PHAGE DISPLAY WORKFLOW

A visual guide to antibody sequence assembly, translation, and structure prediction using DNASTAR Lasergene

DNASTAR
SOFTWARE FOR LIFE SCIENTISTS

ABOUT THE WORKFLOW

Phage display panning is a method used for the discovery of novel ligands against various targets of interest. Which of the tested plasmids in a 96-well ELISA assay have an antibody sequence that will bind well to the antigen of interest? The answer can be found quickly and easily using Lasergene's integrated phage display workflow.

Step 1
Trim and assemble sequence reads

Step 2
Trim assembly to target antibody sequence

Step 3
Translate DNA to amino acid sequence

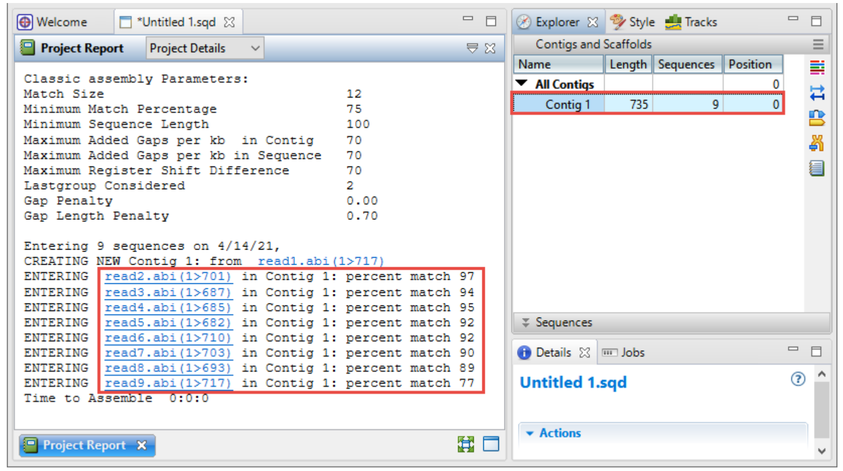
Step 4
Align sample sequences and create phylogeny

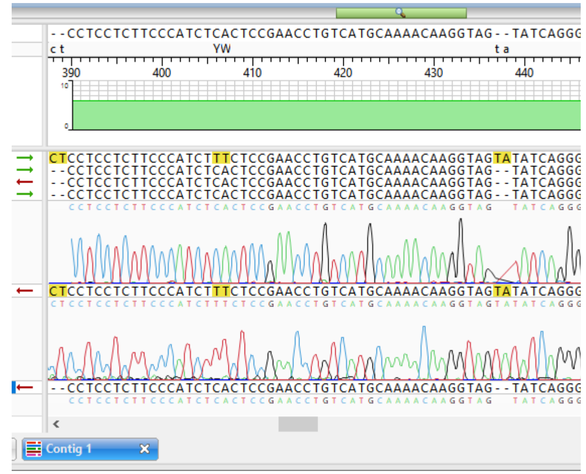
Step 5
Predict and visualize antibody structure

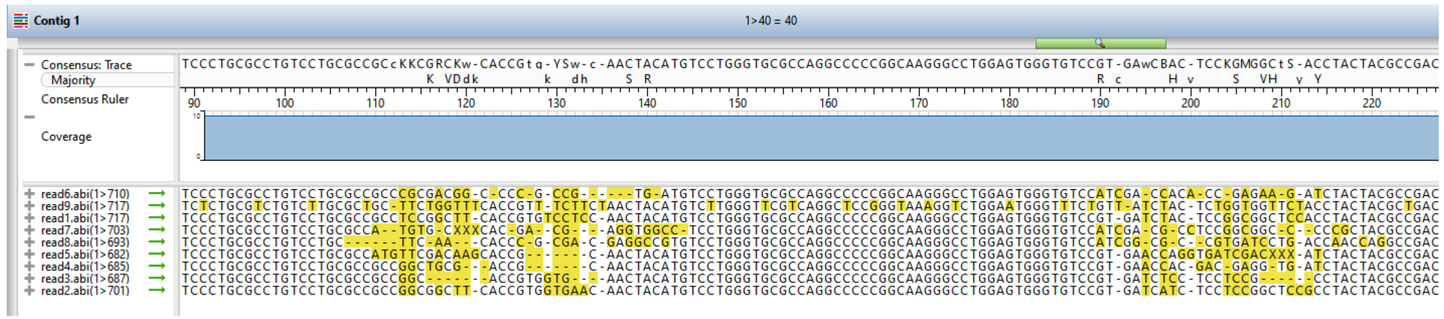
Step 6
Simulate antibody-antigen docking

STEP 1

Trim and assemble sequencing reads in SeqMan Ultra.



