

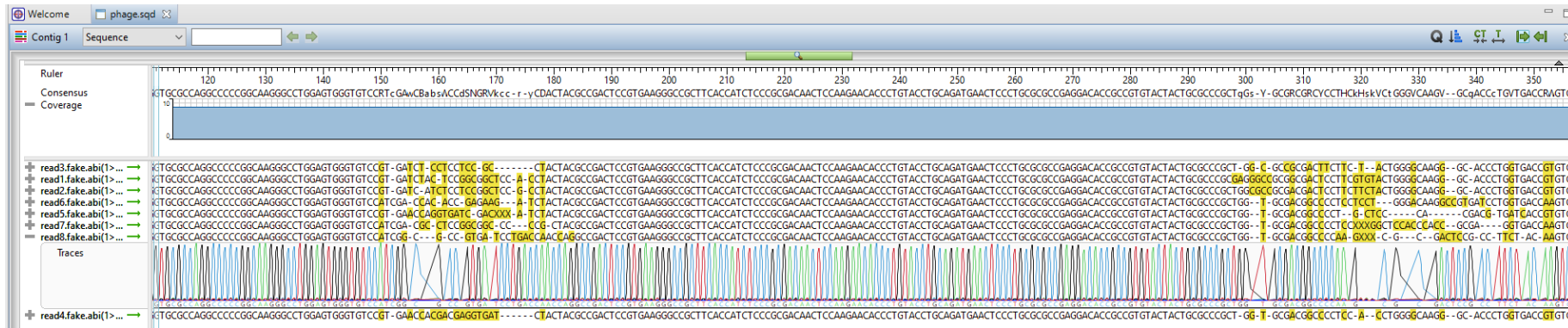
# Phage display assembly, translation and prediction workflow

DNASTAR Inc. 2019

**Date type:** Sanger Abi

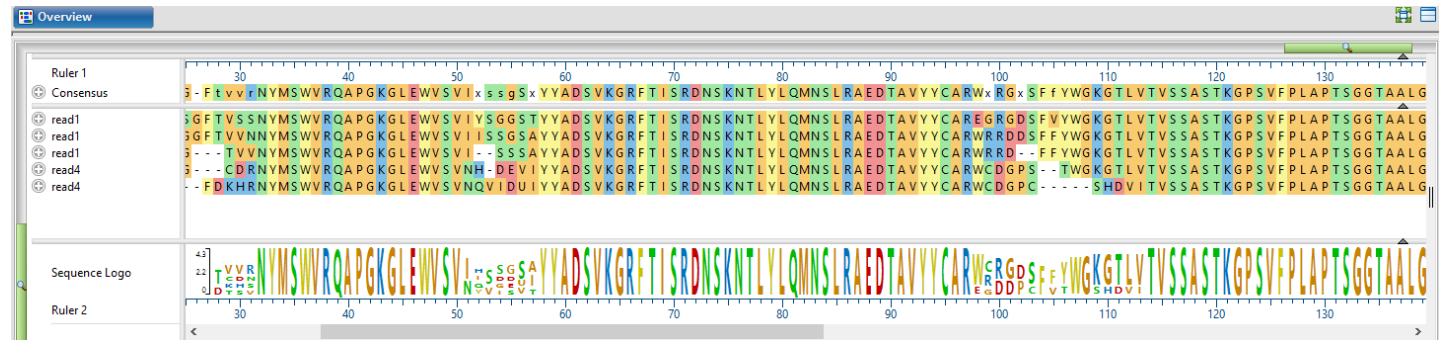
**Programs used:** SeqMan Pro, SeqNinja, MegAlign Pro, NovaFold Ab, NovaDock

1. Assemble of phage display abi reads using SeqMan Pro default deNovo assembly values
2. Use SeqMan Pro's editing mode to trim bases to start codon and stop codon for target antibody translation
3. Export trimmed reads in correct reading frame to SeqNinja for batch translation.



4. Open translated phage sequences in MegAlign Pro to create a phylogenetic tree and multiple/pairwise sequence alignment

5. Create homology model of sequence in NovaFold Antibody and or NovaFold (with custom redundant antibody library)



6. Simulate Docking of predicted antibody structures to target epitope using NovaDock's flexible docking simulation.