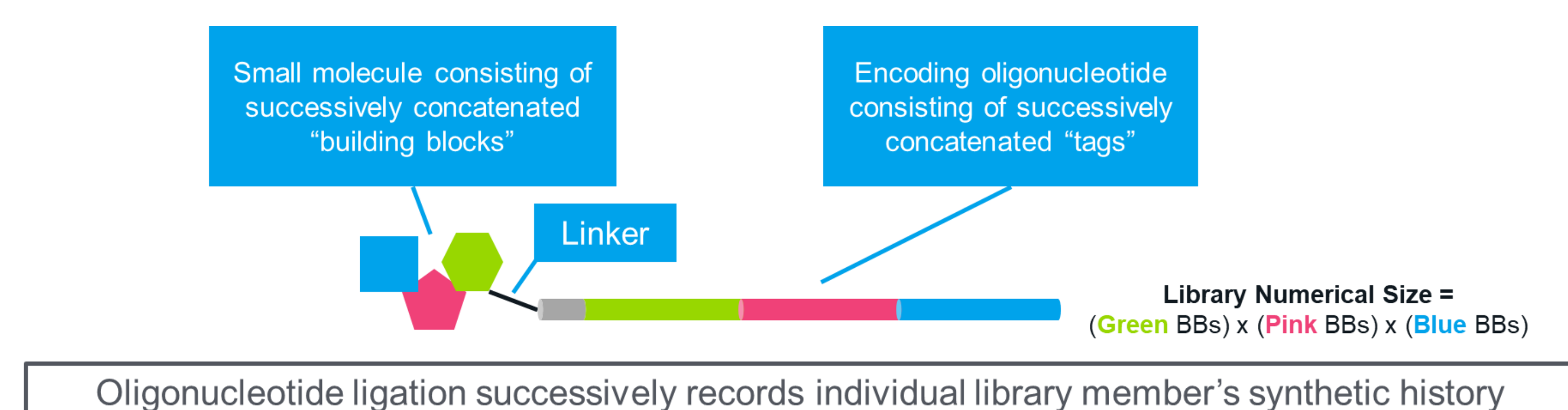


# New inhibitors of oncology targets discovered using the affinity-mediated selection of DNA-encoded chemical libraries followed by machine-learning

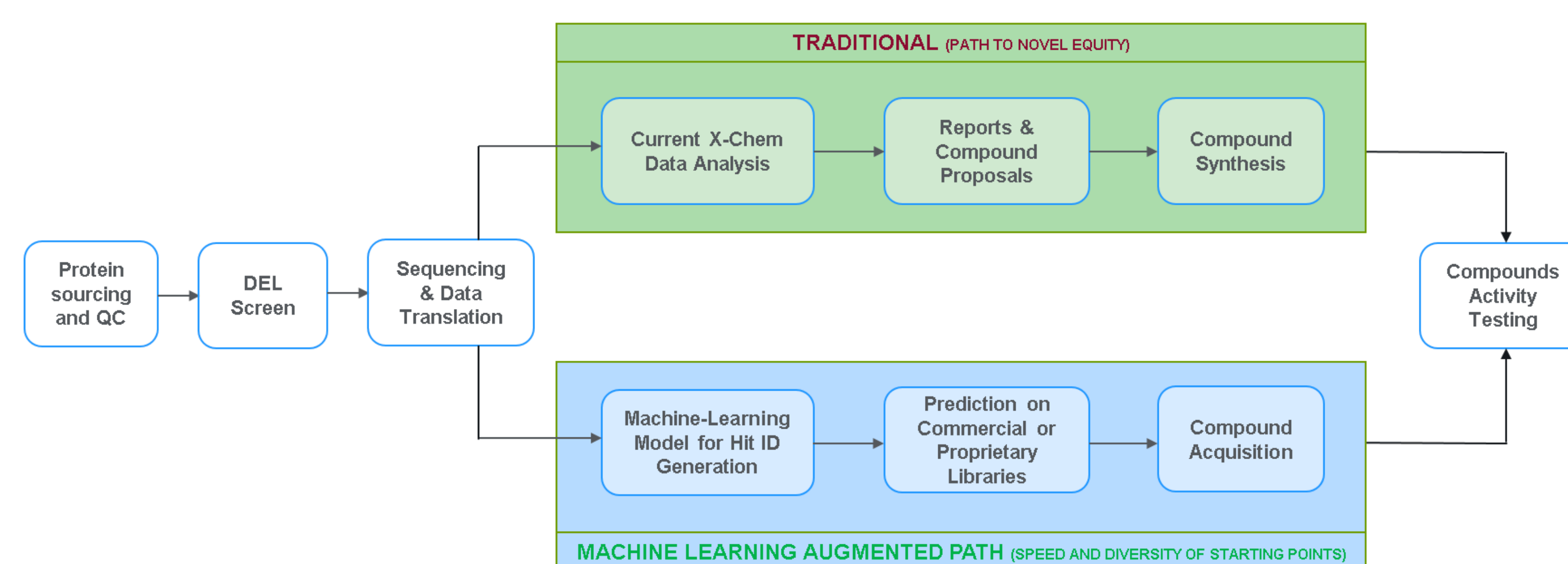
Anthony D. Keefe, Mohamed AbouZleikha, AJ Baghaie, Matthew A. Clark, Marie-Aude Guie, John P. Guilinger, Ryan Walsh, Ying Zhang X-Chem, Inc., Waltham MA, USA

