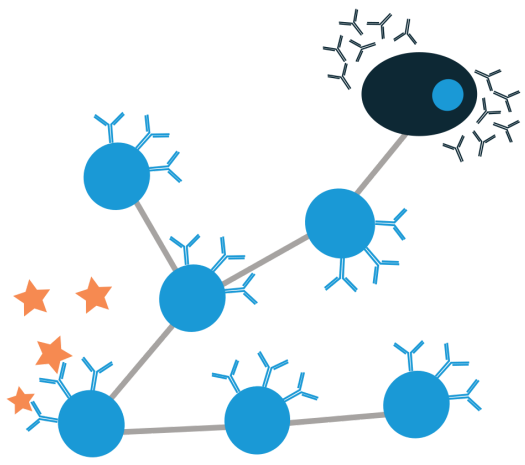
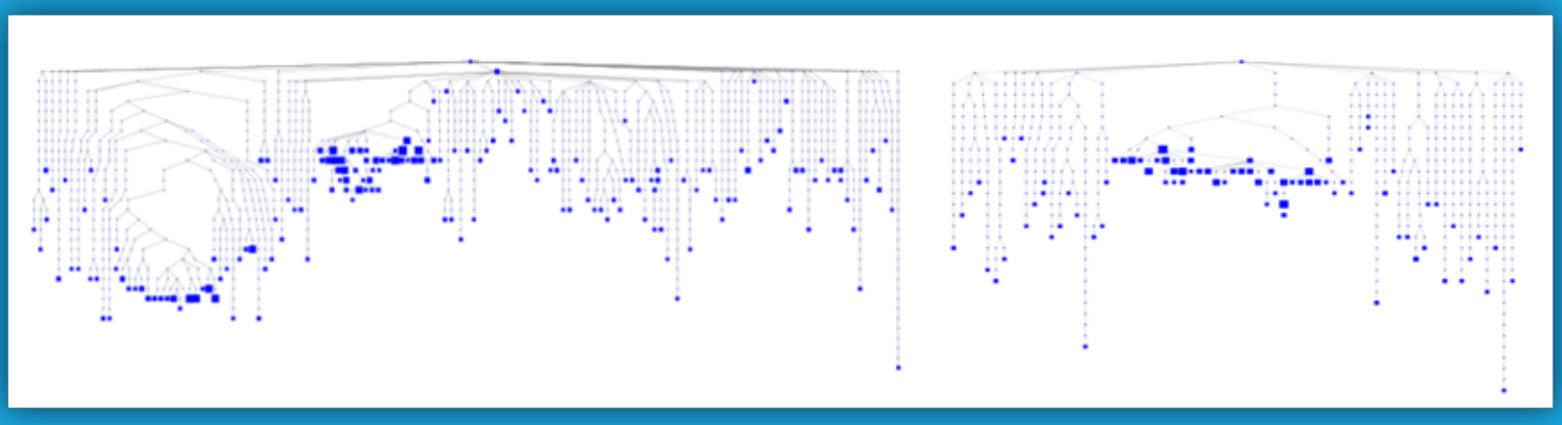
CLONAL HIT-EXPANSION CASE STUDY

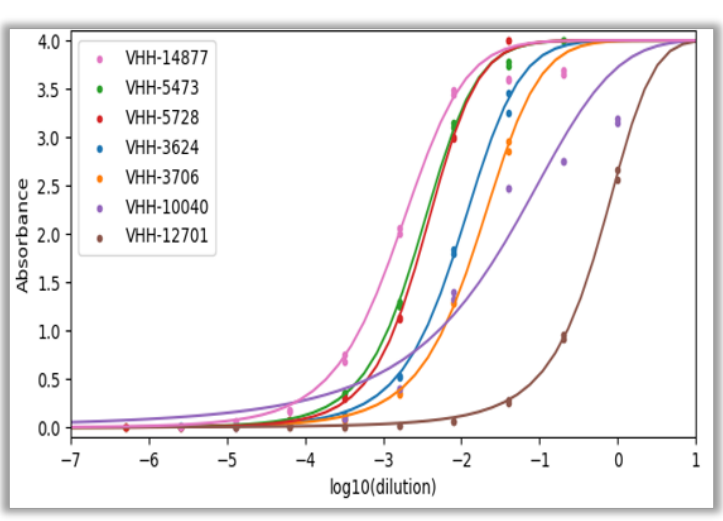


The B-cell receptor (BCR) repertoire contains a wealth of valuable antibodies that are missed in antibody discovery campaigns. In this case study, we expand antibody hits from an antibody discovery campaign by mining the BCR repertoire for relatives within the same clone.

