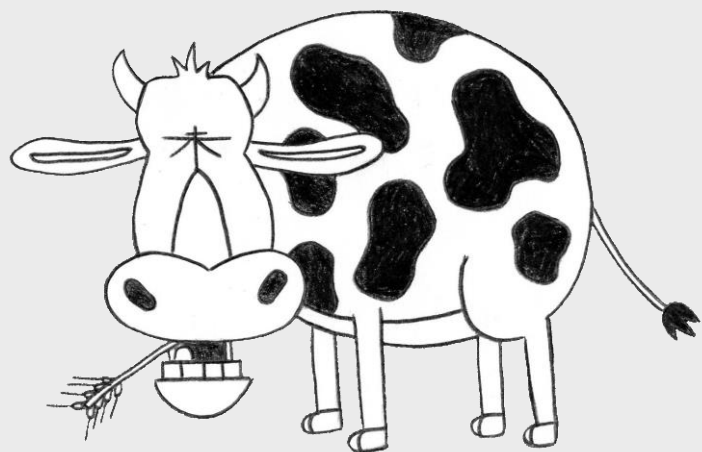


# Early Stages of Drug Discovery in the Pharmaceutical Industry

Daniel Seeliger / Jan Kriegl, Discovery Research,  
Boehringer Ingelheim  
September 29, 2016

