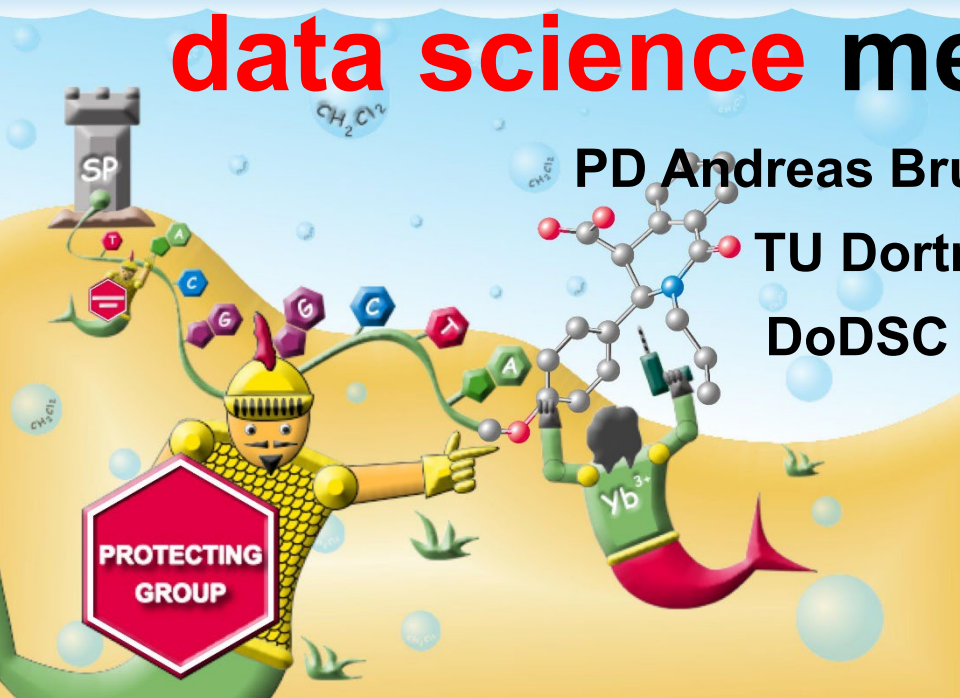


# DNA-encoded libraries:

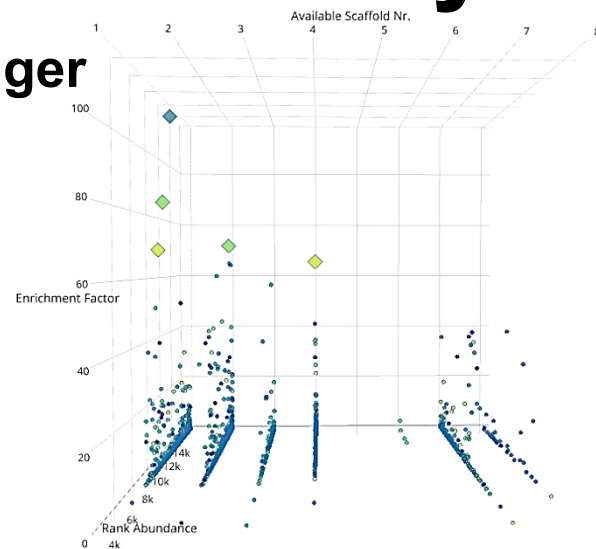
## data science meets chemistry



PD Andreas Brunschweiger

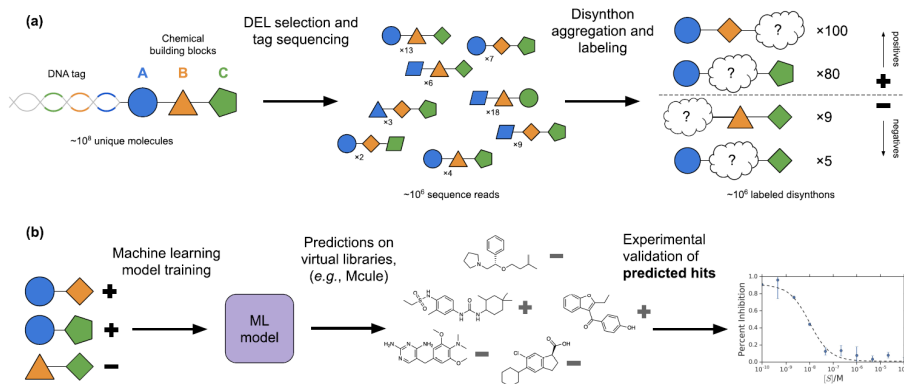
TU Dortmund

DoDSC 2022



## Machine Learning on DNA-Encoded Libraries: A New Paradigm for Hit Finding

Kevin McCloskey,<sup>‡</sup> Eric A. Sigel,<sup>‡</sup> Steven Kearnes, Ling Xue, Xia Tian, Dennis Moccia, Diana Gikunju, Sana Bazzaz, Betty Chan, Matthew A. Clark, John W. Cuozzo, Marie-Aude Gué, John P. Guilinger, Christelle Huguet, Christopher D. Hupp, Anthony D. Keefe, Christopher J. Mulhern, Ying Zhang, and Patrick Riley<sup>\*</sup>



VIP **Peptidomimetics** Very Important Paper

How to cite:

International Edition: doi.org/10.1002/anie.202006280

German Edition: doi.org/10.1002/ange.202006280

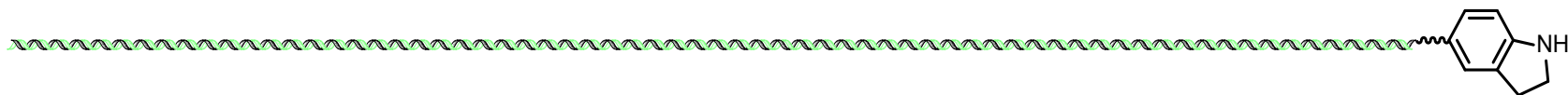
## TEAD–YAP Interaction Inhibitors and MDM2 Binders from DNA-Encoded Indole-Focused Ugi Peptidomimetics

Verena B. K. Kunig, Marco Potowski, Mohammad Akbarzadeh, Mateja Klika Škopič, Denise dos Santos Smith, Lukas Arendt, Ina Dormuth, Hélène Adihou, Blaž Andlovic, Hacer Karatas, Shabnam Shaabani, Tryfon Zarganes-Tzitzikas, Constantinos G. Neochoritis, Ran Zhang, Matthew Groves, Stéphanie M. Guéret, Christian Ottmann, Jörg Rahnenführer, Roland Fried, Alexander Dömling, and Andreas Brunschweiler<sup>\*</sup>

## Navigating Chemical Reaction Space – Application to DNA-encoded Chemistry

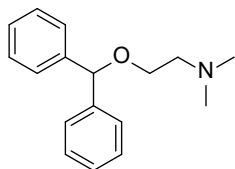
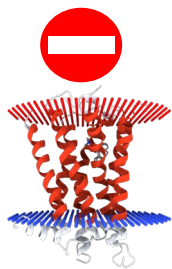
Silvia Chines,<sup>a</sup> Christiane Ehrt,<sup>b</sup> Marco Potowski,<sup>a,c</sup> Felix Biesenkamp,<sup>a</sup> Lars Grützbach,<sup>a</sup> Susanne Brunner,<sup>d</sup> Frederik van den Broek,<sup>e</sup> Shilpa Bali,<sup>e</sup> Katja Ickstadt,<sup>d</sup> and Andreas Brunschweiler,<sup>a\*</sup>