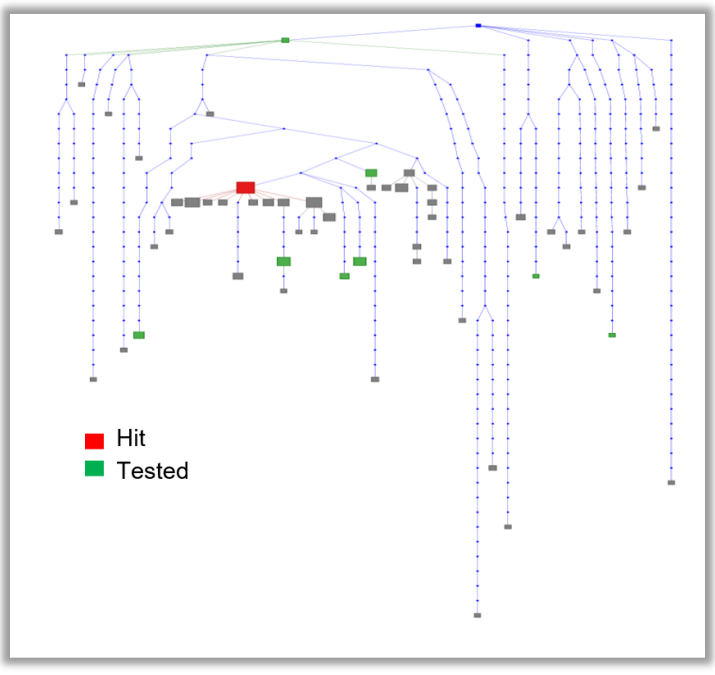
Watch the full PEGS Boston presentation here.



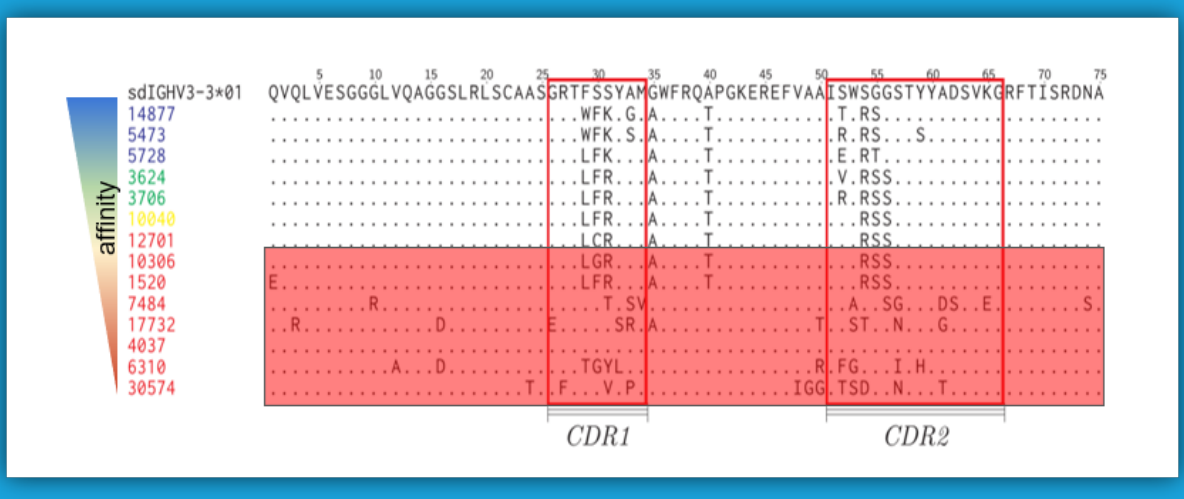
In the BCR repertoire, many antibodies share an identical CDR3 and are considered members of the same clone. While antibody discovery methods sub-sample an immune response, hit expansion uses next-generation sequencing (NGS) to rescue relatives of hits that are within a clone. Above, phylogenetic trees of llama single domain antibody hits discovered by Alicanto are shown.



Single domain antibodies sharing the exact CDR3 as the Alicanto-identified hit were expressed as VHHs and screened via ELISA. The tested VHHs showed a range of affinity to the target.



The phylogenetic tree of the clonal lineage shows how the tested VHHs (green) relate to the original hit (red).



The multiple sequence alignment of clone members shows a pattern of mutations that may be essential for strong target binding, particularly in the CDR1 and CDR2.

Key Benefits:

- NGS repertoires extend hits by finding more members of the same clone.
- Hit expansion identifies 10-100x more antibody candidates per campaign.