# Historical Drug Discovery

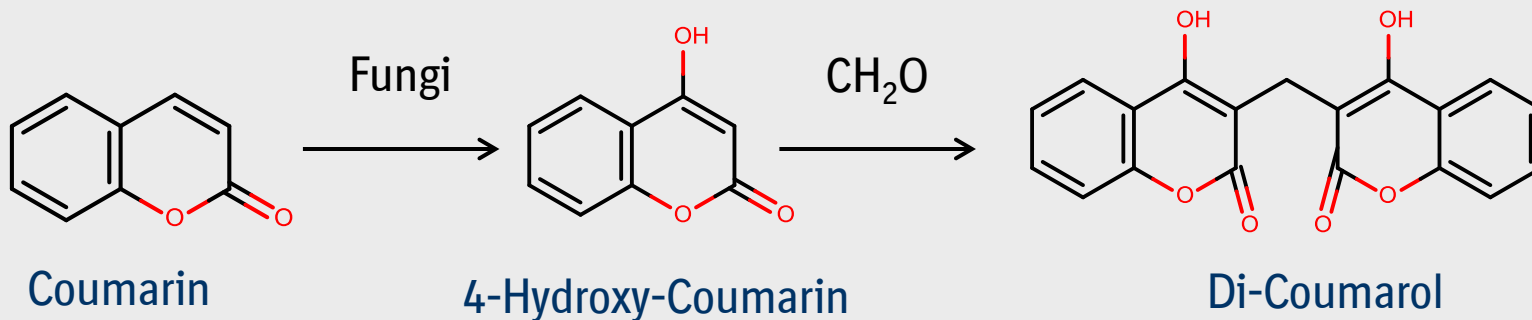
## From Accidental Discovery to a Drug



Cattle, 1920s, North Dakota



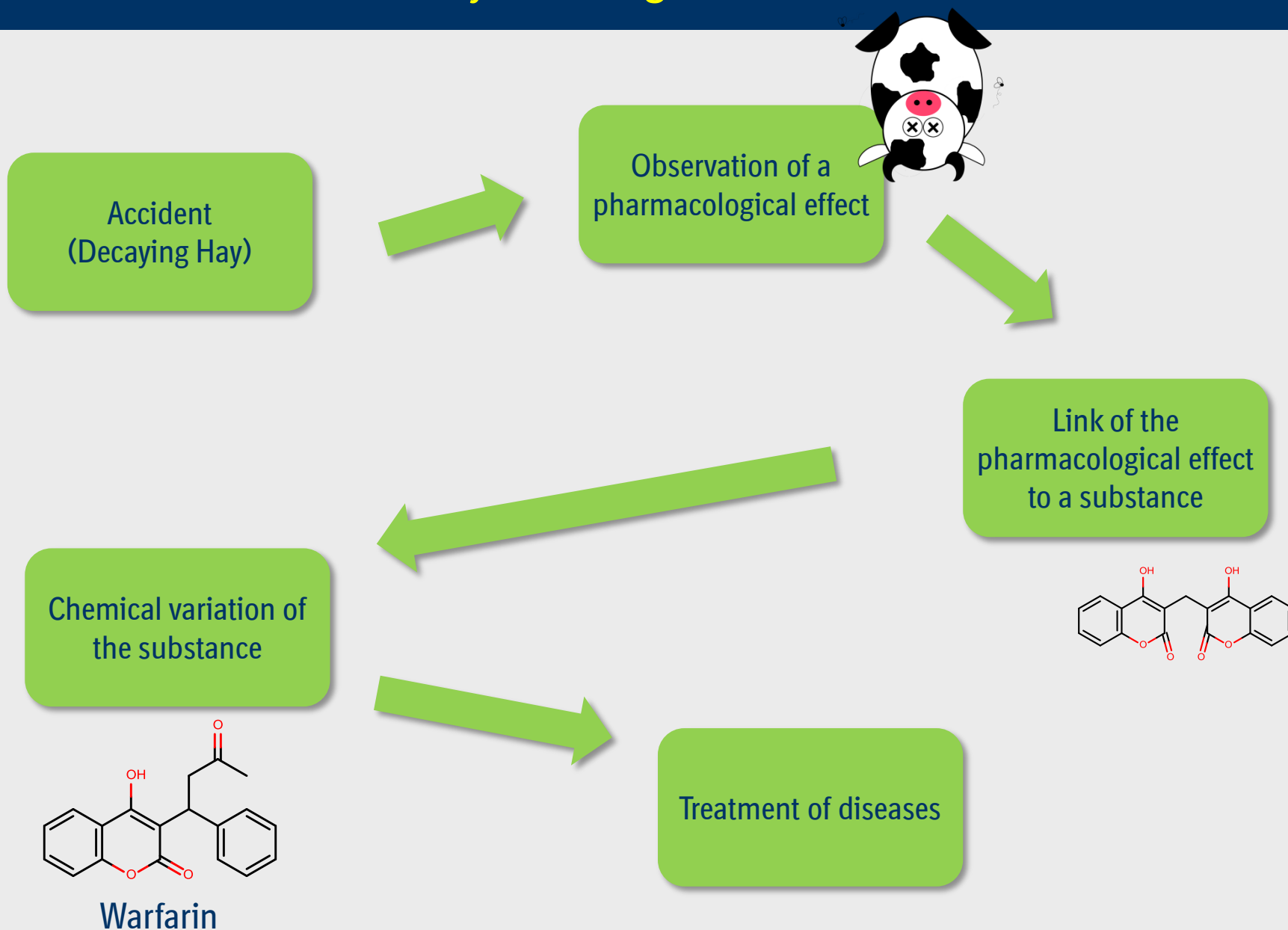
Dead Cattle, 1920s, North Dakota



Strong anti-coagulant

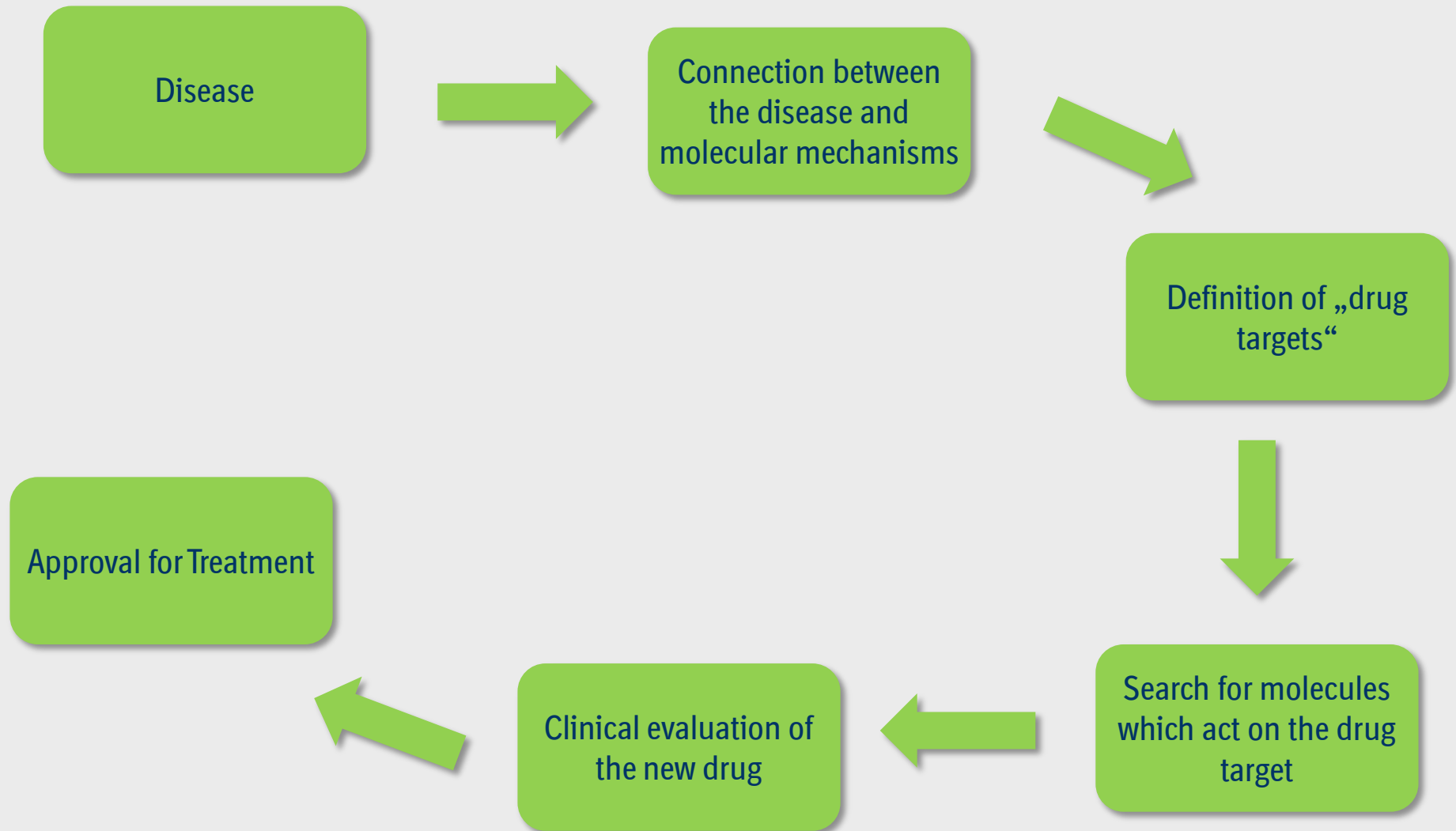
# Historical Drug Discovery

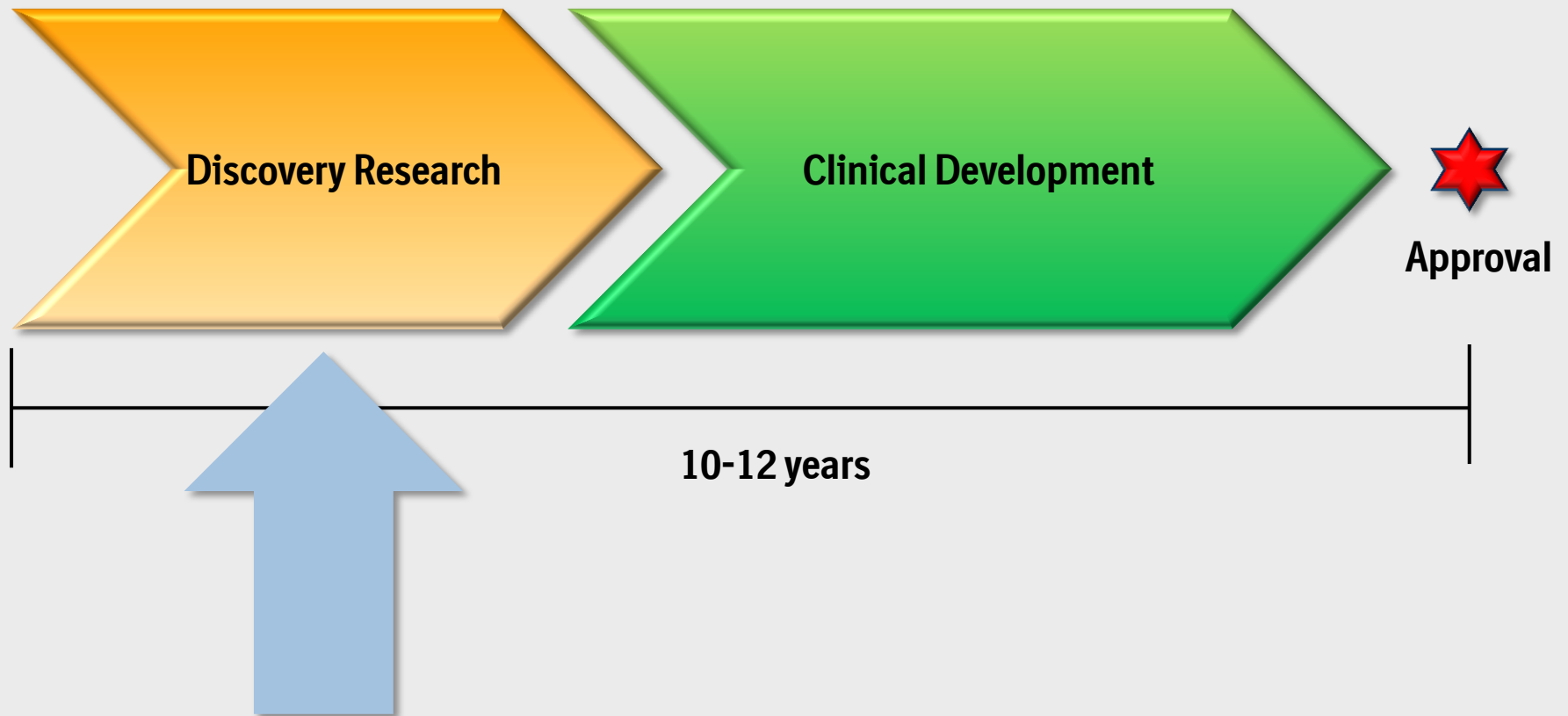
## From Accidental Discovery to a Drug

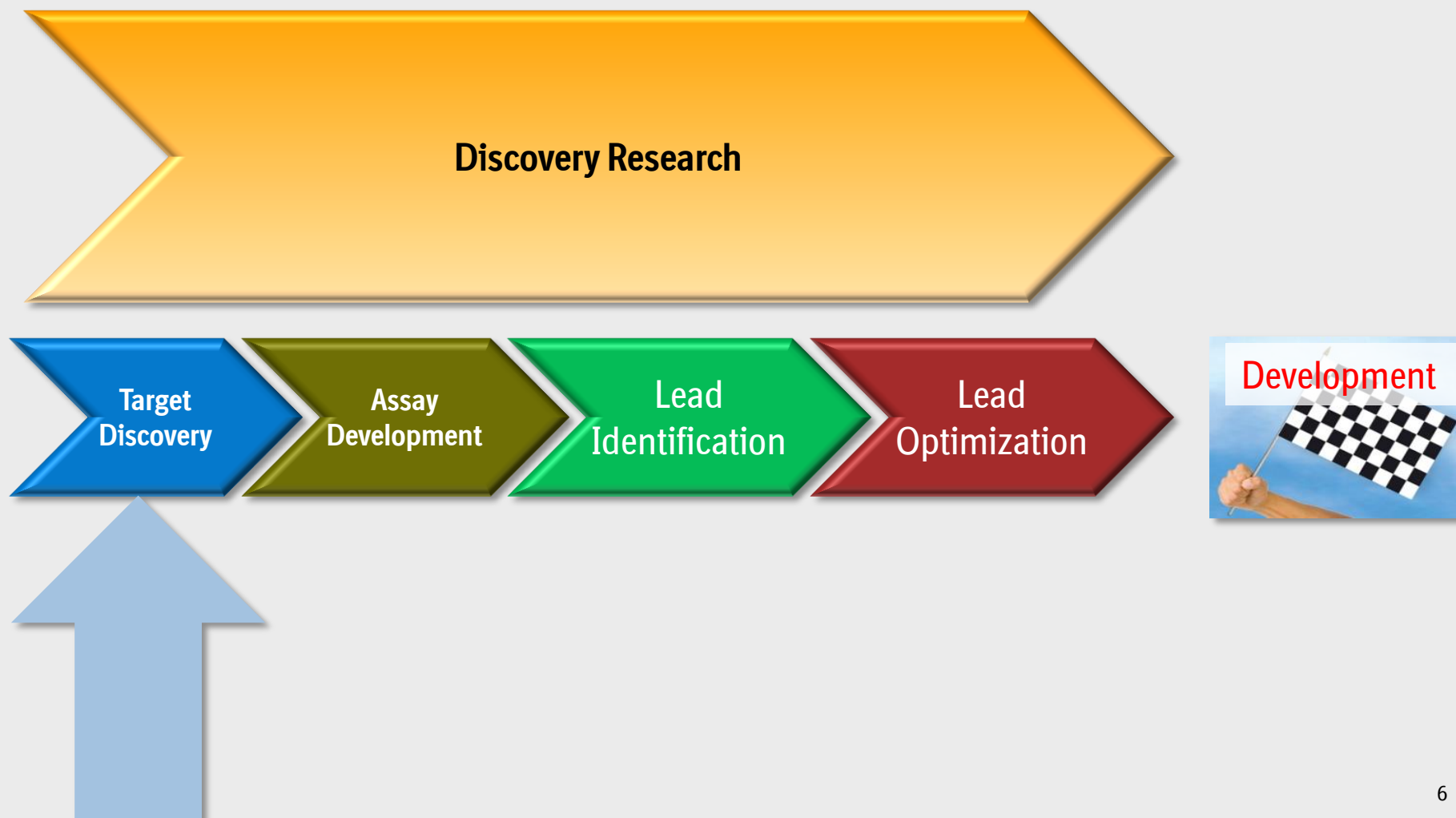


# Modern Drug Discovery

## From the Disease to the Drug

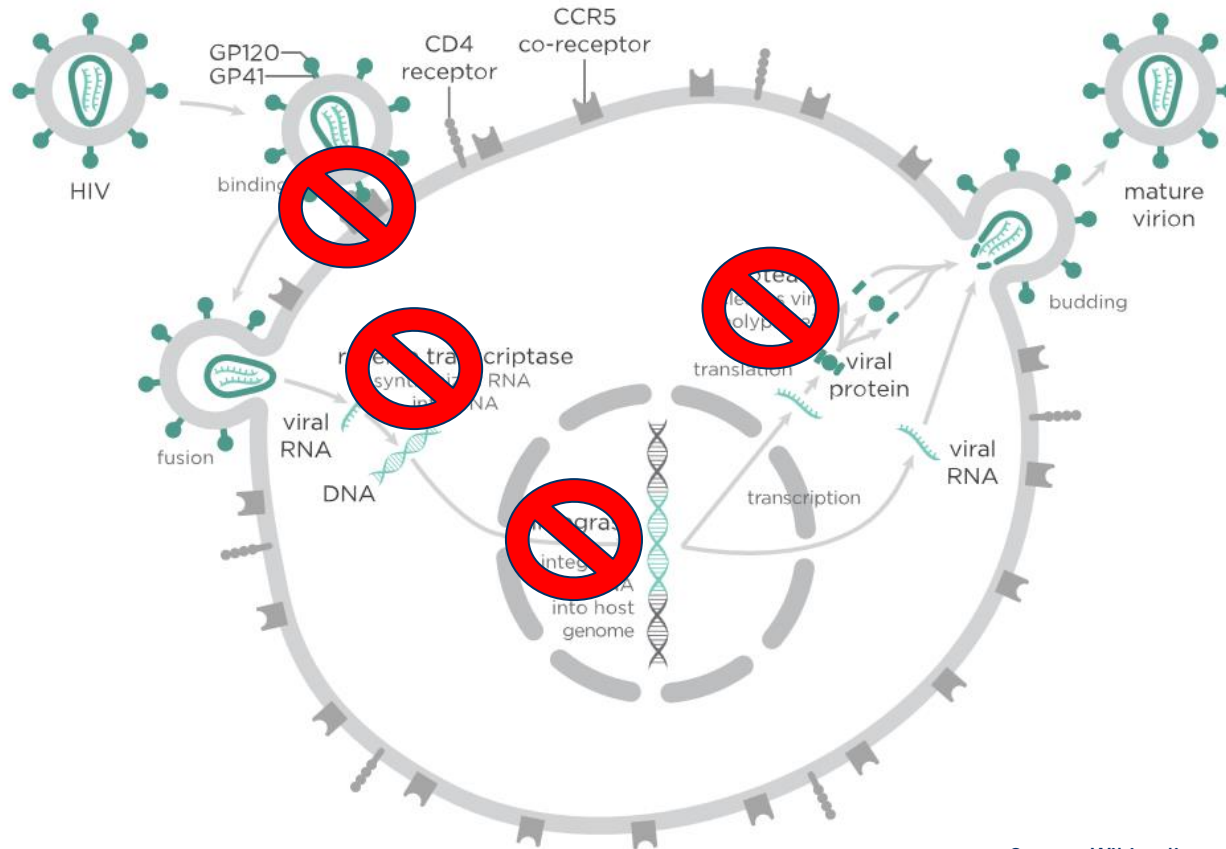




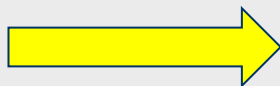