*Chemical Science, in revision*



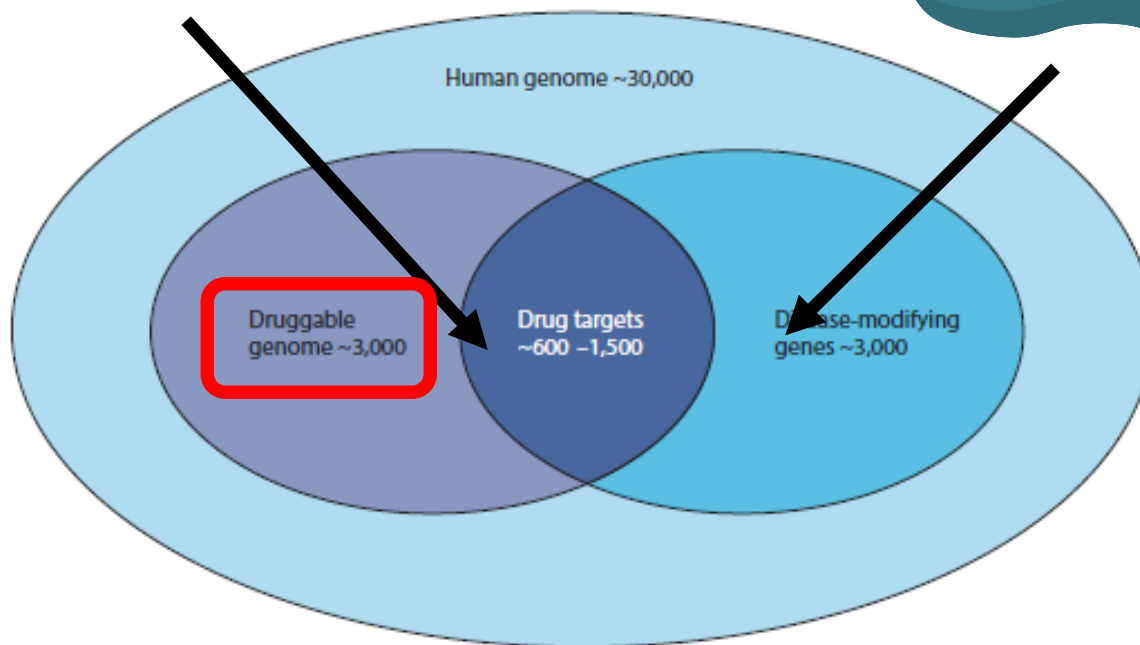
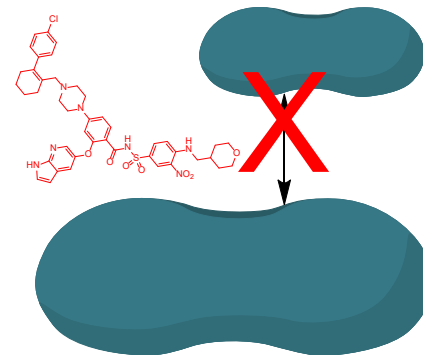
# The background

receptor block

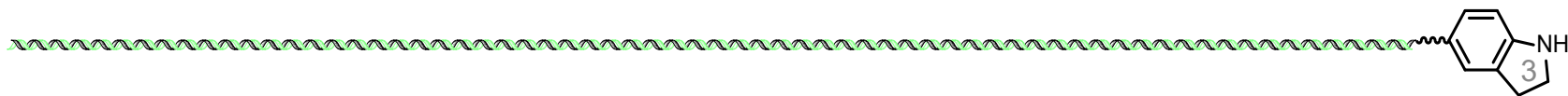


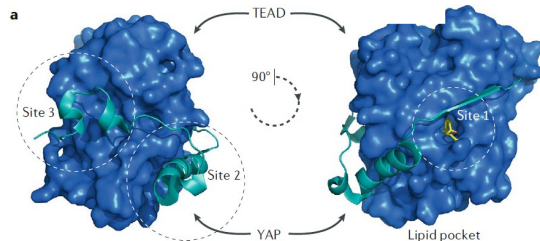
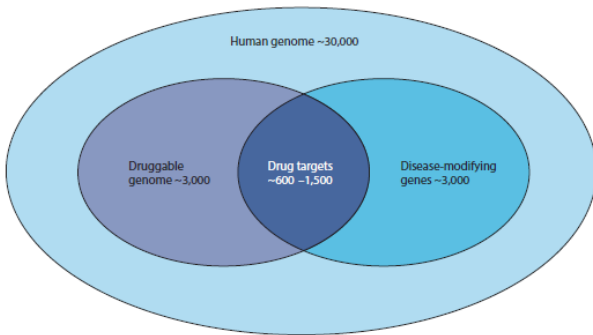
Diphenhydramine

protein-protein interaction



druggable versus undruggable





Exhaustive Repertoire of Druggable Cavities at Protein–Protein Interfaces of Known Three-Dimensional Structure

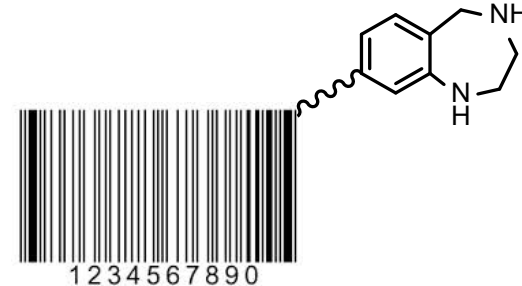
Franck Da Silva,<sup>†</sup> Guillaume Bret,<sup>†</sup> Leandro Teixeira,<sup>‡</sup> Claudio F. Gonzalez,<sup>‡</sup> and Didier Rognan<sup>\*†§</sup>

