

OVERVIEW

Deeptope has developed a methodology, using a combination of surface display, flow cytometry and high-throughput sequencing technologies, which allows to

- Substitute each amino acid of a sequence (either an antibody* or an antigen) with the 19 other amino acids,
- Express all the variants (every single mono-mutant),
- Functionally correlate the impact of each single mutation on the Ab* / Ag interaction.

Our offer consists in characterizing antigen / antibody* interactions (epitope / paratope mapping) and optimizing antibodies*.

In the context of molecule development, we provide in short time frames (6/8 weeks) for

- **Epitope mapping:**
 - o Data equally reliable whether the epitope is conformational or linear,
 - o Accurate to the nearest amino acid,
 - o Prediction of cross reactivity,
 - o Economies of scale (the same antigen single-mutant library can be re-used for several antibodies).
- **Paratope mapping:**
 - o In vitro functional data (customizable parameters: antigen species, off target, temperature, pH),
 - o Accurate to the nearest amino acid,
 - o Comprehensive, reliable, robust and reproducible.
- **Optimization:**
 - o A 360 screening, via the identification of all mutations of interest
 - Ex: Modulation of affinity, cross-reactivity, selectivity; pH switch; Improvement of thermal stability; Humanization / hyper-humanization; Suppression of undesirable motifs (PTM)...
 - o A simultaneous multi-parametric process, which allows the identification of an optimized sequence as well as the associated family of variants (IP protection),
 - o Definitive and comprehensive results.

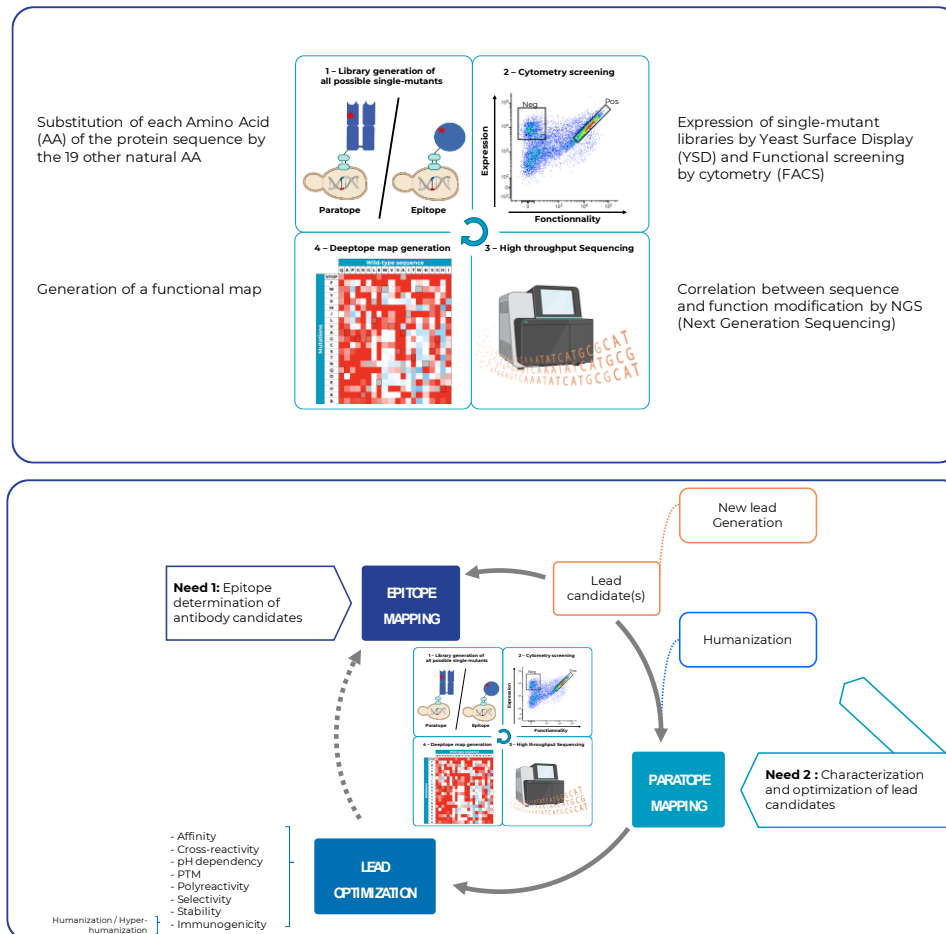
For more information, please contact us

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* Antibodies are the main therapeutic leads we work with, but many other proteins can be optimized as well.

Methodology & Services offered:



Pubmed References (Deeptope is a CEA Paris-Saclay spinoff):

- 2023: Combining deep mutational scanning to heatmap of HLA class II binding of immunogenic sequences to preserve functionality and mitigate predicted immunogenicity - PubMed (nih.gov)
- 2023: Deciphering cross-species reactivity of LAMP-1 antibodies using deep mutational epitope mapping and AlphaFold
- 2022: Deep mutational engineering of broadly-neutralizing nanobodies accommodating SARS-CoV-1 and 2 antigenic drift
- 2021: An antibody targeting type III secretion system induces broad protection against Salmonella and Shigella infections

They have trusted us:

