

# 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.



Project Report Project Details

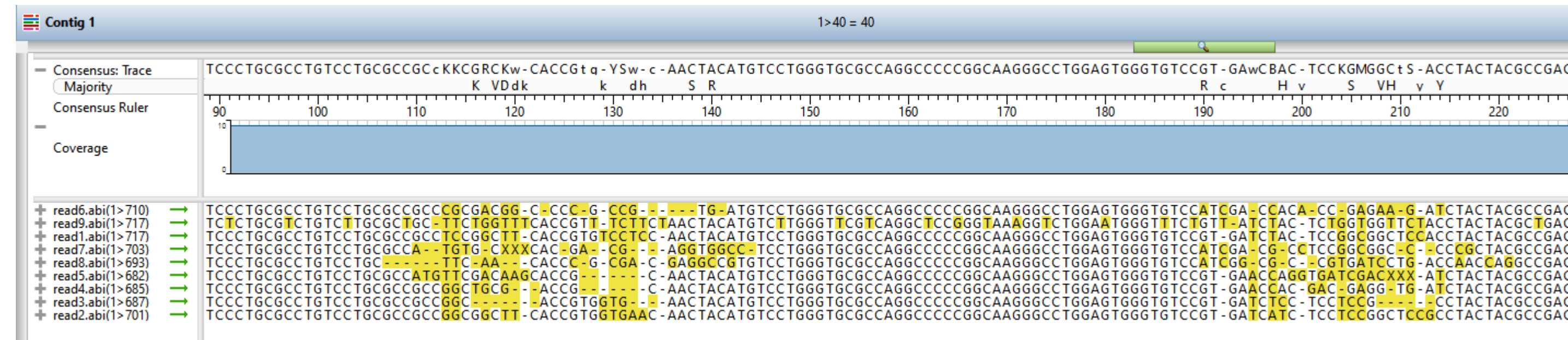
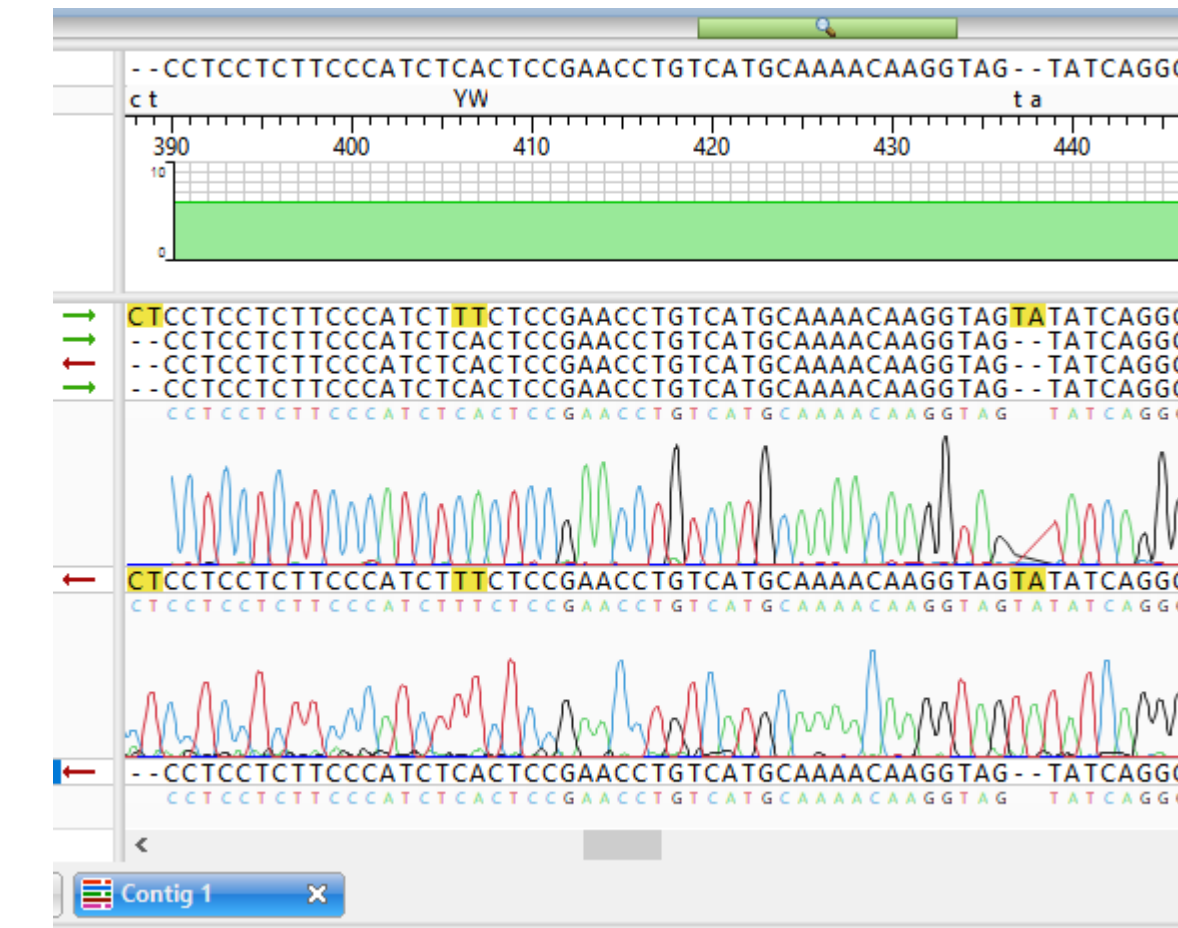
Classic assembly Parameters:

