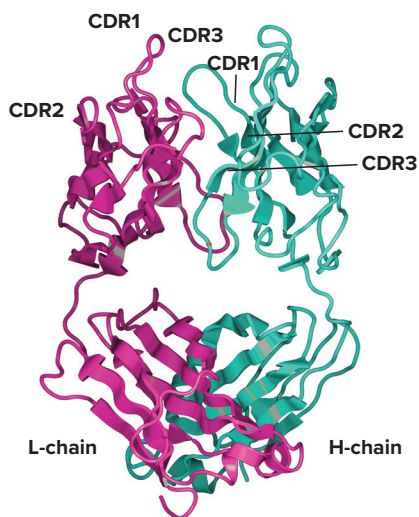


# Twist Antibody Optimization Platform

Quickly generate high-diversity, high quality molecules inspired by the human repertoire



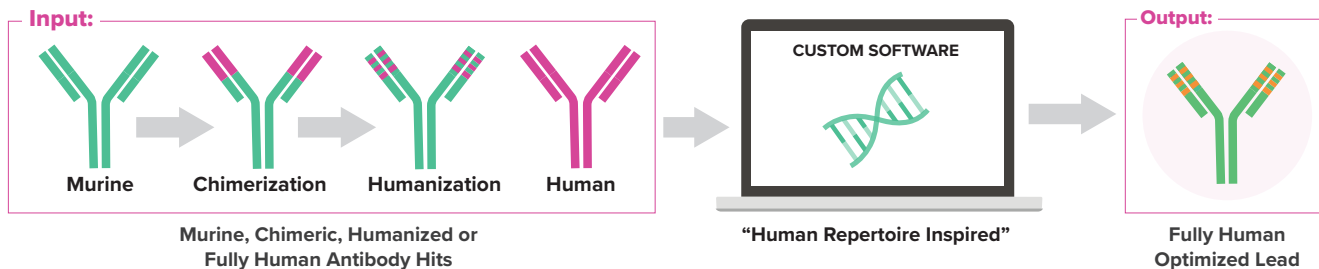
## Why TAO?

Use natural human antibody sequence data to create an optimization library that exactly matches the human repertoire

- Liabilities are removed, e.g. isomerization, cleavage, deamidation, glycosylation sites, liability dipeptide motifs
- Rational sampling from desired sequence space
- Accurate representation: motif sequences explicitly encoded in oligos

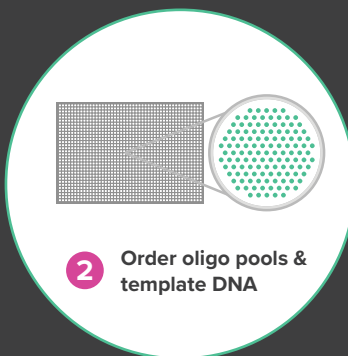
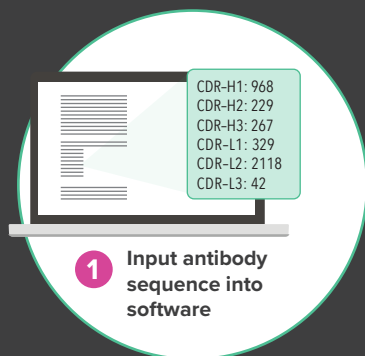
## Optimize for:

- Affinity (pM)
- Expression
- Solubility
- Processability
- Half-life
- Immunogenicity
- Druggability