“almost no overlap in property space between PPI and „druggable“ pockets“

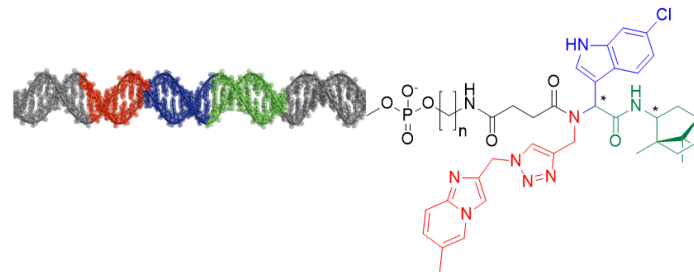
druggable versus undruggable



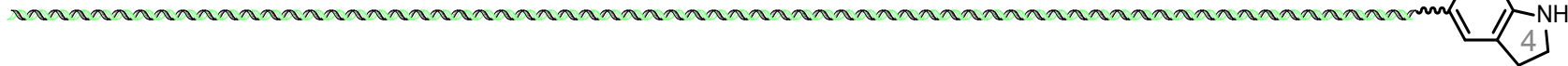
discrete, static



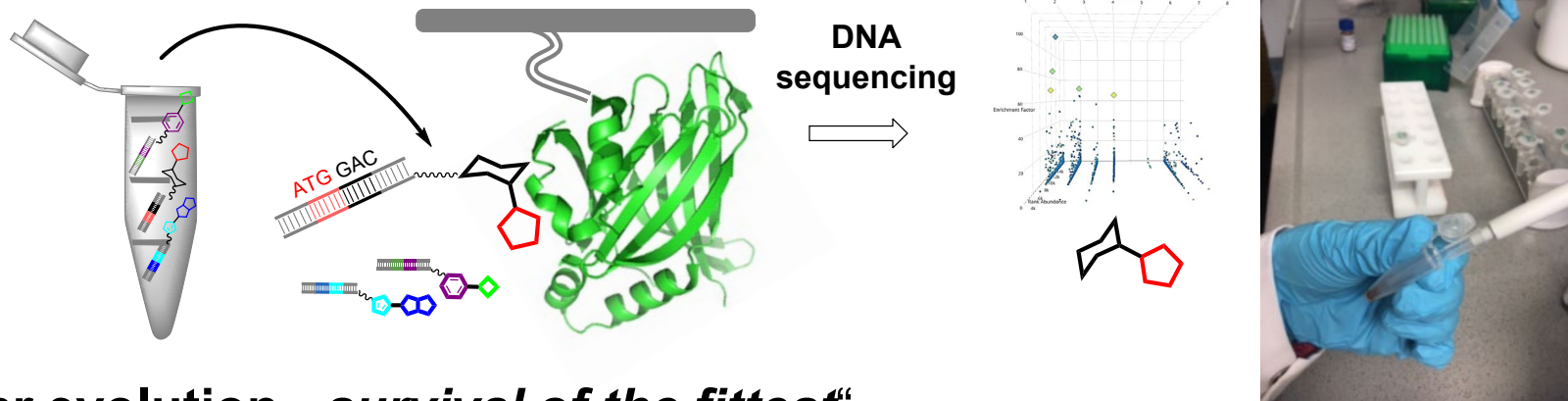
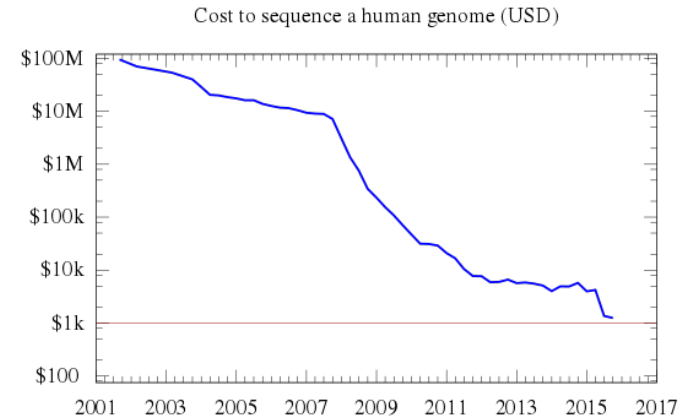
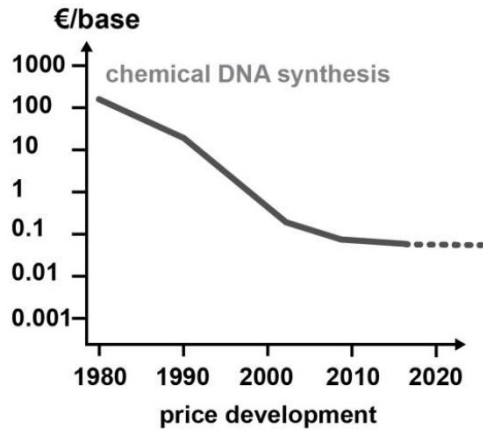
genotype - phenotype



pooled, dynamic

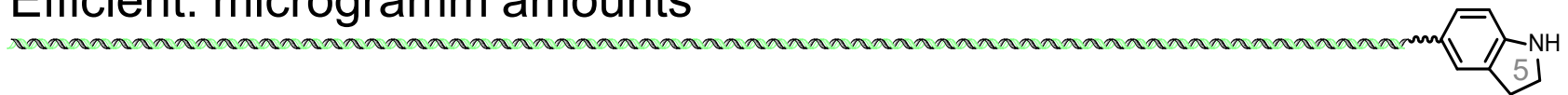


# DNA as a compound barcode

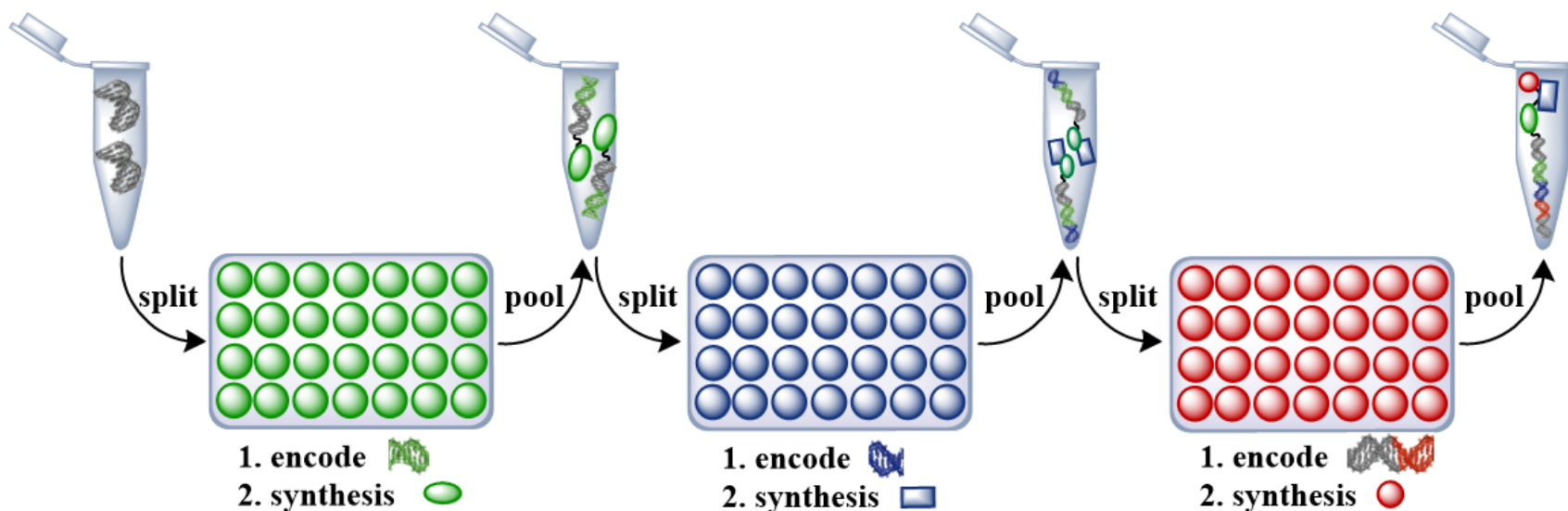


## Molecular evolution, „*survival of the fittest*“

- Generic, disease- and target-agnostic assay design
- Purified recombinant tagged proteins
- Efficient: microgramm amounts



# Encoded combinatorial chemistry



$100 \times 100 \times 100 = 1.000.0000$  compounds

Scalable, efficient

Expanding chemical space, de novo library design

Chemical reaction space?

Building block selection?

Reactivity of chemicals?