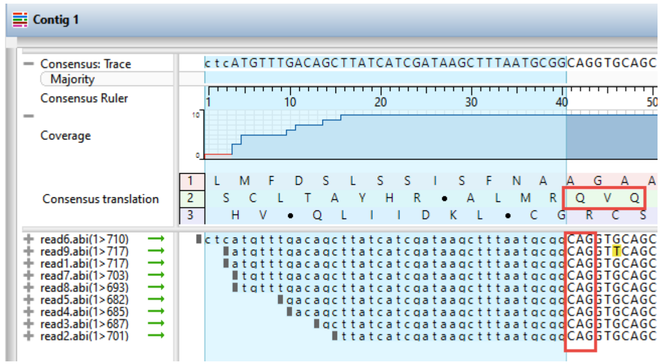




After sequencing. trim and assemble your Sanger or NGS sequencing data using SeqMan Ultra. Assembly usually takes just a few seconds to a few minutes. Here you can also view the completed assembly and the underlying trace and read quality data.

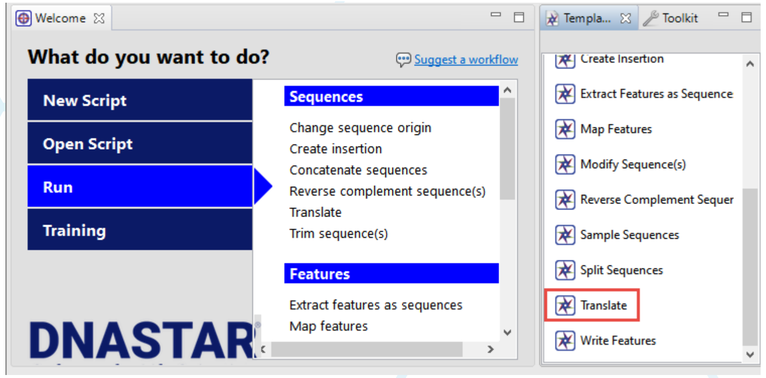
STEP 2

Trim assembly to target antibody translation sequence in the correct reading frame.



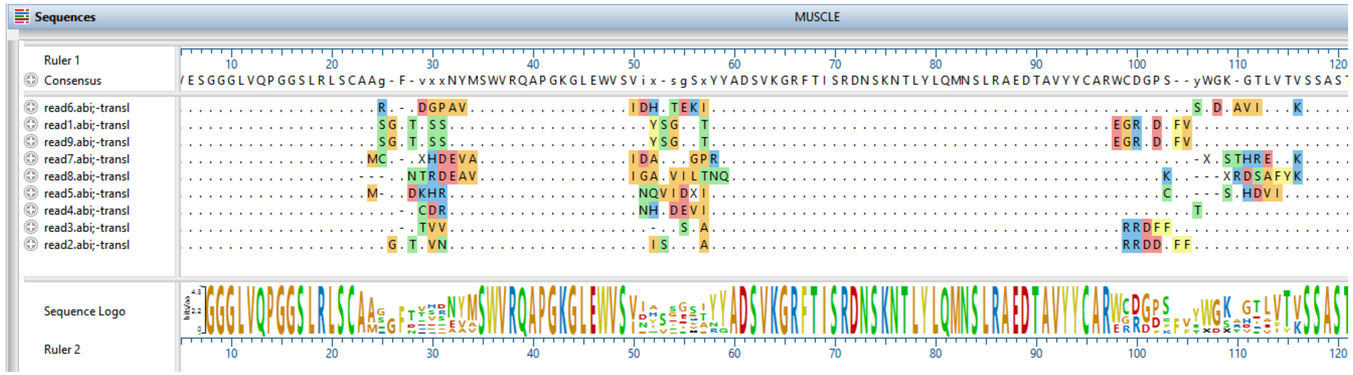
STEP 3

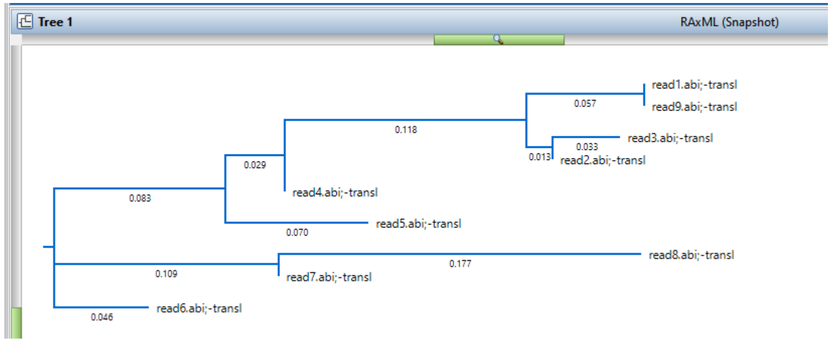
Batch translate sequences in SeqNinja.



STEP 4

Align sequences and create a phylogenetic tree in MegAlign Pro.