## DNA-Encoded Chemistry

DNA-Encoded Chemical Library (DEL) technology enables the rapid discovery of small molecules that bind to distinct protein targets of therapeutic value. Individual compounds are synthesized and screened as mixtures enabling the screening of very large numbers of compounds. Affinity-mediated selection enriches target-engaging compounds which are subsequently identified by deep sequencing to recover encoded chemical information.

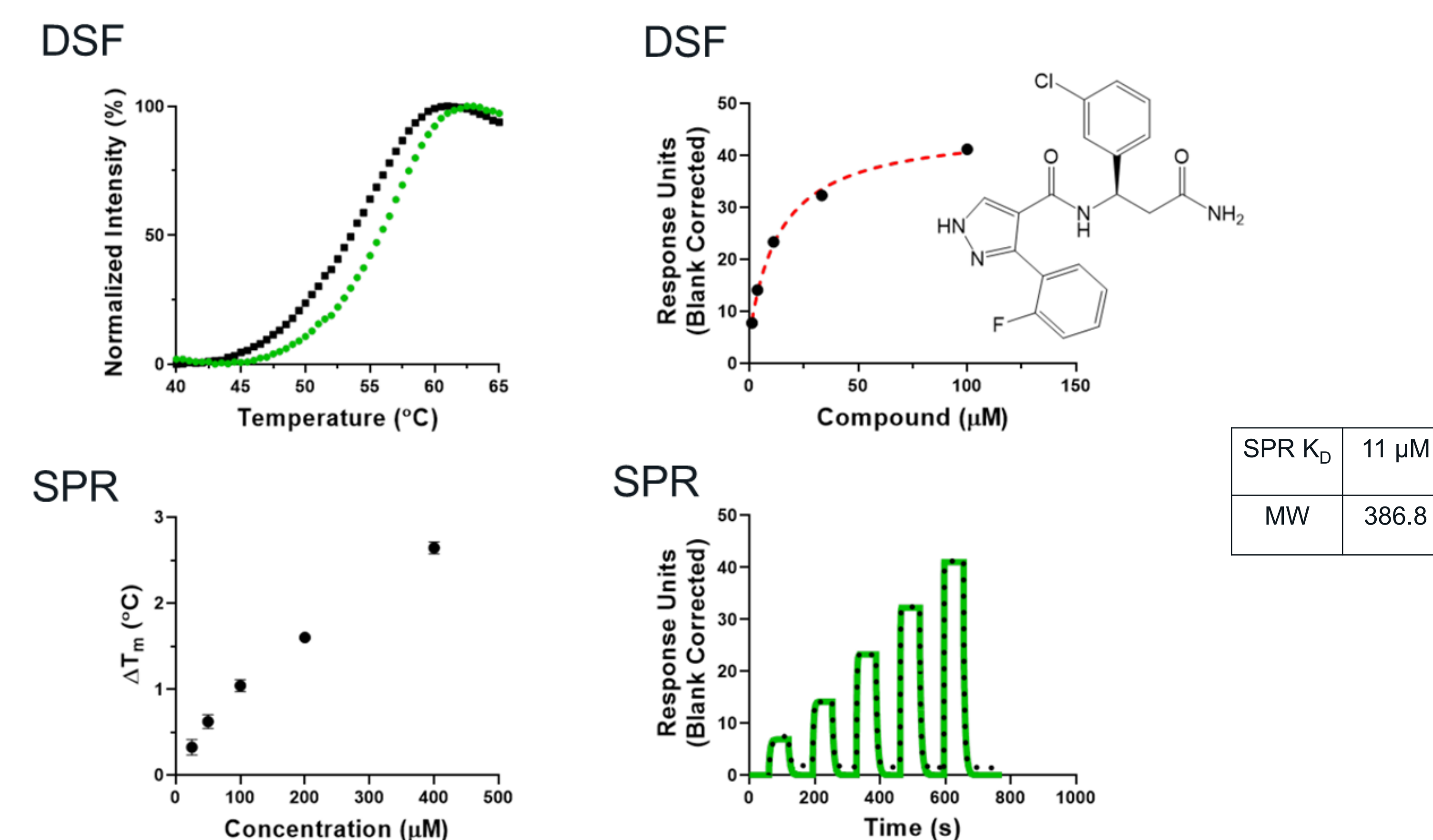


## DEL>ML>Catalog: An Alternative Approach to Hit ID

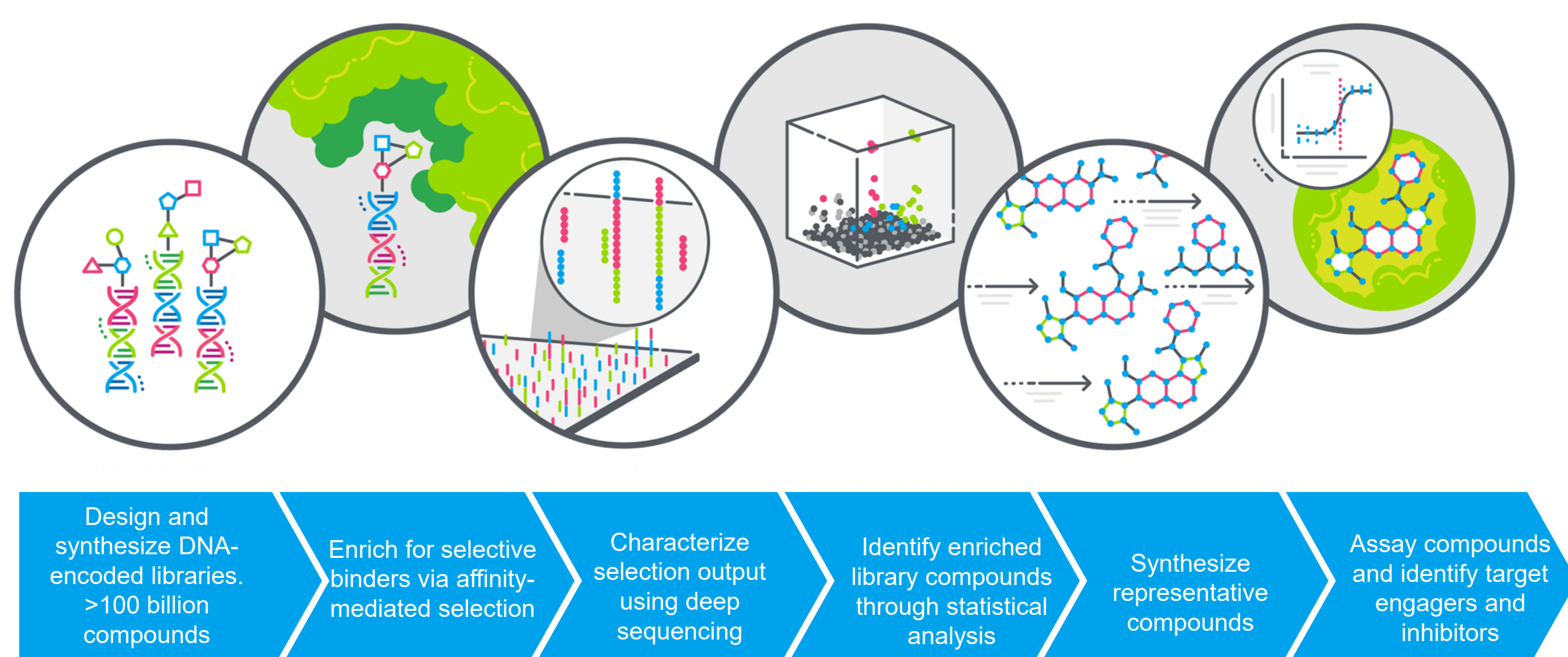


## Case Study 2: DCAF1

DCAF1 is the substrate-recognition component of an E3 ligase complex that is associated with the proliferation of colon cancer cells.