# What are Drug Targets?

## The Life Cycle of the HI Virus



Source: Wikipedia



Blocking a step in the virus life cycle stops viral reproduction

# What are Drug Targets

## The Link between a Target and a Disease

Cleavage of the HIV poly-protein is essential for viral reproduction.

Understand the biology of the disease

Inhibition of the catalytic mechanism will prevent viral reproduction.

Propose drug target

Lower viral reproduction rate will slow down or even halt the progression to AIDS.

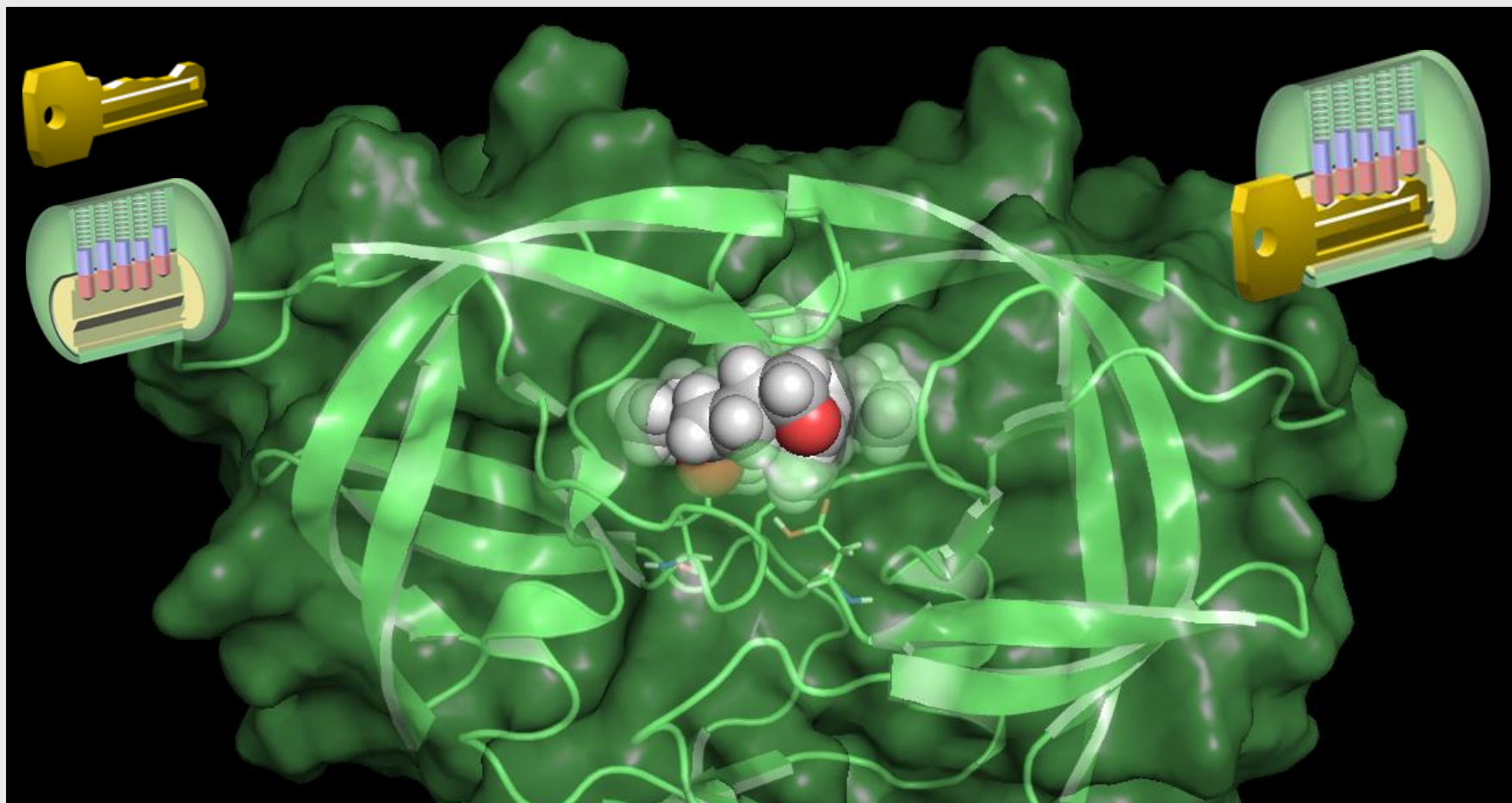
Postulate hypothesis of the link between a drug target and the disease.