Journal of Medicinal Chemistry

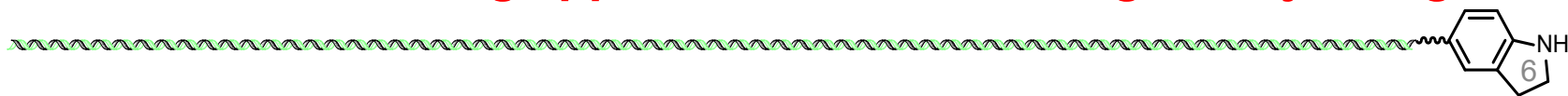
Article  
Cite This: *J. Med. Chem.* 2019, 62, 9732–9742 [pubs.acs.org/jmc](https://pubs.acs.org/jmc)

Exhaustive Repertoire of Druggable Cavities at Protein–Protein Interfaces of Known Three-Dimensional Structure

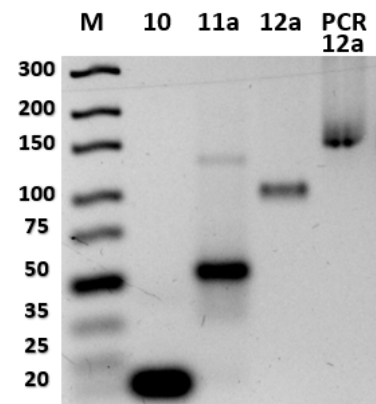
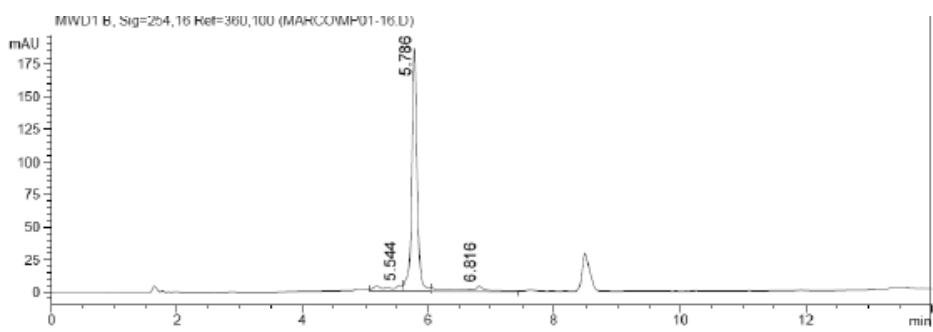
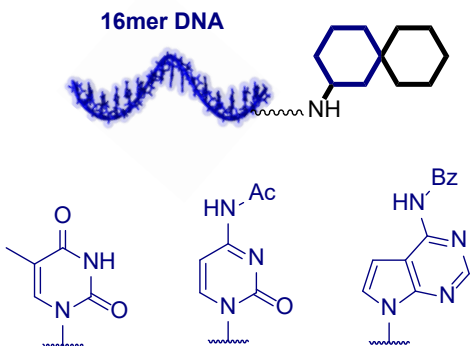
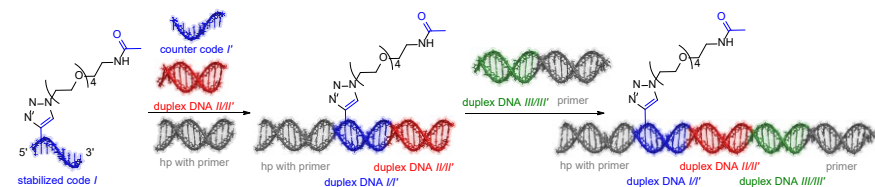
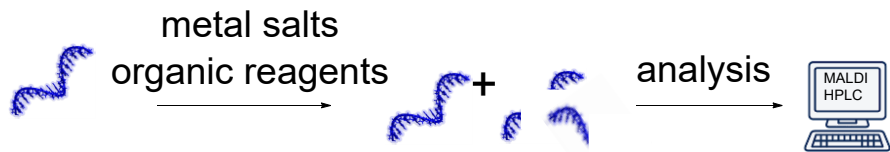
Franck Da Silva,<sup>1</sup> Guillaume Bret,<sup>2</sup> Leandro Teixeira,<sup>3</sup> Claudio F. Gonzalez,<sup>3</sup> and Didier Rognan<sup>4,5</sup>

*“almost no overlap in property space between PPI and „druggable“ pockets“*

## 1. Machine-learning approaches for screening library design?



# Chemically stabilized DNA



after treatment with 10 % TFA

## 7-deazaA-DNA

chemically stable to protic acids and to many Lewis acids  
 ligatable, amplifiable, readable code for DEL  
 → *expanding chemical reaction space for DEL*

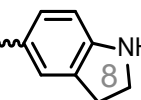
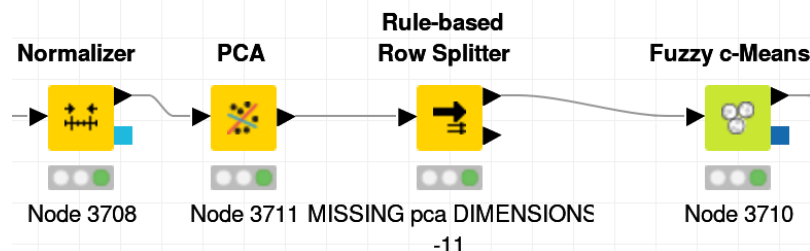
A barcode with enhanced chemical stability