Match Size	12
Minimum Match Percentage	75
Minimum Sequence Length	100
Maximum Added Gaps per kb in Contig	70
Maximum Added Gaps per kb in Sequence	70
Maximum Register Shift Difference	70
Lastgroup Considered	2
Gap Penalty	0.00
Gap Length Penalty	0.70

Entering 9 sequences on 4/14/21,  
CREATING NEW Contig 1: from read1.abi (1>717)

read2.abi (1>701)	in Contig 1: percent match 97
read3.abi (1>687)	in Contig 1: percent match 94
read4.abi (1>685)	in Contig 1: percent match 95
read5.abi (1>682)	in Contig 1: percent match 92
read6.abi (1>710)	in Contig 1: percent match 92
read7.abi (1>703)	in Contig 1: percent match 90
read8.abi (1>693)	in Contig 1: percent match 89
read9.abi (1>717)	in Contig 1: percent match 77

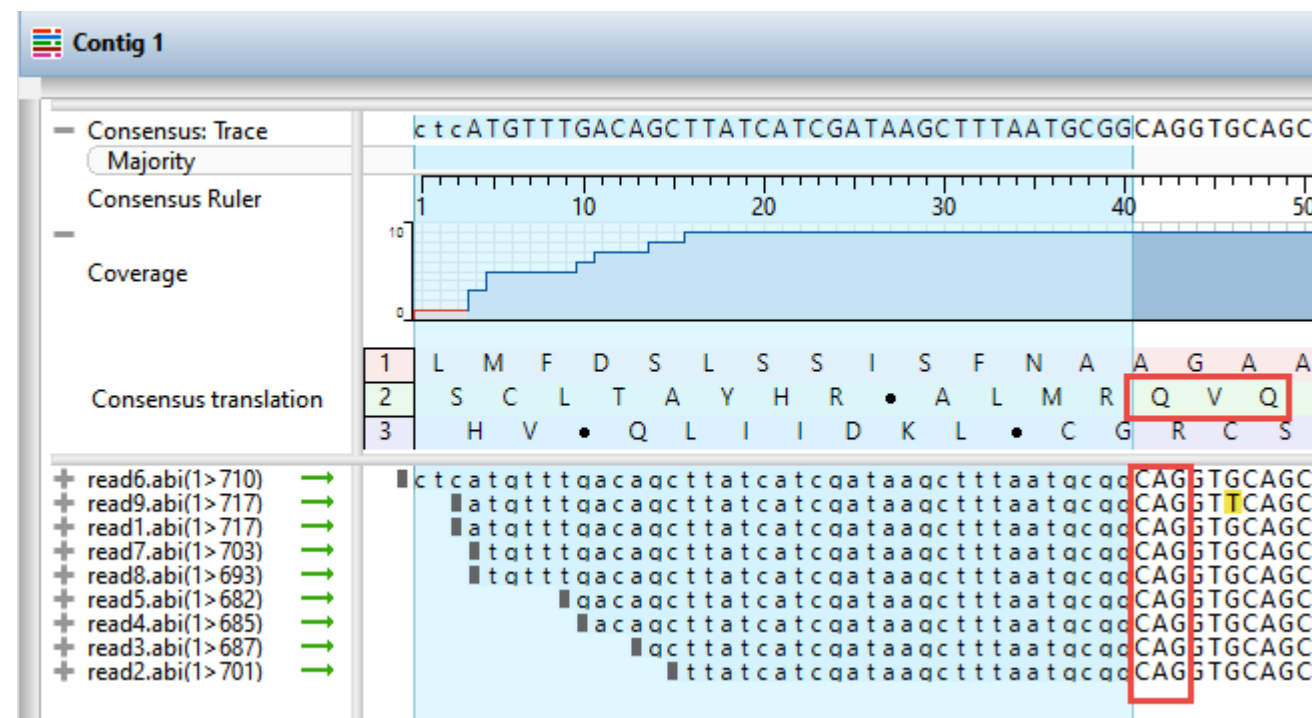
Time to Assemble 0:0:0



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.