## X-Chem Lead Discovery Platform

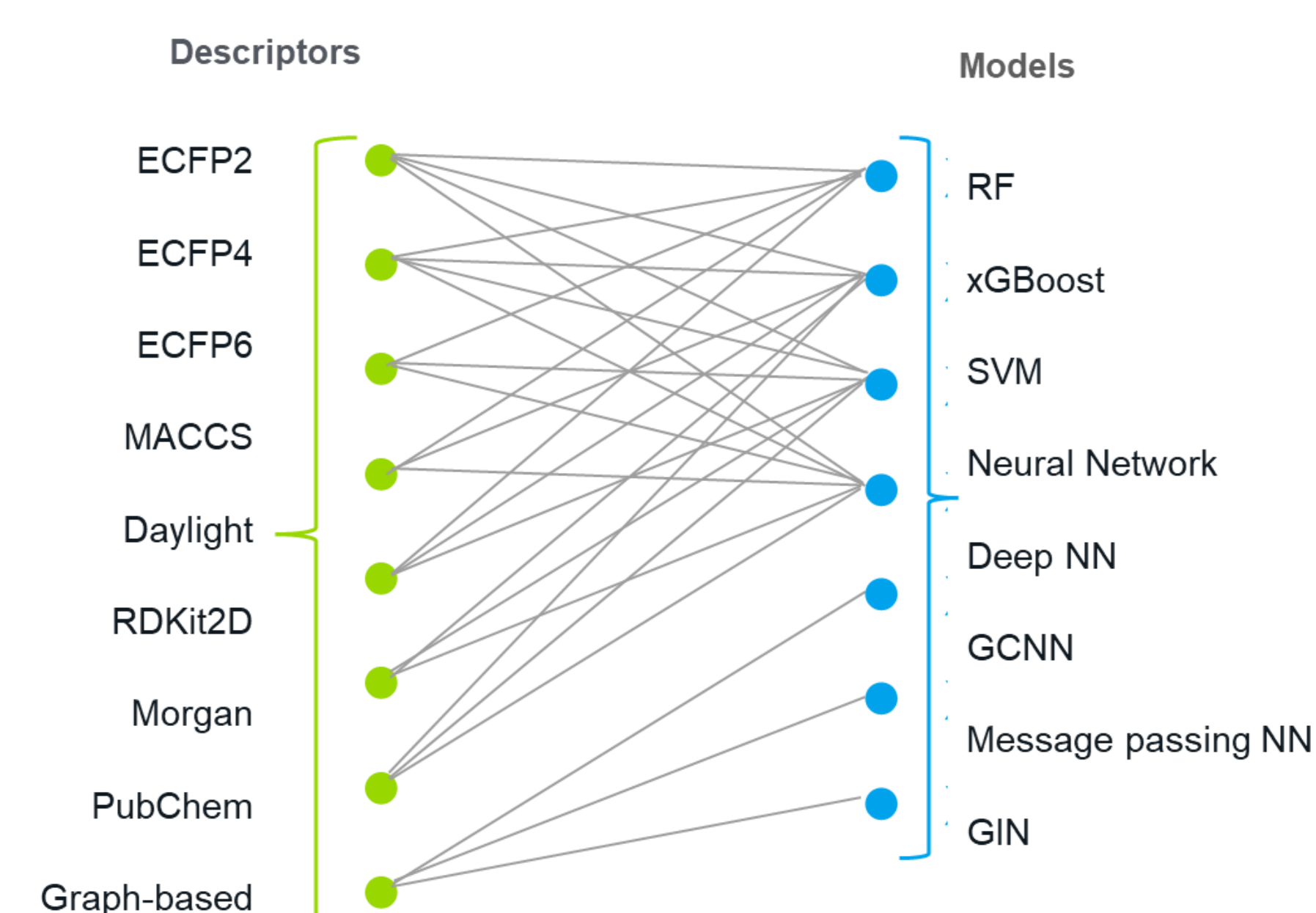


## Searching for the Right Combination of Descriptor and Model

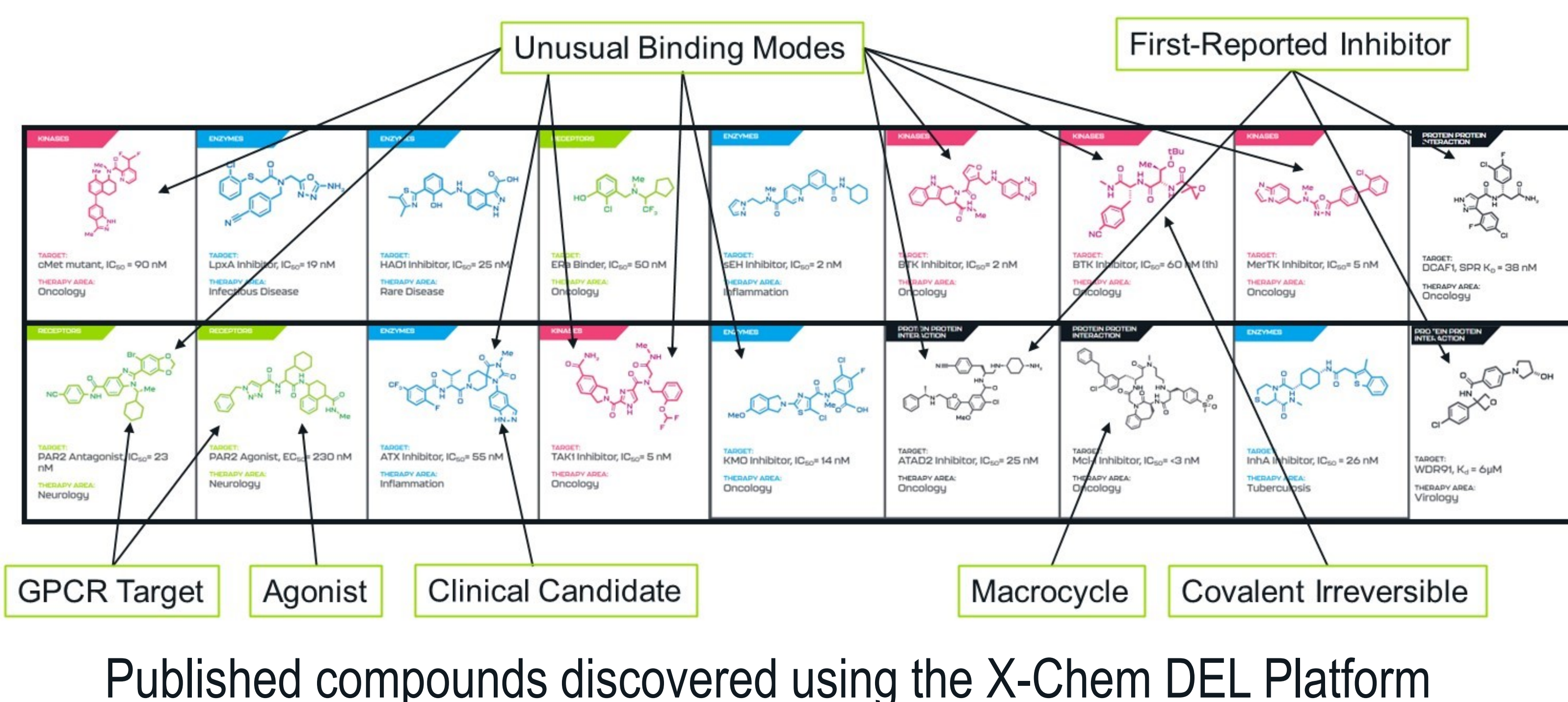
We utilize over 12 different representations and over 10 different ML methods.

Each training process outputs a pool of up to 40 ML models, each model is the result of hyperparameter tuning of around 350 experimental variations.

High-performance computing and scalable infrastructure is required to enable training completion in days.