→ **2. Selection of reactions from vast chemistry databases?**

→ Application of data science tools

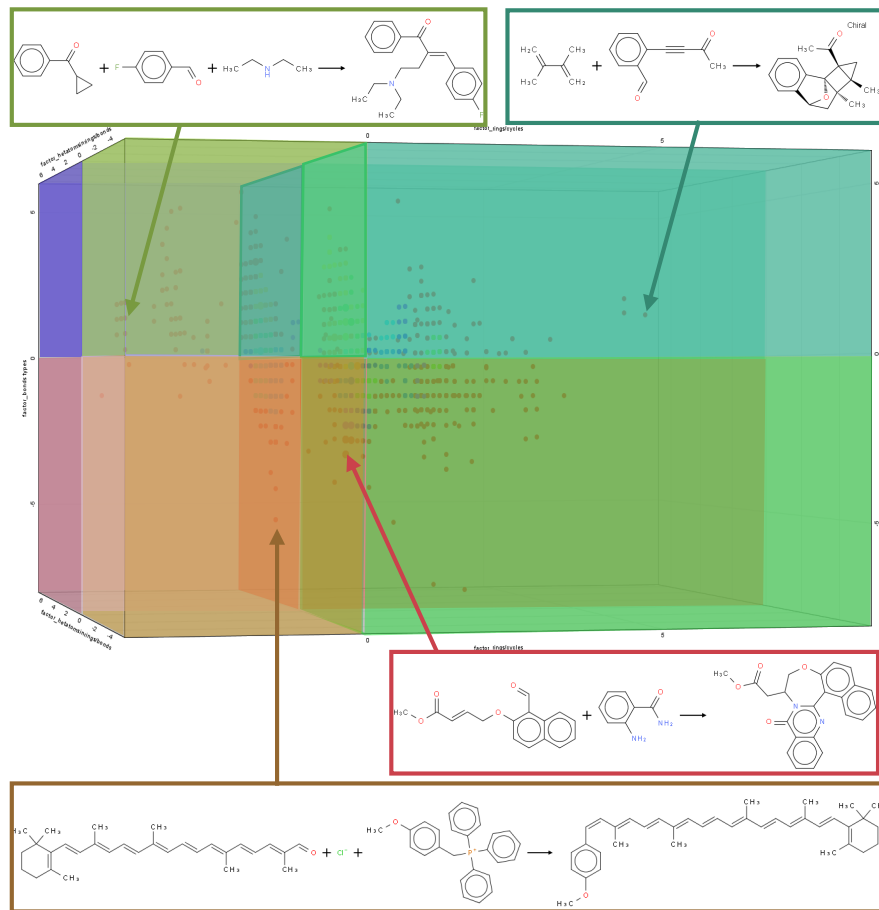
→ Navigate chemical reaction space

100k reactions





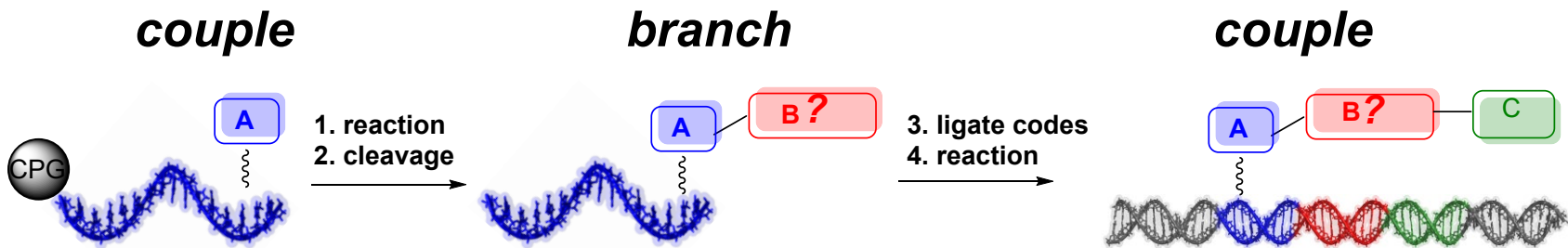
# Navigate chemical reaction space



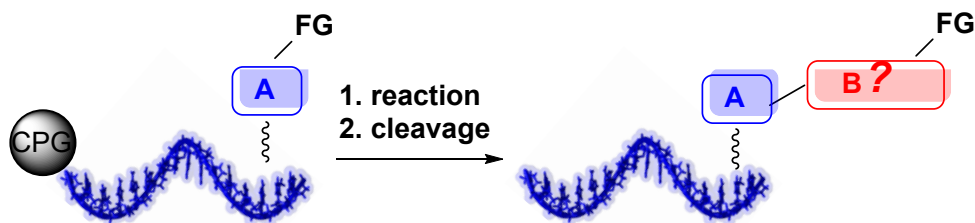
Comprehensive chemistry databases are commercial.

## 3. Access to chemistry data, e.g. from patents?

# DEL design



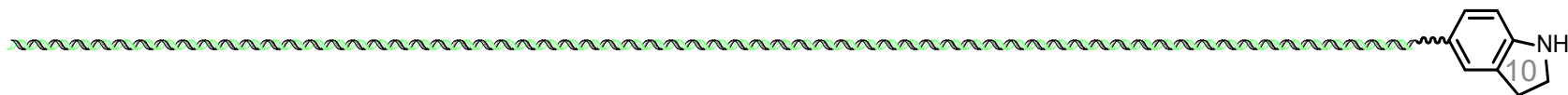
*branch*: key step - structural diversity from reactions



- aim: DELs w. 1 mio compounds
- bifunctional starting materials
- diverse chemistries

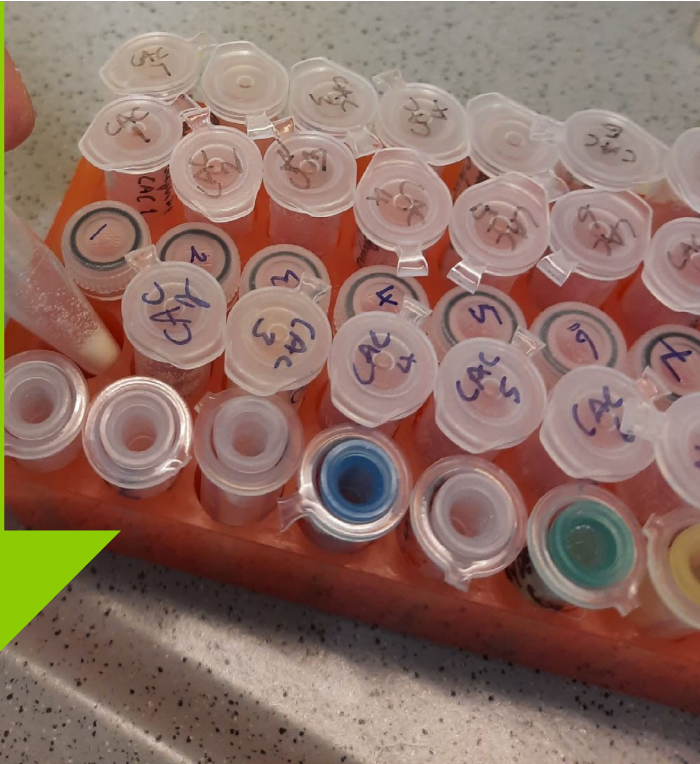
## on-DNA reactions:

|              |                               |
|--------------|-------------------------------|
| Klika Škopić | Chem. Sci. 2017               |
| Klika Škopić | Org. Biomol. Chem. 2017       |
| Potowski     | Chem. Sci. 2019               |
| Kunig        | Org. Lett. 2019               |
| Potowski     | Bioorg. Med. Chem. Lett. 2020 |
| Klika Škopić | J. Am. Chem. Soc. 2019        |
| Kunig        | Angew. Chem. Int. Ed. 2020    |
| Potowski     | Org. Lett. 2021               |
| Potowski     | Angew. Chem. Int. Ed. 2021    |
| Klika Škopić | Org. Lett. 2022               |



# A glimpse into the lab

**DNA  
and  
Building  
Block  
in one  
row**



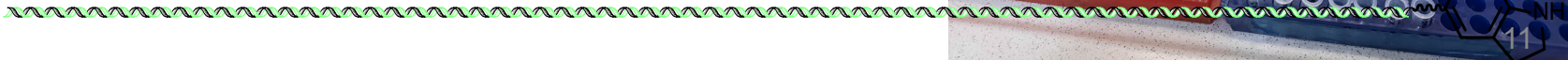
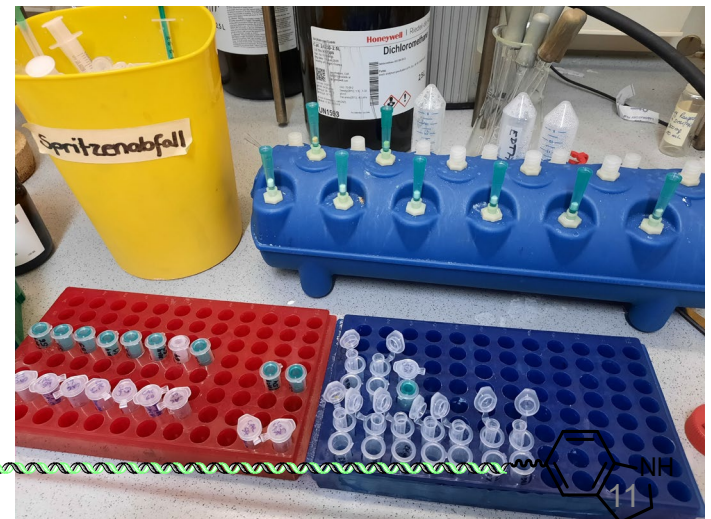
*Reaction solution*

