Twist Ancestral scFv Library

Build on previous expertly built antibody discoveries

The Twist Ancestral scFv Library is a new synthetic antibody library developed using trends observed in a curated, yet broad, set of therapeutic and diagnostic antibodies. By capturing the diversity observed in examined antibody sequences and mimicking the human antibody repertoire, this library offers higher quality sequences than naïve libraries to help you identify better hits against any target.

KEY BENEFITS

Produce robust scFv antibodies against any target

- Fully human antibody sequences
- Proven, highly manufacturable framework
- Developability liabilities removed
- 1 x 10^9 diversity

Capitalize on binding motifs from examined antibodies

- Binding sites informed by 22,426 existing antibodies
- Superior binding affinity and specificity

Synthetic library advantage

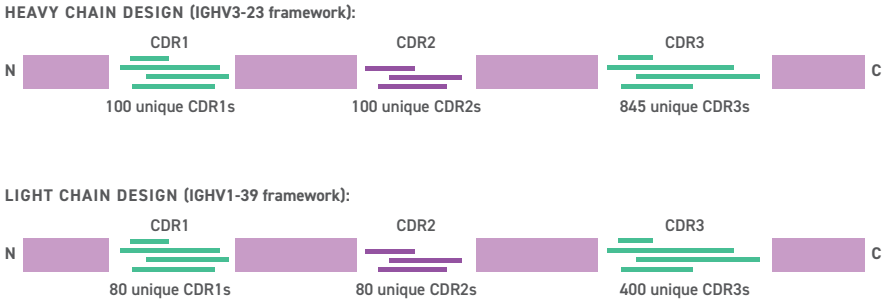
- Avoid immunization
- Focus on effective sequence space
- Screen multiple targets simultaneously
- Engineer and optimize antibodies with ease

APPLICATIONS

Therapeutic antibody discovery and development for any indication

Library Specifications

The Twist Ancestral scFv Library leverages information from 22,426 existing human, monkey, and alpaca antibodies. The library excludes potential development liability motifs while selecting for optimal complementarity-determining region (CDR) sequences and lengths that generate the diversity of this antibody set. The heavy chain library permutates CDR sequences from 100 unique CDR1s, 100 unique CDR2s, and 845 unique CDR3s within the human IGHV3-23 framework. The light chain library assembles diverse combinations of CDRs from 80 unique CDR1s, 80 unique CDR2s, and 400 unique CDR3s within the human IGKVK1-39 framework. When combined, the assembled heavy and light chain libraries yield a fully human scFv library with a diversity of 1 x 10^9.



Library Panning & Screening

Go from panning to functional assays in 10-12 weeks. The process starts with phage screening the diverse Twist Ancestral scFv Library against target antigens and ends with reformatting candidate antibody fragments to full-length IgG.

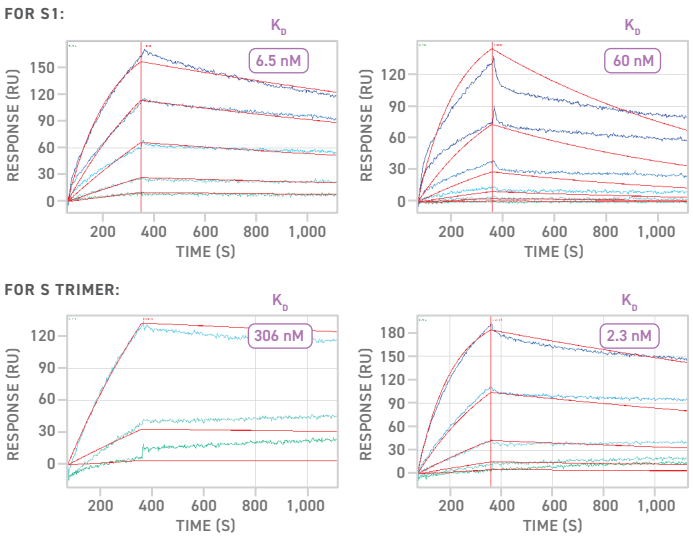
Cell-based or protein-based selections	NGS or Sanger clone sequencing	Reformatting to IgG and DNA scale-up	High-throughput IgG expression and purification	Binding and functional assays
3 WEEKS	2 WEEKS	4 WEEKS	2 WEEKS	1 WEEK

Proof of Concept Data

The Twist Ancestral scFv Library was successfully panned against SARS-CoV-2 Spike Protein S1. A large number of unique clones with diverse binding affinities were identified.

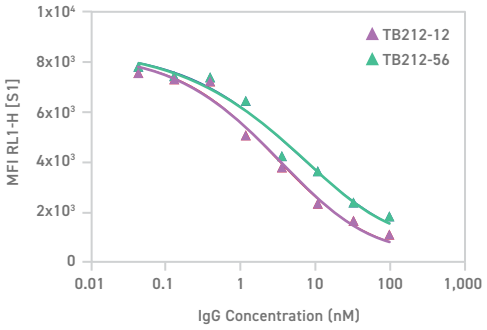
Uncover Anti-S1 Antibodies with High Binding Affinity

Kinetics with directly coupled anti-S1 antibodies via surface plasmon resonance identifies antibodies like TB212-12 and TB212-56 with high binding affinity for S1 and S trimer.



Potent Inhibition of VERO E6 Cells by FACS

Flow titration demonstrates that TB212-12 and TB212-56 show inhibition of S1 binding to ACE2-expressing VERO E6 cells.



ANTIBODY NAME	EC_{50} (nM)
TB212-12	3.07
TB212-56	6.22