Many drug discovery programs fail because the hypothesis about the target/disease link turns out to be wrong!



# Inhibition of Drug Targets

## HIV-1 Protease Inhibitors

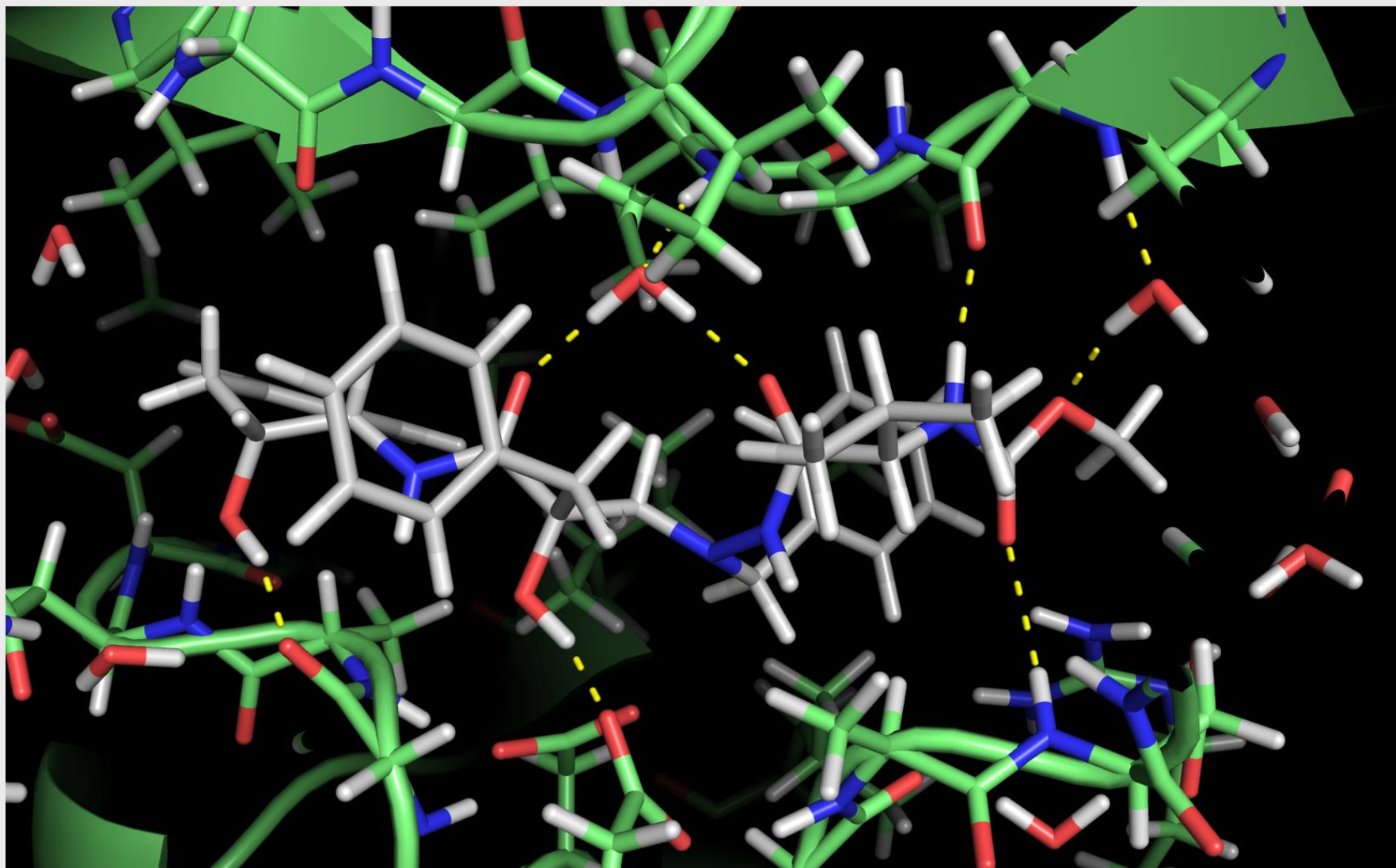


### Inhibitors:

- Bind with high affinity to the active site of the enzyme
- Prevent entry and cleavage of the normal substrate of the enzyme

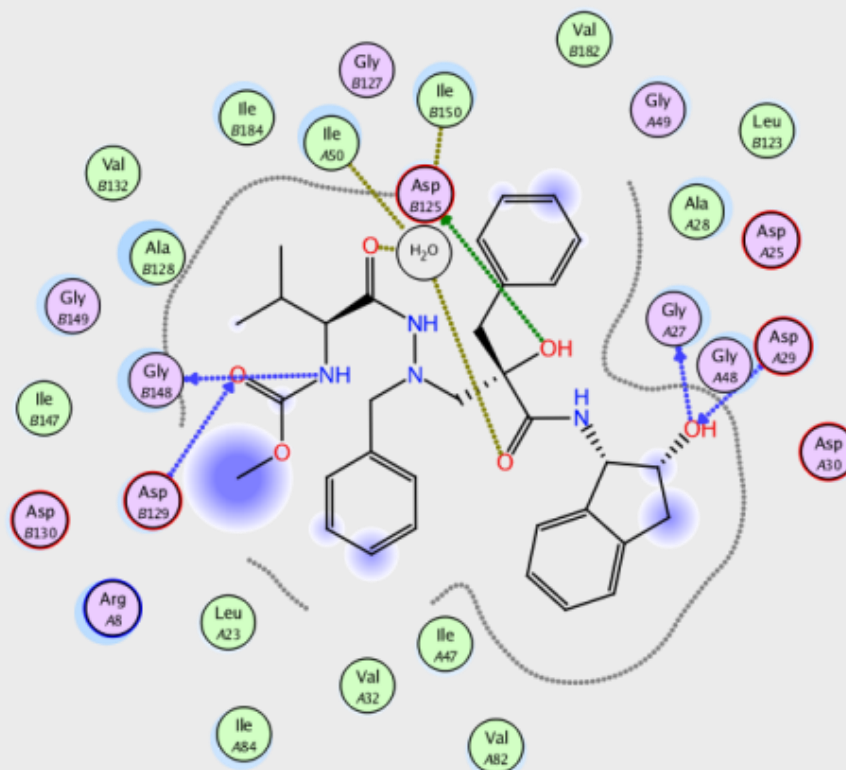
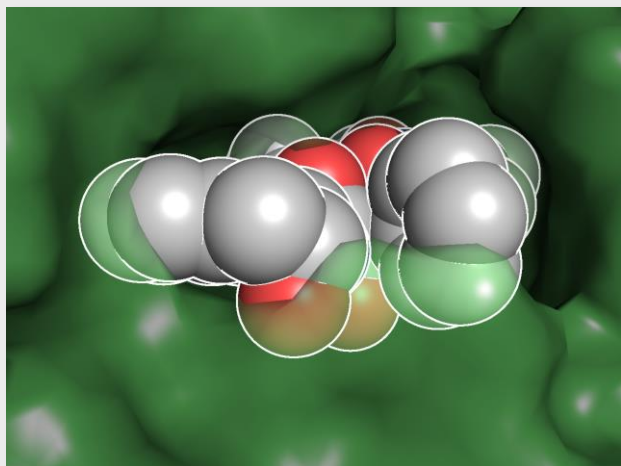
# Inhibition of Drug Targets

