A NEW CHALLENGE IN MEDICINE: DISCOVERY OF NOVEL THERAPEUTIC LEADS

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SELEXIS

Problem – Challenge

The challenge of any protein therapeutic development campaign is to rapidly identify optimal clinical candidate(s) that can be stably produced at high levels in the manufacturing cell line.

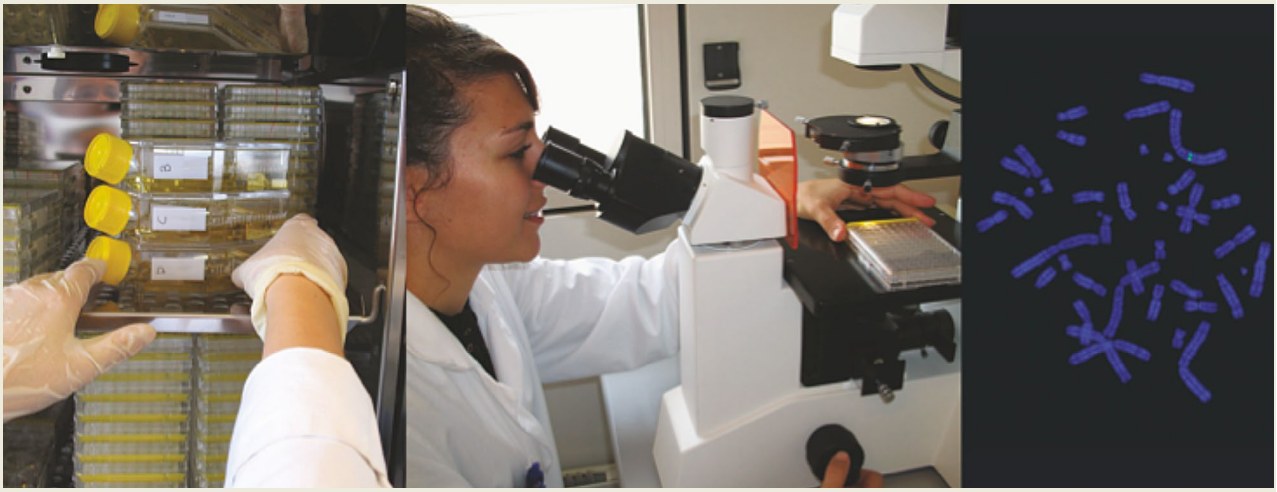
To achieve this goal, the current approaches are based on the transient expression of the lead candidate(s) and stepwise selection by expression level and then the required biological activity. In addition, the overall cell line development process is compromised by the use of different recipient cell lines for discovery and manufacturing, a limited number of variants expressed simultaneously, labor-intensive screening process and long timelines.

Solution

Selexis, a start-up of the University of Lausanne, pioneered the novel Selexis D2 Platform™ to overcome these hurdles. This CHO cell-based platform takes advantage of Selexis Genetic ElementsTM boosting protein expression to enable:

- *Selection based on both titer and activity*
- *Screening of 10 – 1000 protein variants*
- *Use of the same mammalian cell line along the whole process*
- *Reduced timelines and costs*
- *Earlier clinically relevant data*

Most importantly, Selexis D2 Platform™ decreases the attrition rates today observed in Discovery to identify new therapeutic entities in medicine.



Case Study: Screening and identification of a new therapeutic neutralizing antibody

A CHO-based (Chinese Hamster Ovarian) combinatorial repertoire containing 10 heavy chains (HC) and 25 light chains (LC) was established. The objective was the identification of the best neutralizing antibody against an infectious agent. Each antibody gene was cloned into a Selexis SUREtech DNA expression vector, and a combinatorial transfection (10 VH x 25 VL) generated a library of 250 antibody-CHO expressing cell pools. By applying Selexis D2 Platform™ the library was constructed and assayed in only 8 weeks from the transfection date. Both the titer and the neutralizing activity were measured during this period of time. Based on these criteria the three best candidates out of the 250 were expanded to generate high producing cell clones.