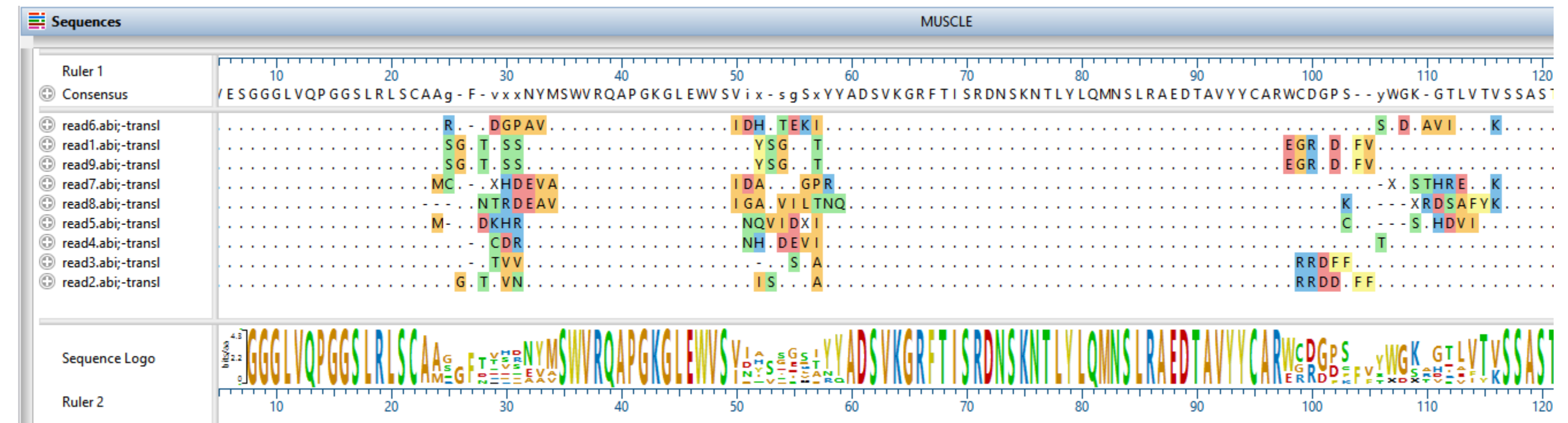
# STEP 2

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