## Molecular Interactions



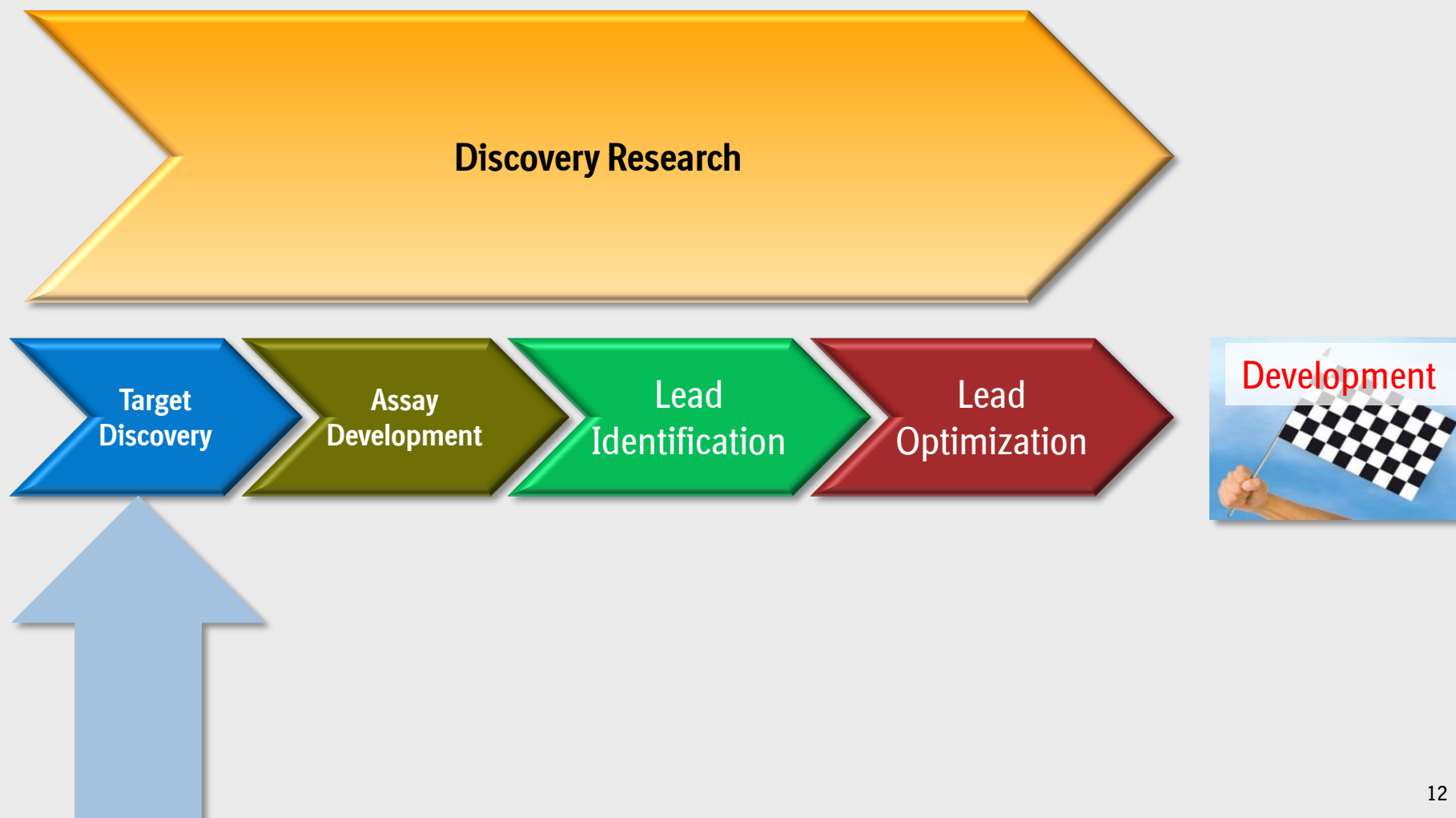
# Inhibition of Drug Targets

## Molecular Interactions



### Principle of Drug Design:

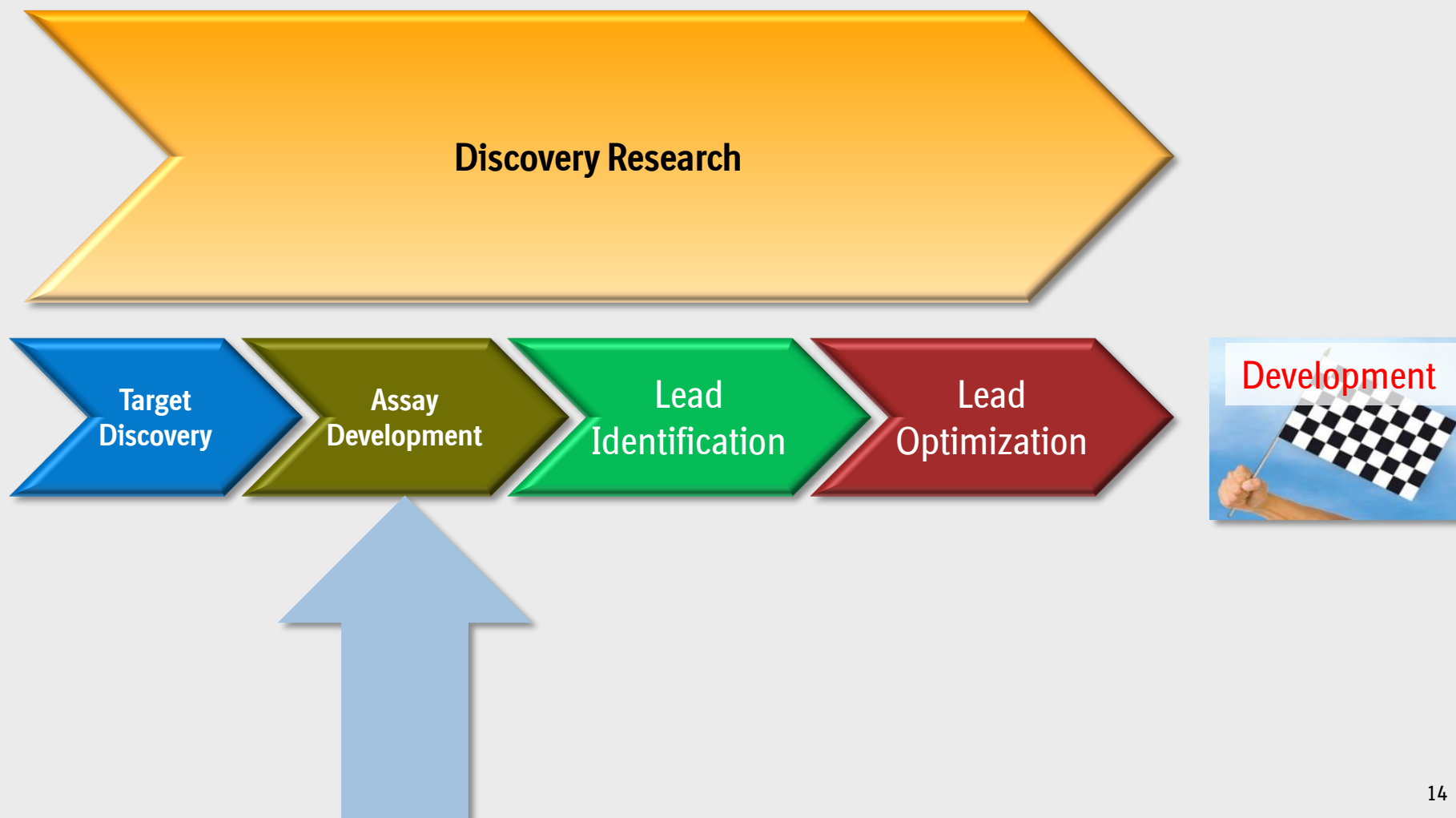
Design molecules which are able to form multiple favorable interactions with the target and which are complementary in shape.