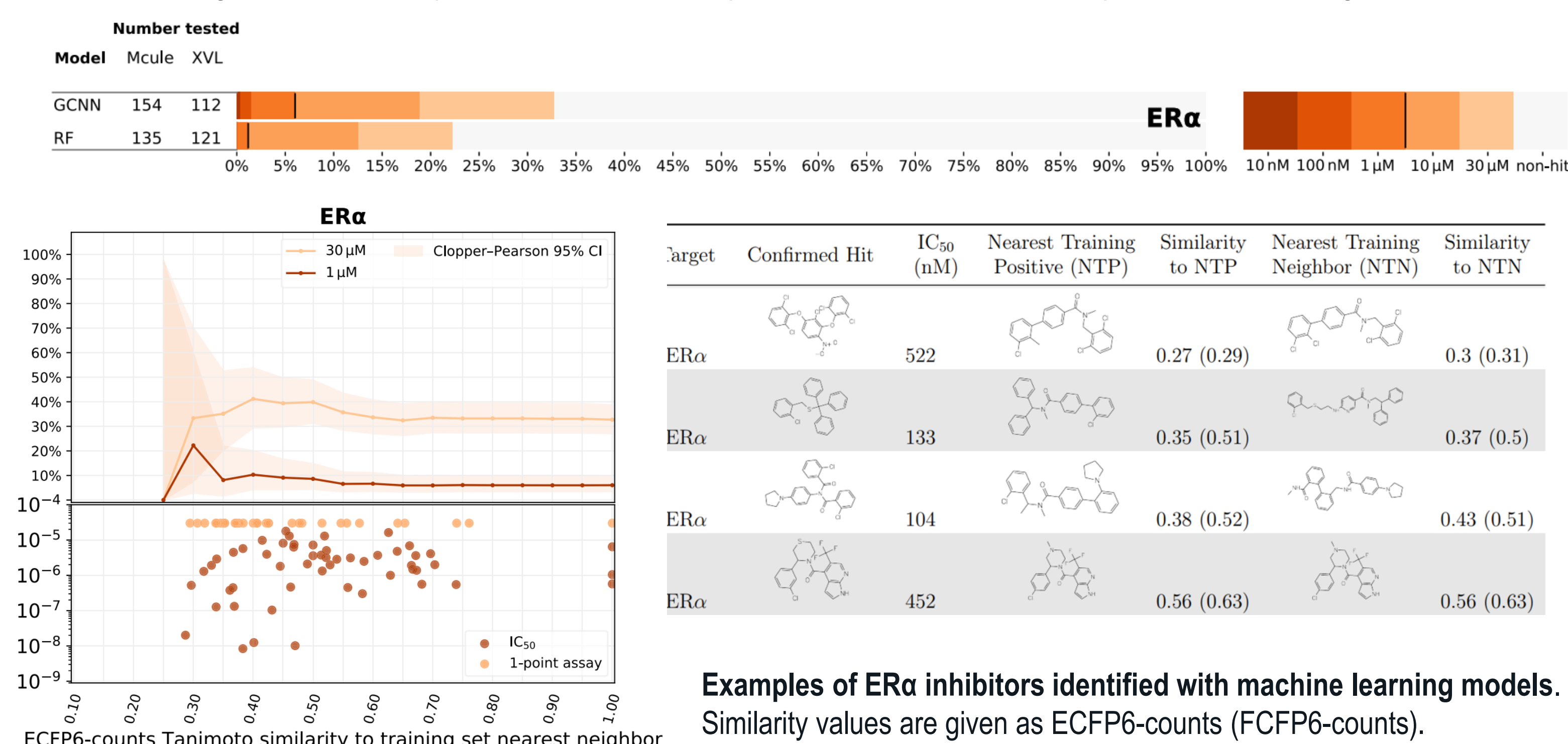


## X-Chem Track Record

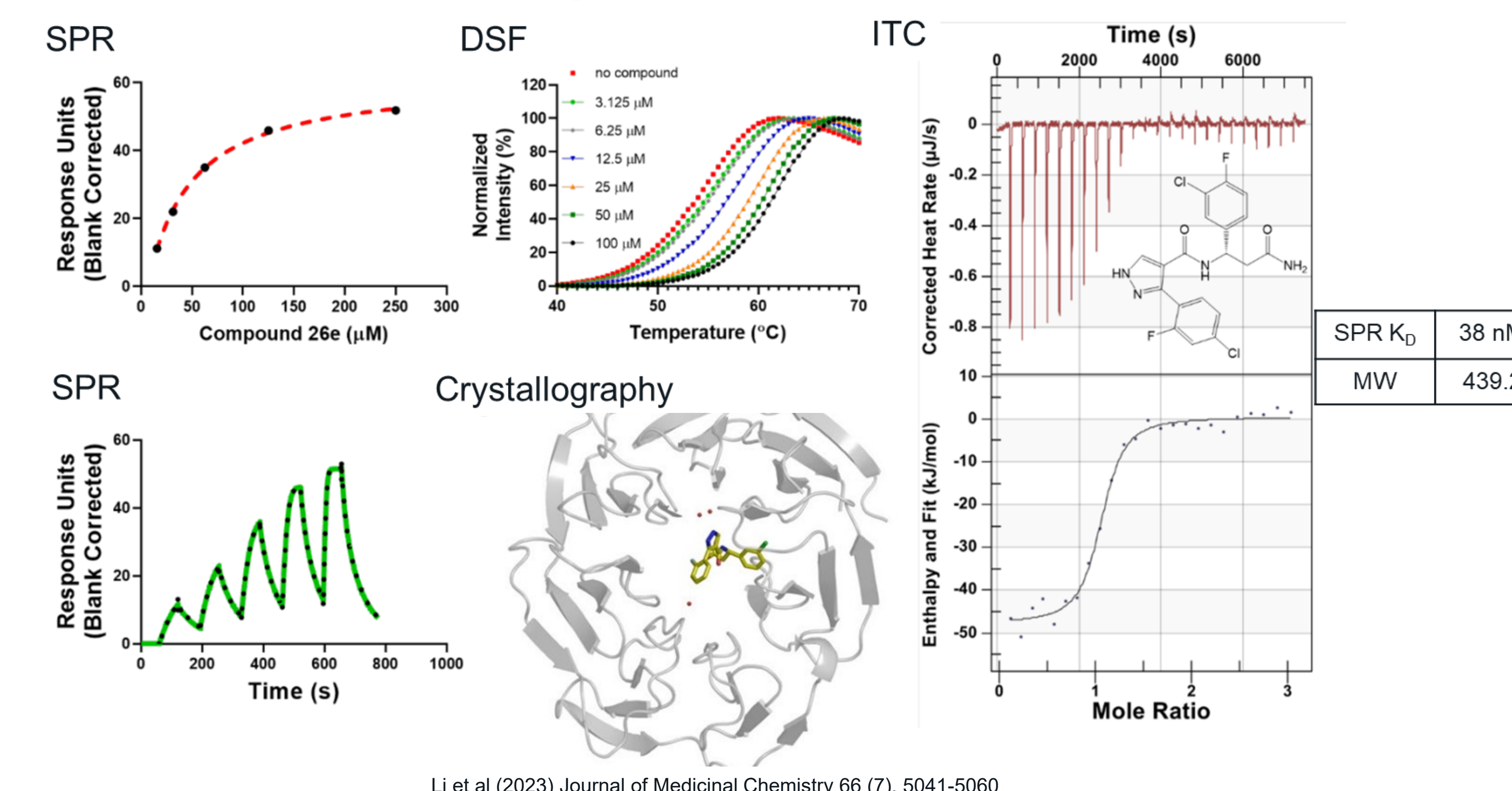


## Case Study 1: ERα

ERα is an estrogen-activated receptor that controls transcription and stimulates breast cell proliferation including in breast cancer.



## DCAF1 Compound Advancement



## Summary

We have established a DEL>ML>Catalog>Hit ID platform that utilizes our deck of DNA-Encoded chemical compounds, affinity-mediated selection and DNA sequencing to identify populations of enriched compounds. The structures of these enriched compounds are then featurized using a range of representations and the resultant fingerprints are subjected to machine-learning using a range of architectures. The most successful models are combined and used to score catalog compounds, the highest scoring of which are then sourced and tested. This strategy has rapidly provided attractive inhibitors for a range of oncology targets including those for which no inhibitors were previously known. Two case studies, DCAF1 and ERα, are presented as examples.