*DNA*

*Carboxylic Acid*

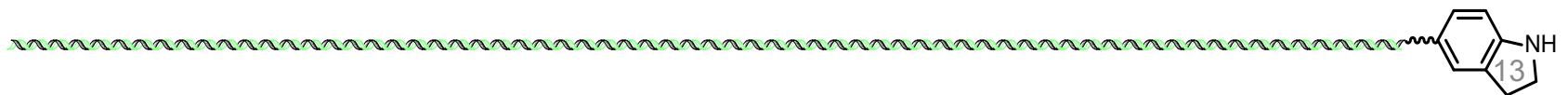
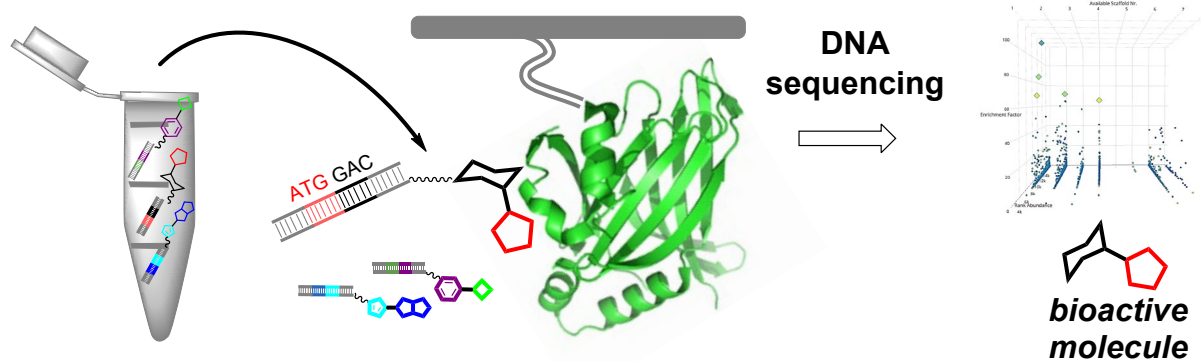
*DNA-wash-column*

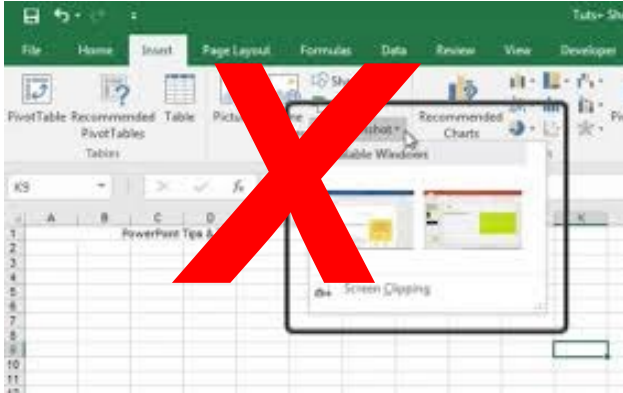
Wash columns and  
rack:  
Same positioning of  
samples!