➤ Develop a robust and reliable assay!

- Reproducible results
- Sufficient throughput
- Physiologically relevant

No drug discovery program without reliable assay





# Lead Identification

## High-Throughput Screening

Big pharma companies have large compound collections

- Historically grown over decades of research
- Permanently updated with compounds from vendor catalogs
- Permanently updated through inhouse syntheses (combinatorial chemistry)

Boehringer Ingelheim has ~ **2 000 000** compounds registered in the central database

Boehringer Ingelheim's large screening pool currently contains ~ **850 000** compounds.

# Lead Identification

## High-Throughput Screening



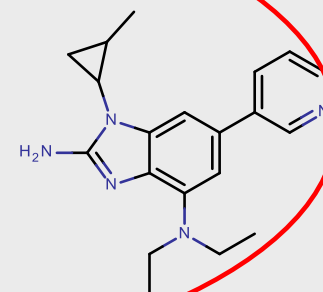
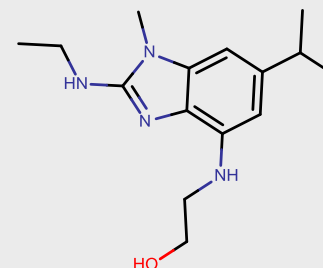
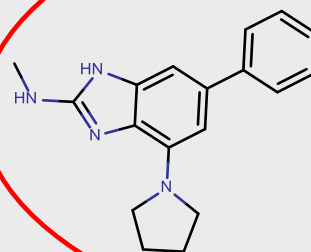
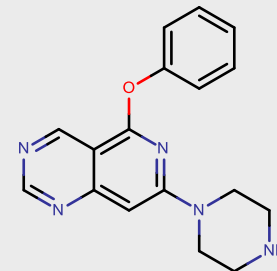
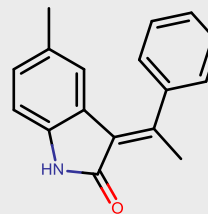
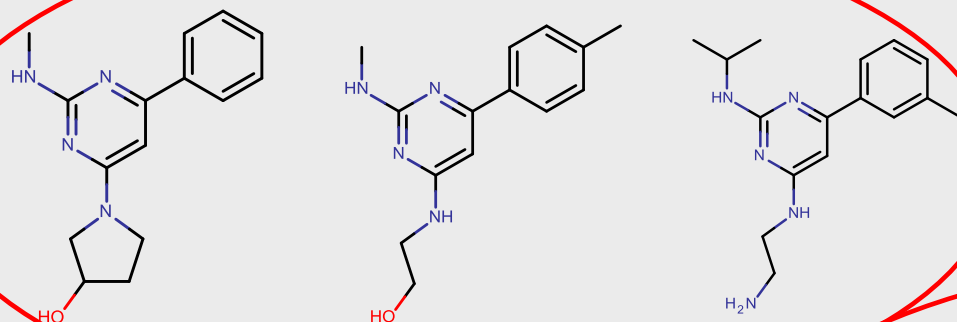
Throughput ~ 50 000 cpds/day