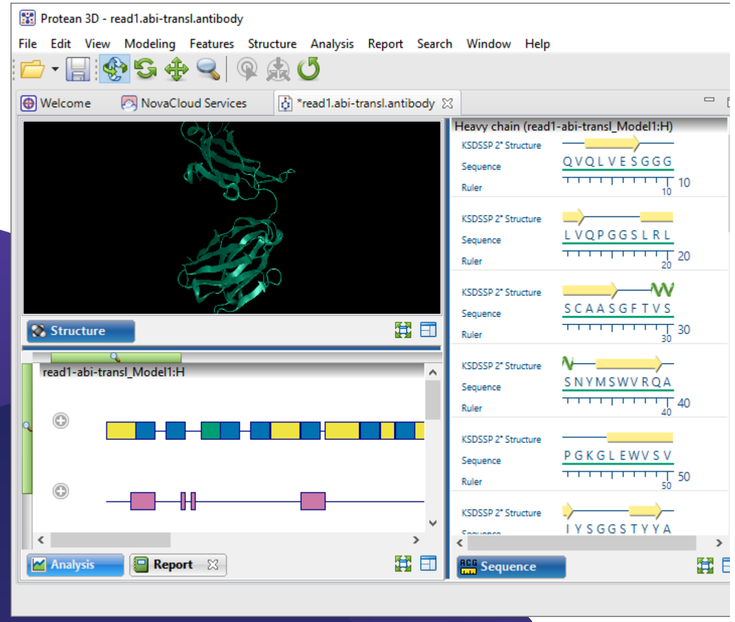




After assembly, use Lasergene Molecular Biology applications for sequence analysis and editing. Use SeqMan Ultra to further trim your sequences to the desired location, and SeqNinja to batch translate from DNA to amino acid sequence for downstream analysis. You can then quickly and easily create a multiple sequence alignment, visulaize conserved CDR regions, and build phylogenetic trees in MegAlign Pro.

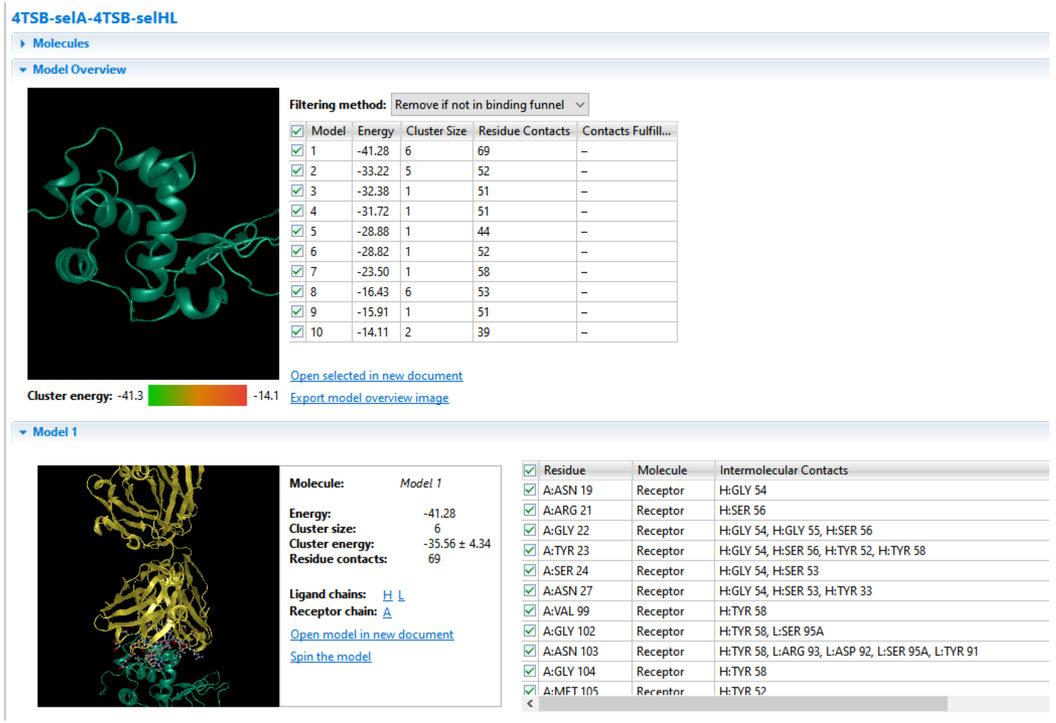
STEP 5

Use Protean 3D with NovaFold Antibody to create a homology model of the sequence .



STEP 6

Use Protean 3D with NovaDock to simulate docking of the predicted antibody structures to the target antigen.



Using the sequence data from previous steps, model and visualize the antibody structures. Optionally, you can also model immune complexes by simulating docking interactions between the antibody and antigen structures.

READY TO TRY THIS WORKFLOW WITH YOUR DATA?

FOR A FREE DEMO OF THE SOFTWARE,
CONTACT US AT SUPPORT@DNASTAR.COM

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