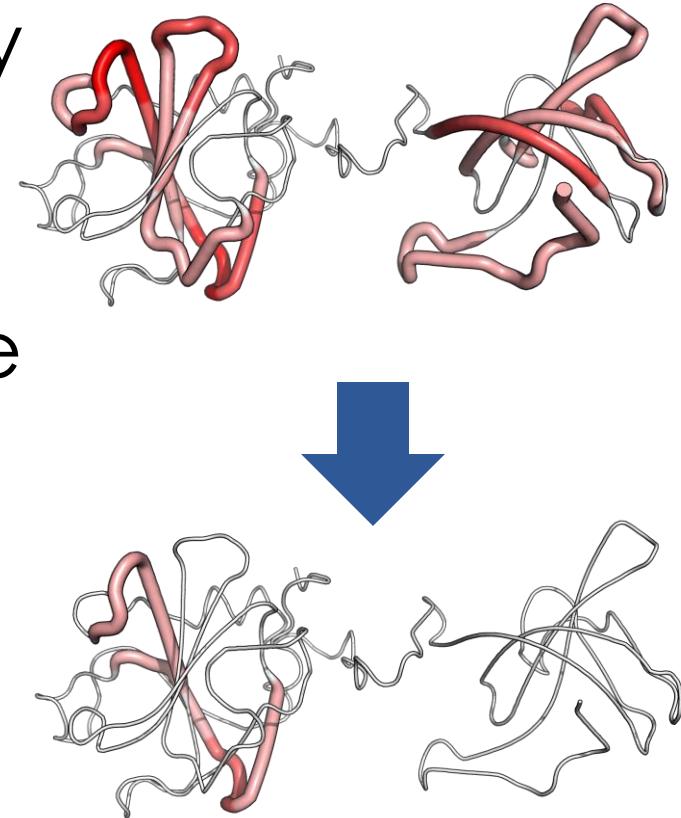
Conclusion

Goal: reduce immunogenicity while maintaining function

Methods: both objectives are predictable and designable

- sequence/structure
- individual/library

Results: reduced immunogenicity & *improved* efficacy



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