# Lead Identification

## From Data to Information – HTS Analysis

HTS usually yields several thousand hits

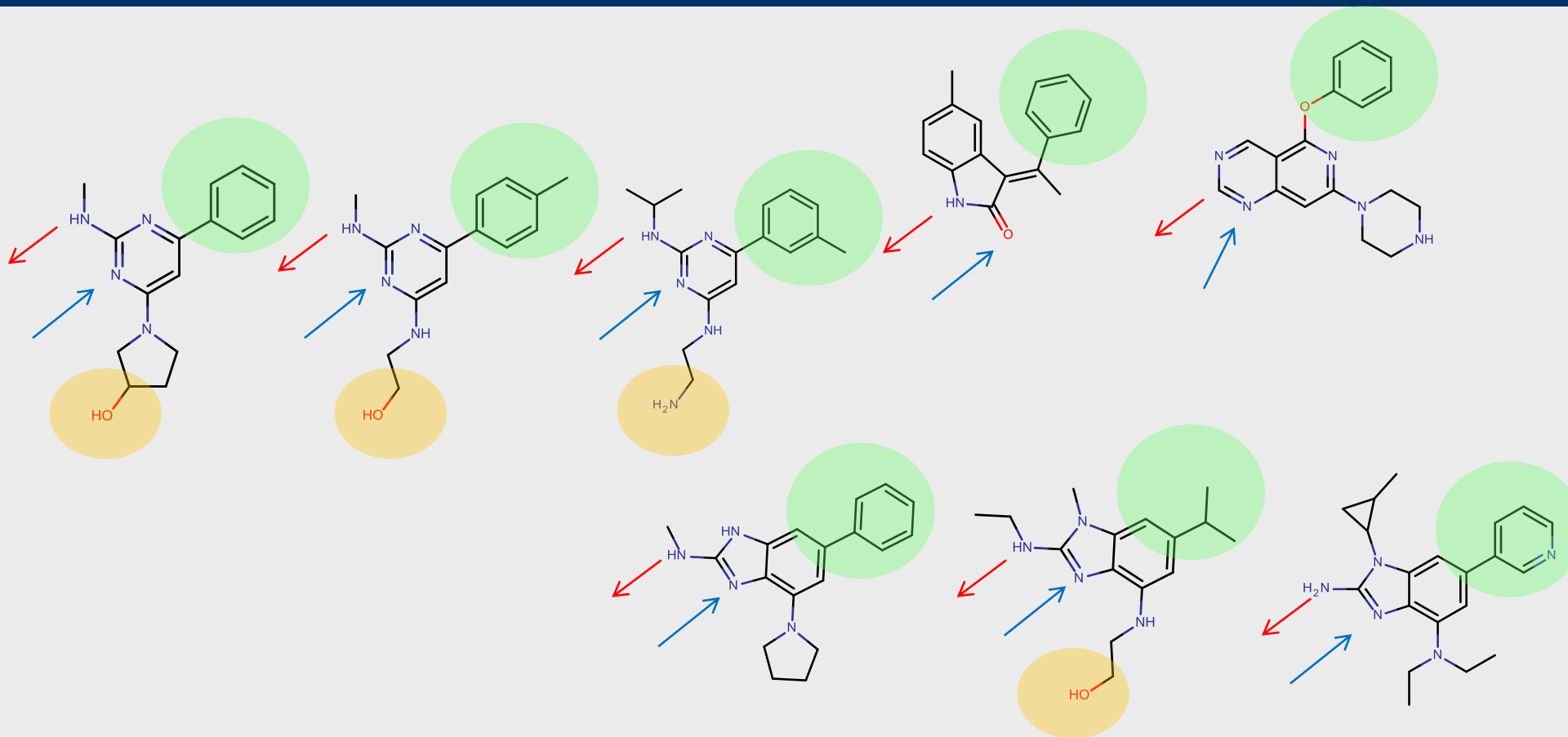


### HTS data analysis:

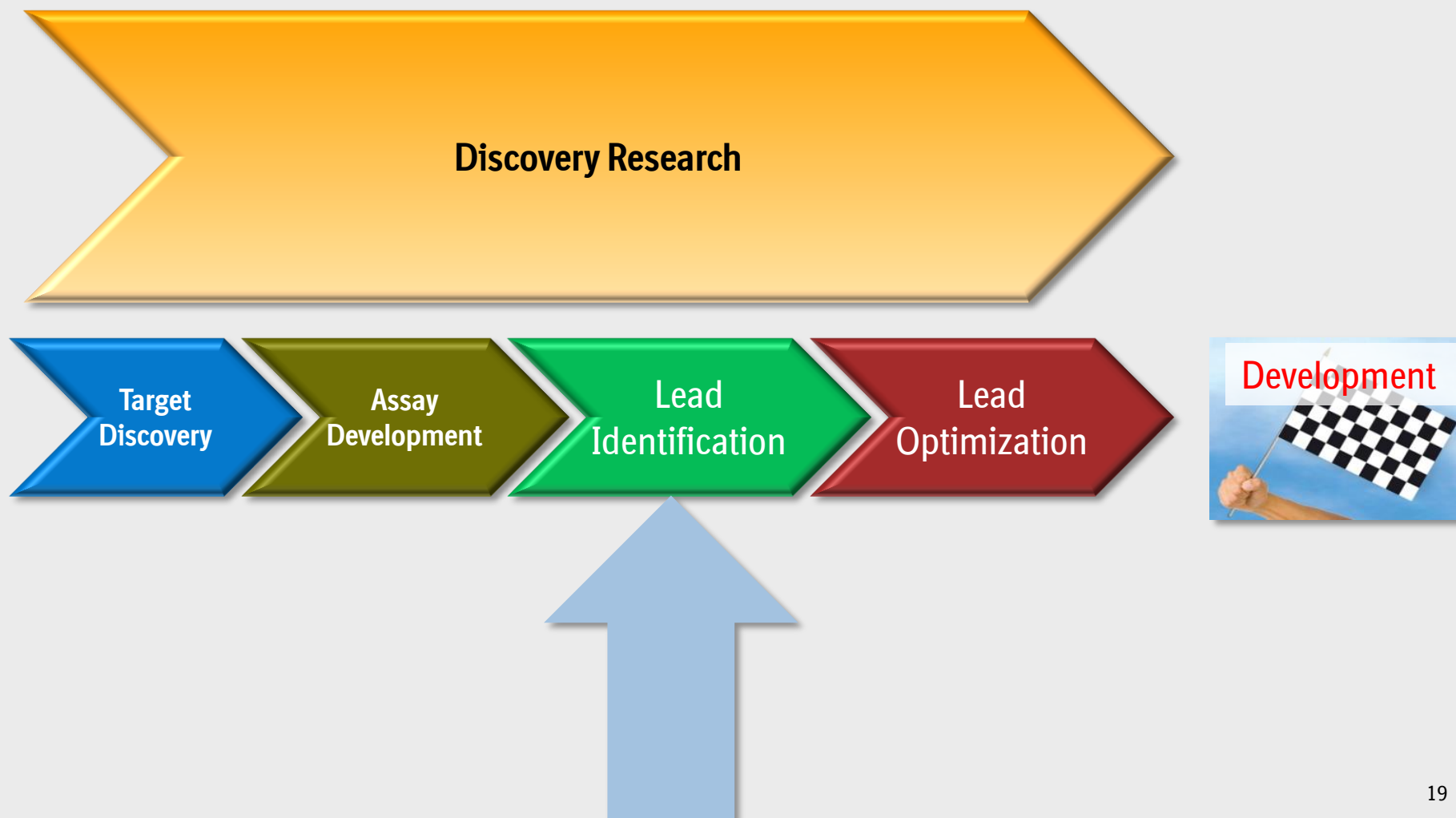
- Clustering of molecules based on chemical similarity
- Identify common patterns among hits (structure-activity relationships, SAR)

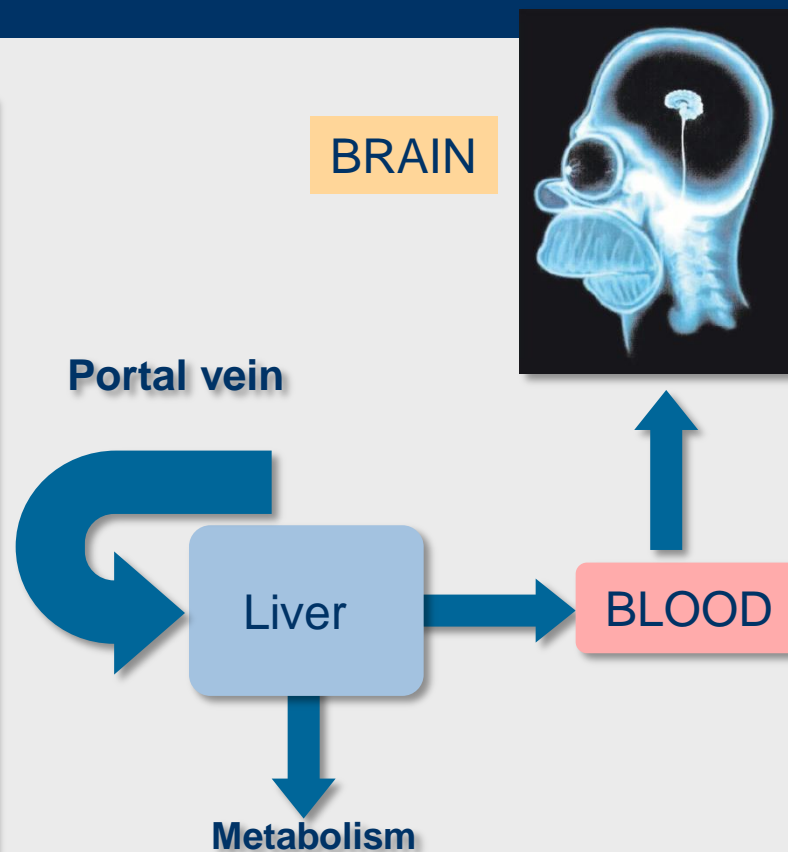
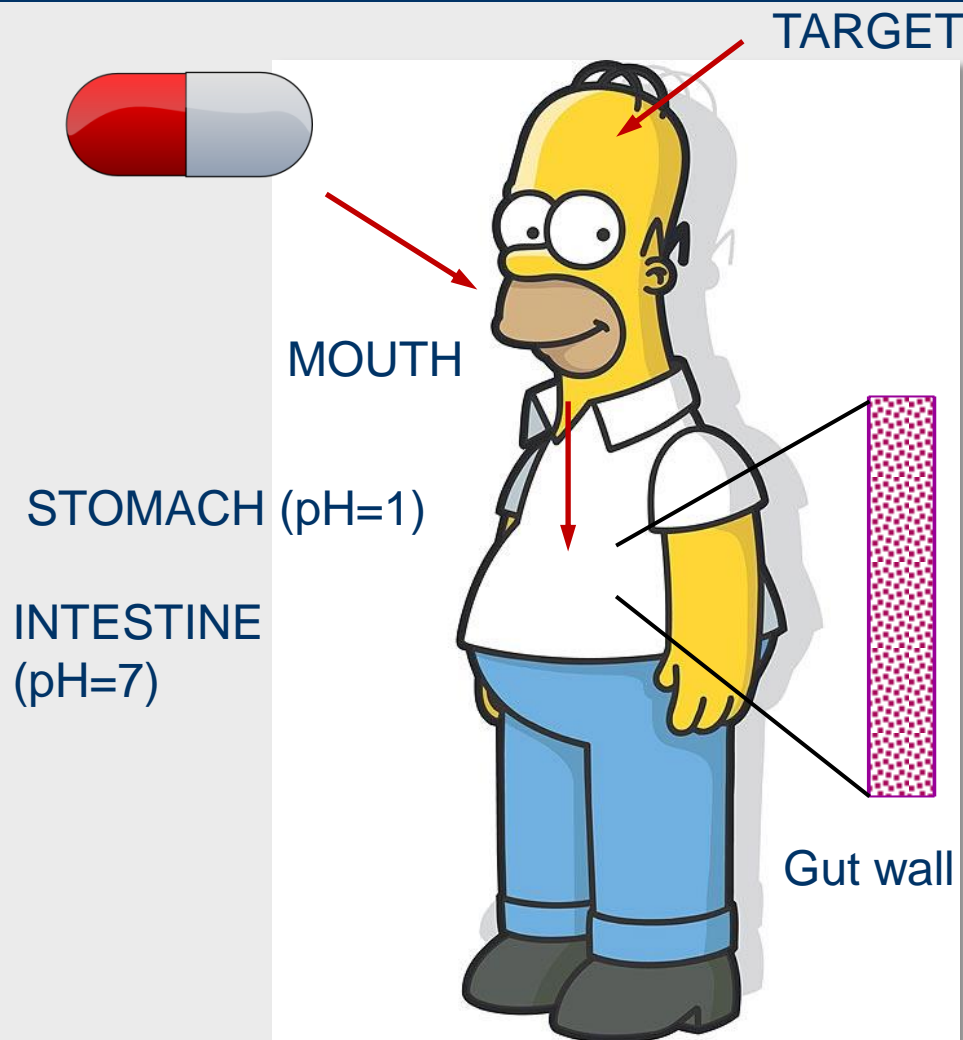
# Lead Identification