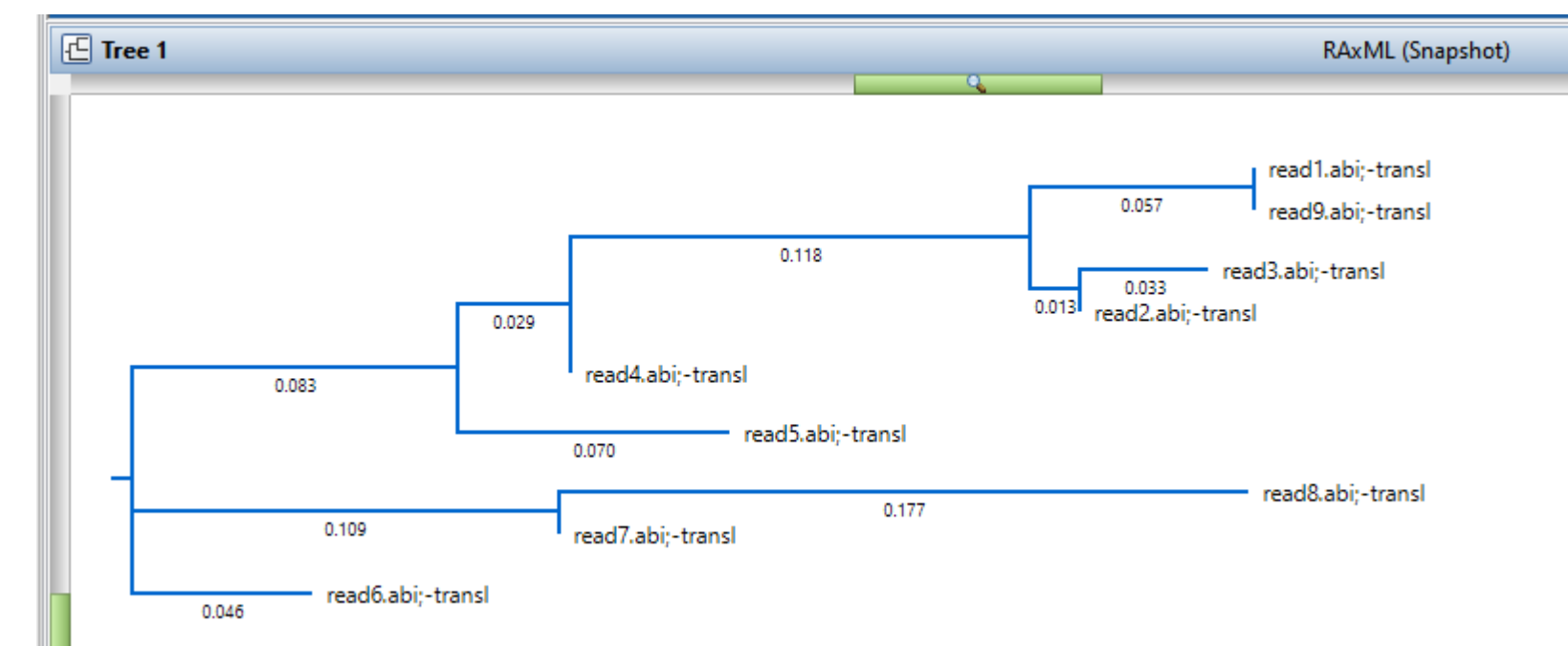
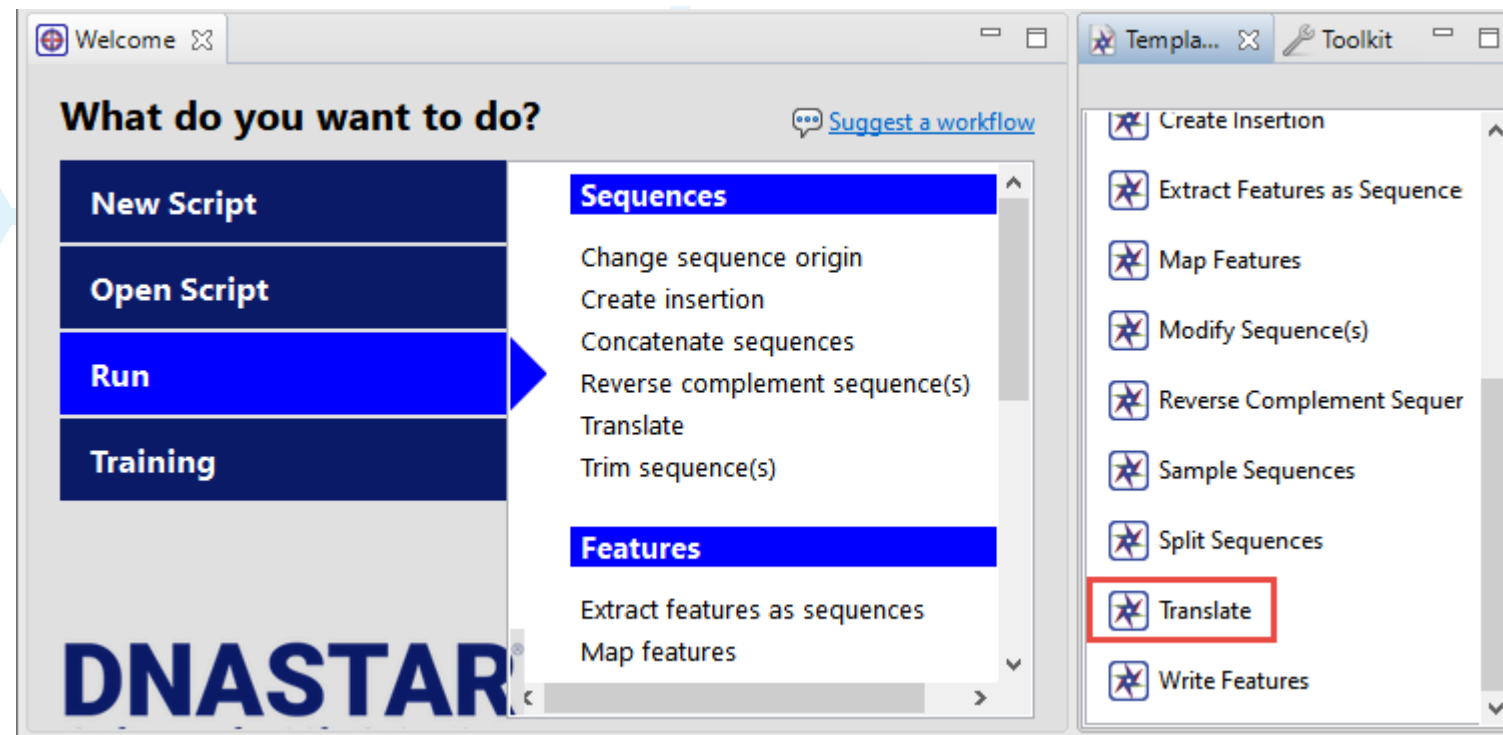
# STEP 4