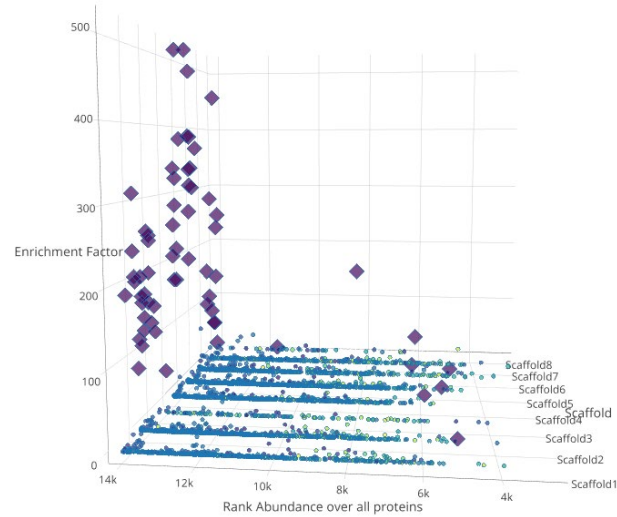


# From DEL synthesis to compound identification



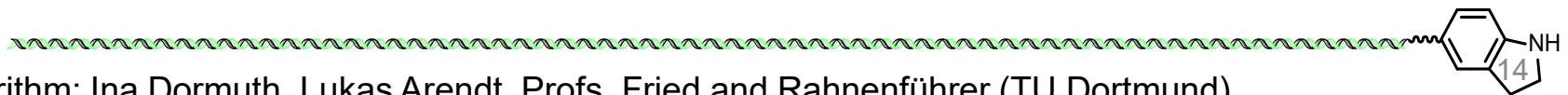


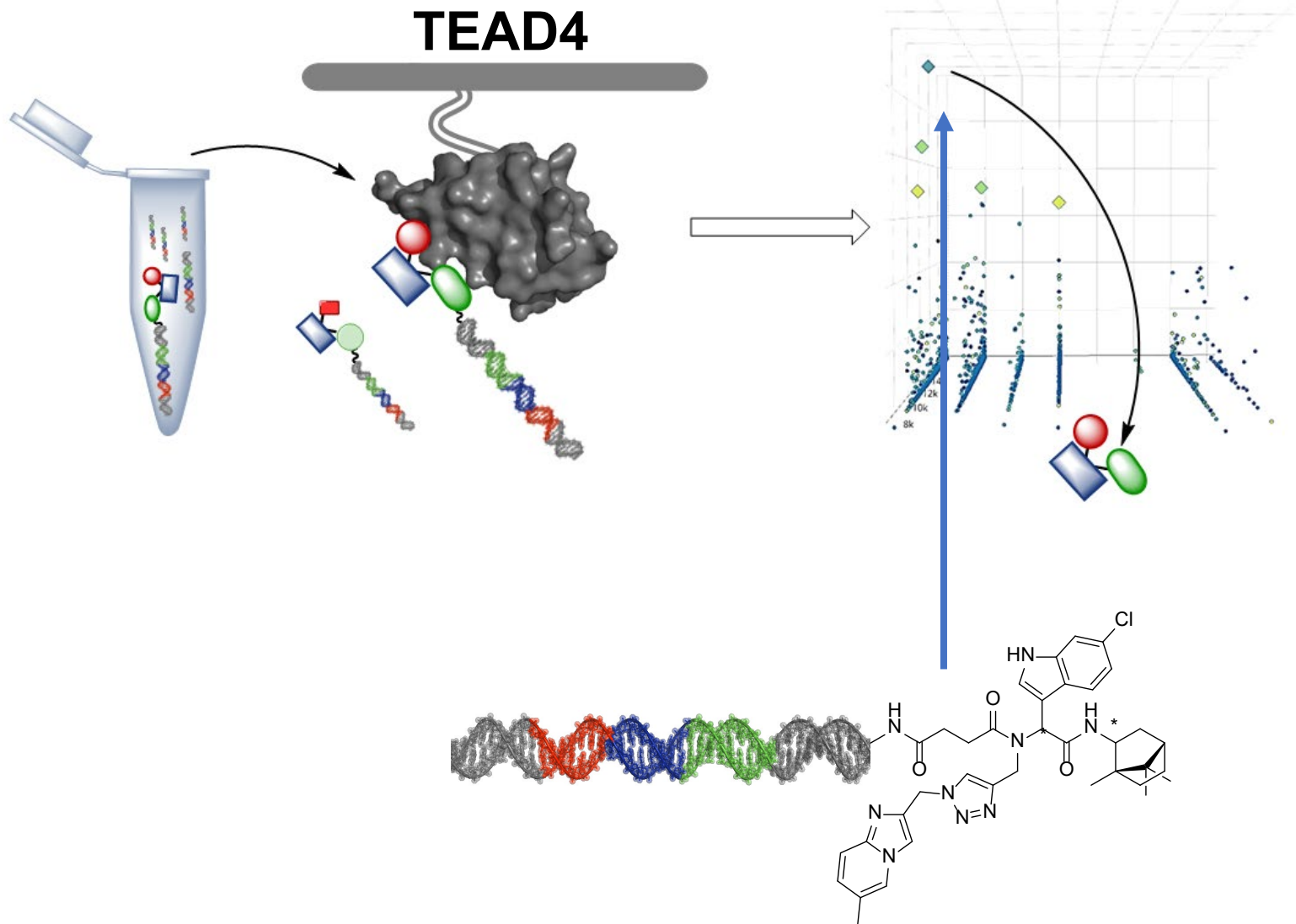
## manual analysis



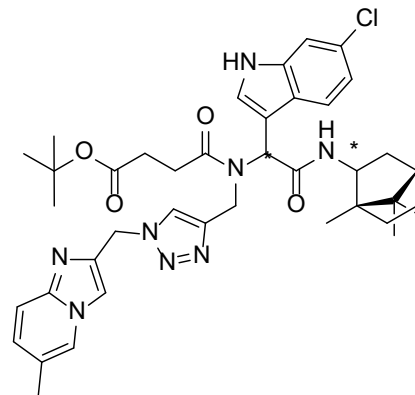
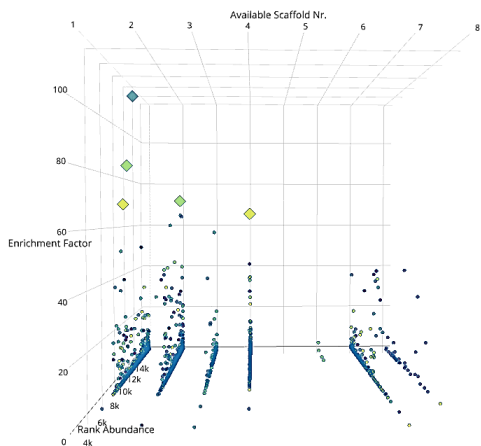
## enrichment factor analysis

- barcode PCR encodes selection experiments
- algorithm calculates enrichment factors
- accounts for differences in individual DNA amplification efficiency

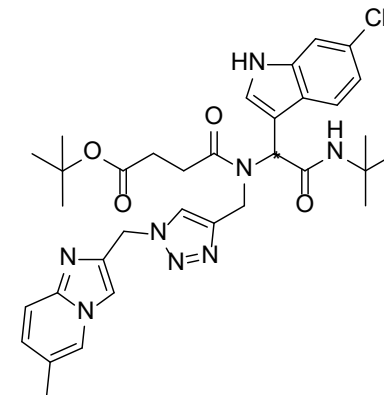




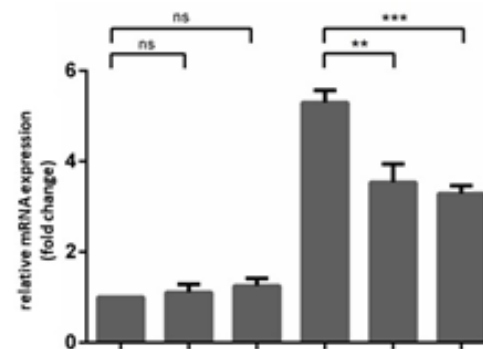
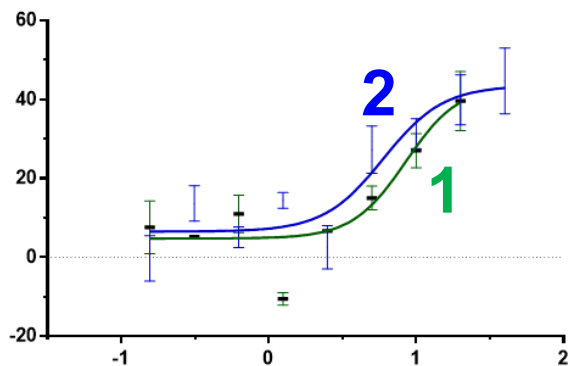
## 5. Machine learning for compound identification?



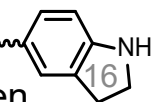
1 (VK57)



2 (VK67)



w/o Hippo-I    w Hippo-I

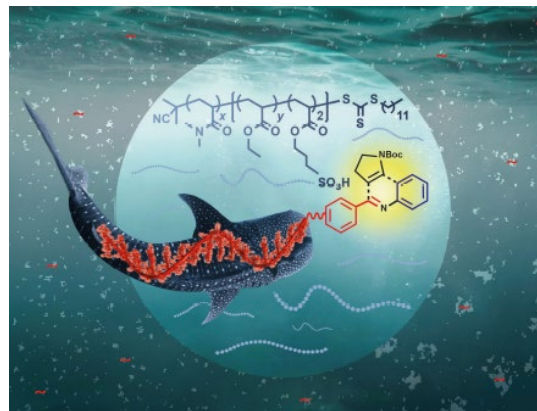
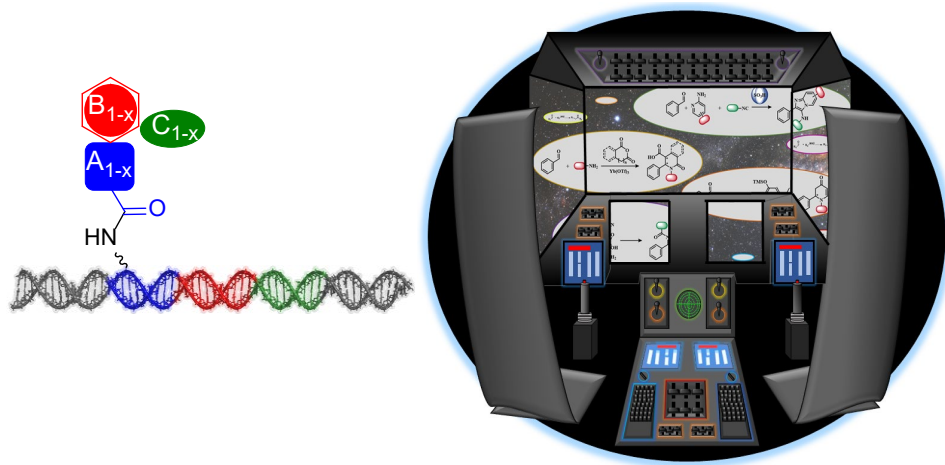