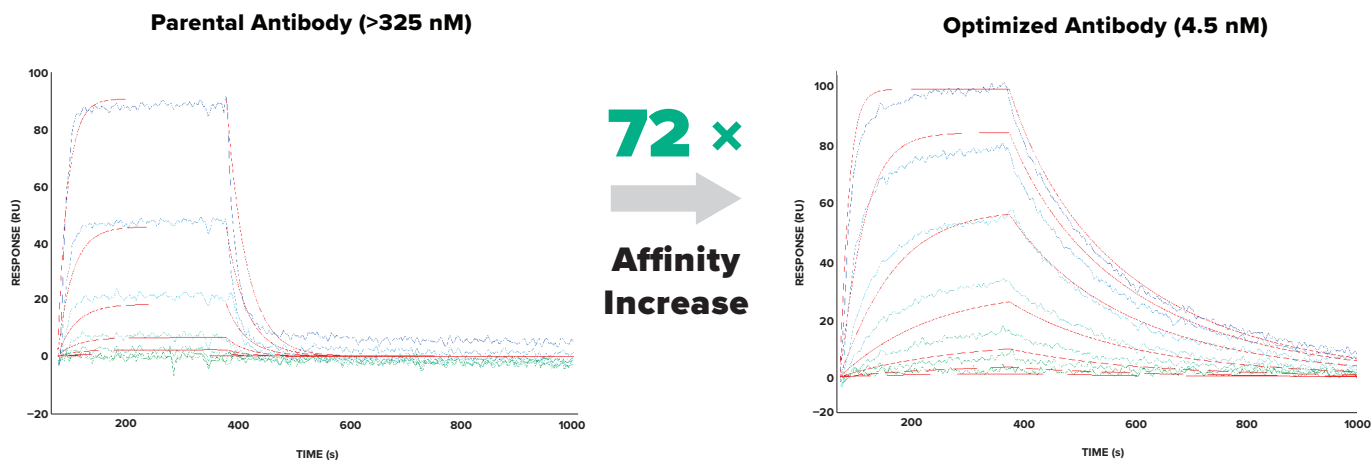


## How it Works

4 MONTHS



# Using Twist Antibody Optimization, PD-1 Inhibitors Have Higher Affinity and Potency



## TAO Optimized IgGs Block PD-1/PD-L1 Interaction

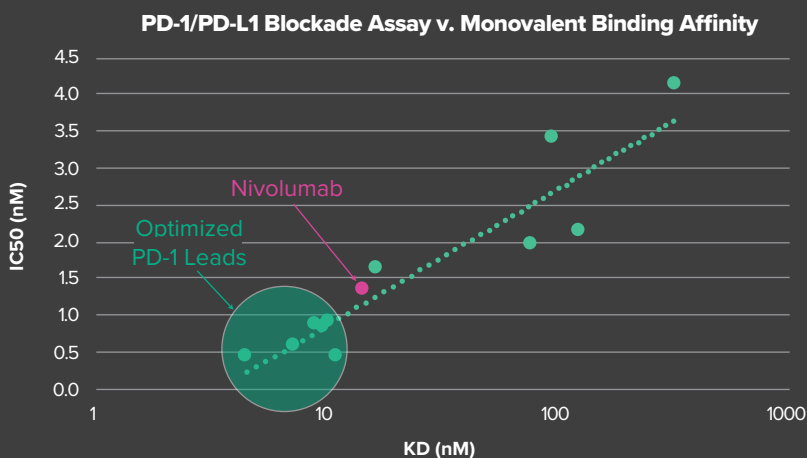
Binding Affinity (IgG)

Clone	SPR KD (nM)	IC50 (nM)	Bmax (RU)
PD1_TAO1	4.5	0.434	693
PD1_TAO15	7.3	0.562	634
PD1_TAO91	9.2	0.868	664
PD1_TAO2	9.8	0.848	661
PD1_TAO7	10.5	0.896	642
PD1_TAO75	11.2	0.418	614
Nivolumab	14.5	1.345	628
PD1_TAO60	16.5	1.614	776
PD1_TAO8	78.1	1.968	436
PD1_TAO58	96.7	3.384	446
PD1_TAO80	125	2.129	450
Parental	325	4.122	449

- After Twist Antibody Optimization:
  - Binding affinity went up 72×
  - Function increased by 9.5×
  - **Six antibodies identified with higher binding affinity and function than nivolumab**

Addition of anti-PD1 antibody blocks the PD-1/PD-L1 interaction, releases inhibitory signal and results in TCR activation and NFAT-RE-mediated luminescence (RU)

### Multiple Optimized Leads



**Tell Us What Twist Biopharma Can Do For You**

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