Align sequences and create a phylogenetic tree in MegAlign Pro.



# STEP 3

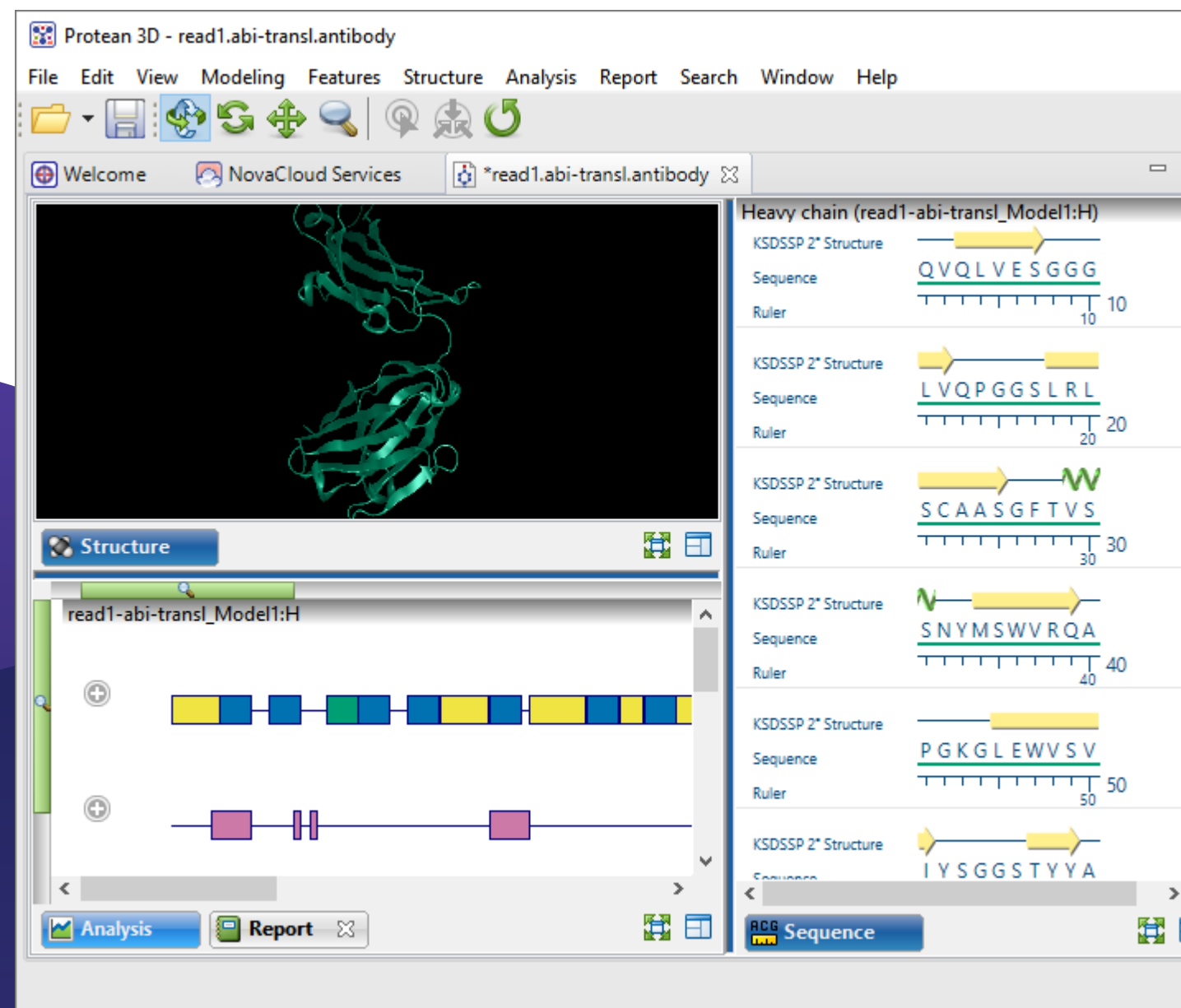
Batch translate sequences in SeqNinja.



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, visualize 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.

4TSB-selA-4TSB-selHL

Filtering method: Remove if not in binding funnel

Model	Energy	Cluster Size	Residue Contacts	Contacts Fulfill...
1	-41.28	6	69	--
2	-33.22	5	52	--
3	-32.38	1	51	--
4	-31.72	1	51	--
5	-28.88	1	44	--
6	-28.82	1	52	--
7	-23.50	1	58	--
8	-16.43	6	53	--
9	-15.91	1	51	--
10	-14.11	2	39	--

Cluster energy: -41.3 -14.1

Residue Molecule Intermolecular Contacts

A:ASN 19	Receptor	H:GLY 54
A:ARG 21	Receptor	H:SER 56
A:GLY 22	Receptor	H:GLY 54, H:GLY 55, H:SER 56
A:TYR 23	Receptor	H:GLY 54, H:SER 56, H:TYR 52, H:TYR 58
A:SER 24	Receptor	H:GLY 54, H:SER 53
A:ASN 27	Receptor	H:GLY 54, H:SER 53, H:TYR 33
A:VAL 99	Receptor	H:TYR 58
A:GLY 102	Receptor	H:TYR 58, L:SER 95A
A:ASN 103	Receptor	H:TYR 58, L:ARG 93, L:ASP 92, L:SER 95A, L:TYR 91
A:GLY 104	Receptor	H:TYR 58
A:MFT 105	Receptor	H:TYR 52

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](mailto:support@dnastar.com)

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