# Data science impacts...

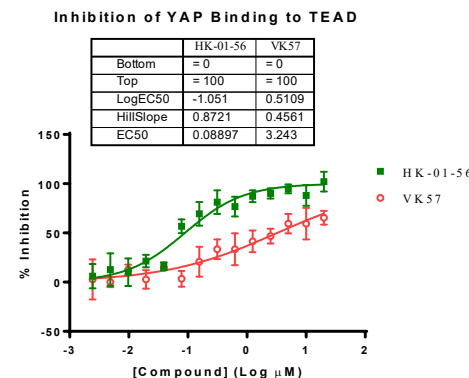
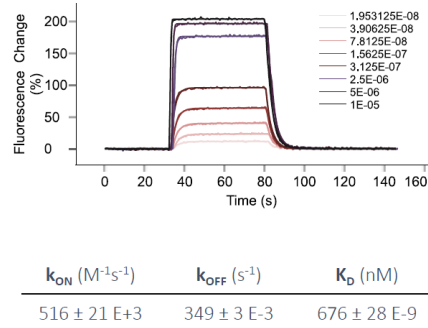
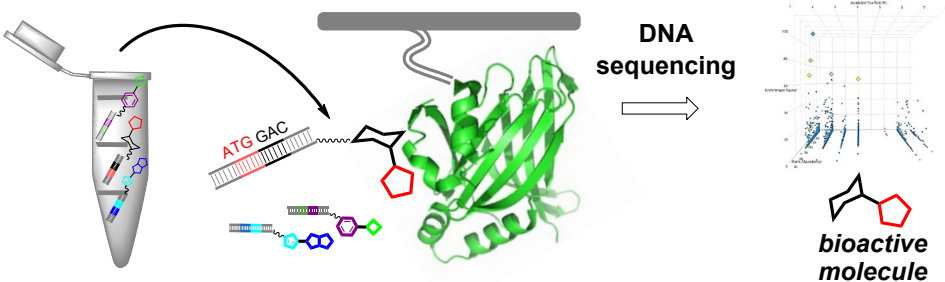
encoded library **design**

reactivity prediction of chemicals

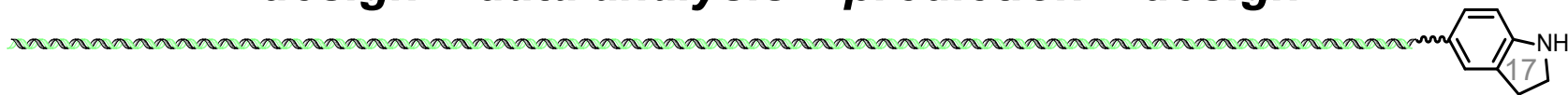


DEL screening data analysis

inhibitor validation and development



**design – data analysis – prediction – design**



*The DEL-Team*

Silvia Chines  
Katharina Götte  
Mateja Klika Škopić  
Verena Kunig  
Marco Potowski  
Avinash Bhat  
Suzanne Willems



*Faculty*

Prof. Rauh  
Prof. Waldmann

*Chemistry*

Prof. Weberskirch, TU Do  
Prof. Kockmann, TU Do  
Prof. Dömling, U. Groningen  
Prof. Bode, ETH Zürich  
Prof. Waring, Newcastle  
Dr. Vakalopoulos, Bayer  
Prof. Fogg, U. Ottawa



für Bildung  
und Forschung



Mercator Research Center Ruhr  
Eine Initiative der Stiftung Mercator  
und der Universitätsallianz Ruhr



Boehringer Ingelheim  
Stiftung



*Analysis of sequencing data*

Ina Dormuth and Lukas Arendt  
Prof. Rahnenführer, TU Do  
Prof. Fried, TU Do

*TEAD assays*

Hélène Adhiou, MPI Do  
Hacer Karatas, MPI Do  
Mahyar Akbarzadeh, MPI Do  
Blaz Andlovic, TU Eindhoven

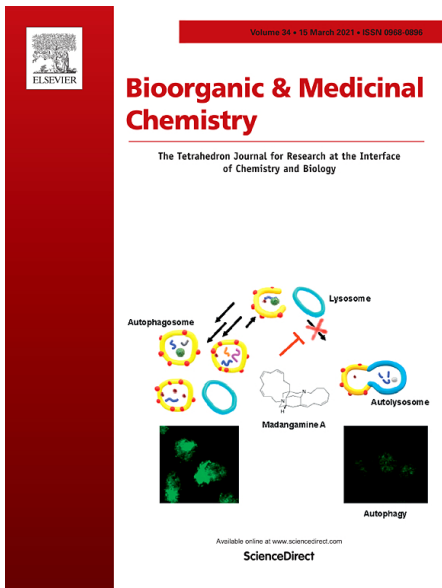
*DNA synthesis*

Lukas Stratmann, TU Do  
Prof. Clever, TU Do

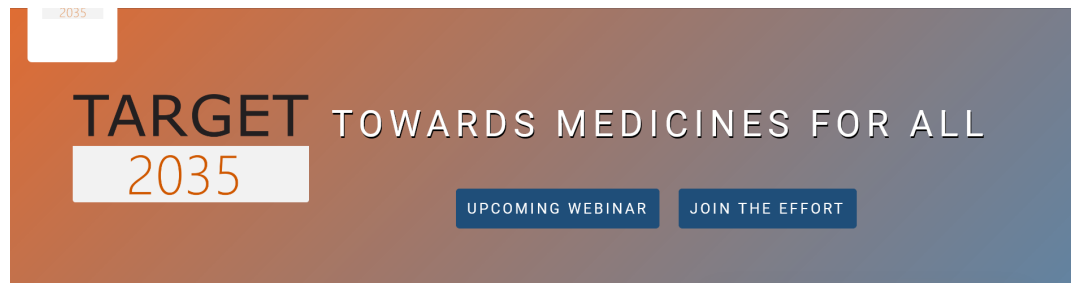
*DEL design, TEAD-I design*

Dr. Christiane Ehrt, HHU  
Julia Jasper  
Lukas Eberlein  
Prof. Kast, TU Do

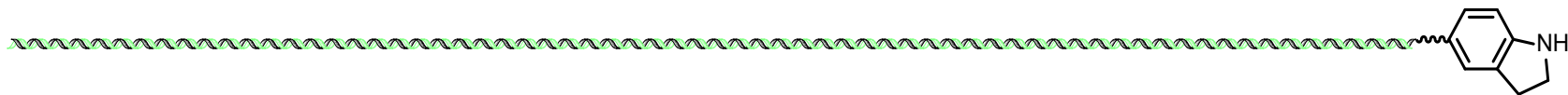
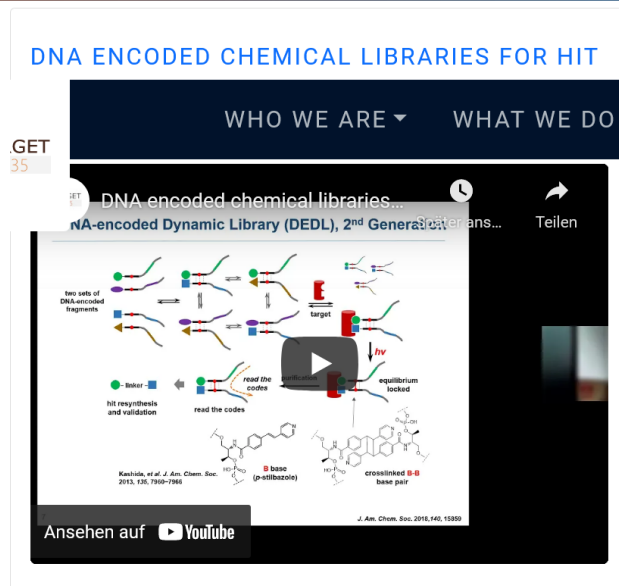
# spreading the message



Special Issue on DELs



Volume on DELs  
w. Prof. Damian Young  
Houston



# Thank you!