## From Data to Information – HTS Analysis



Find Attractive Starting Points for Optimization -> Lead Classes





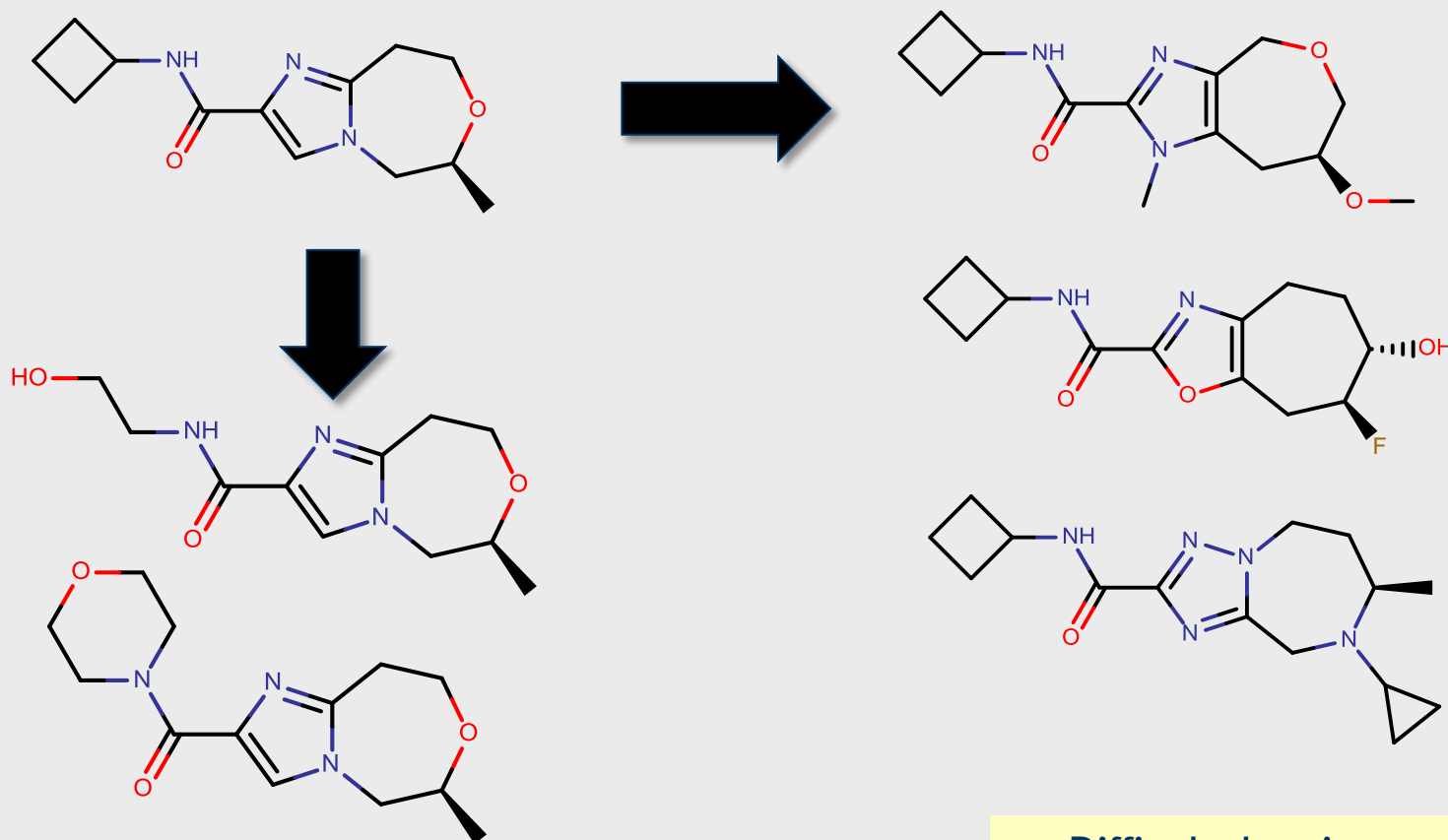
### Drug Design is a Multi-Parameter Optimization

- Potency
- Selectivity
- Bioavailability
- Solubility
- Metabolic Stability
- Plasma Protein Binding
- Cytochrome Inhibition (Drug/Drug Interactions)
- Brain Permeation
- Toxicity
- Pharmacokinetic
- .....

# Lead Optimization

## From a Lead to a Drug Candidate

Lead Optimization essentially means synthesis of close analogs of an active molecule.



- „Easy“ chemistry -> Variation straightforward
- **Cheap!**

- Difficult chemistry
- Different synthetic routes
- **Expensive!**

# Lead Optimization

## Prediction of Molecule Properties

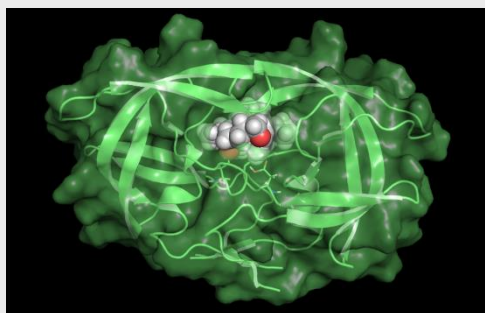
- Synthetic Chemistry can be very expensive ( on average 2000€/molecule)



Make Predictions of Molecule Properties!

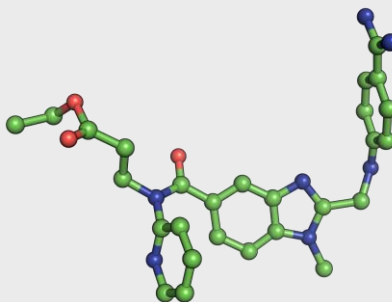
„Predictions are difficult, especially about the future“ (Niels Bohr)

### Structure-based design



- Xray structure(s) required
- Physics-based approaches

### Ligand-based design

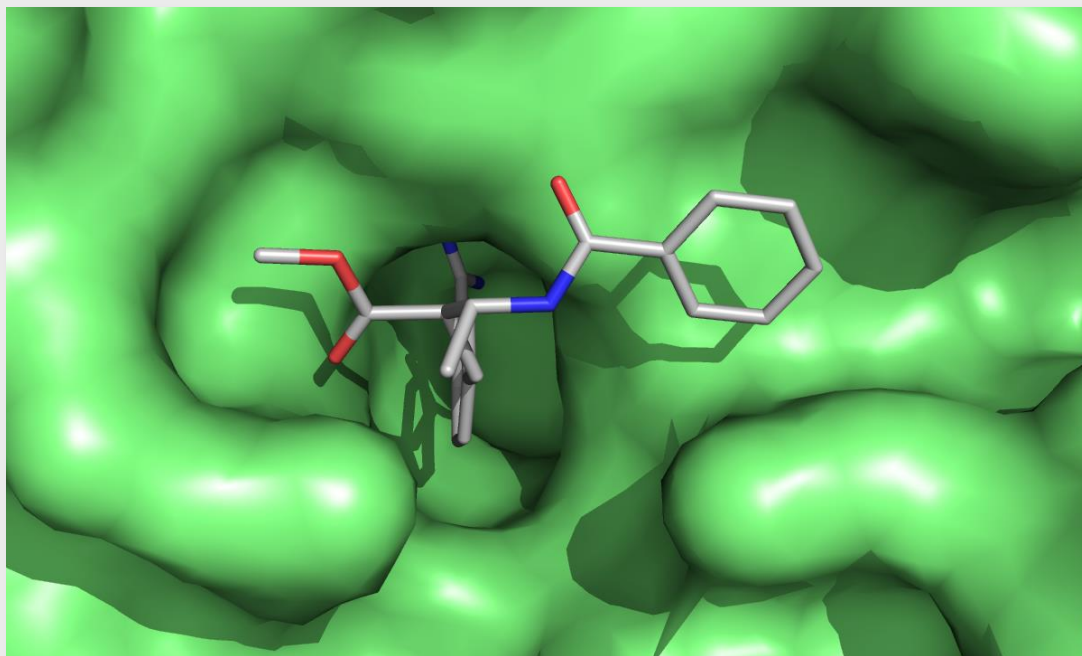


- Known ligand required
- Physics-based approaches
- Chemoinformatics

### Data-driven design



- Lots of data required
- Chemoinformatics
- Machine Learning



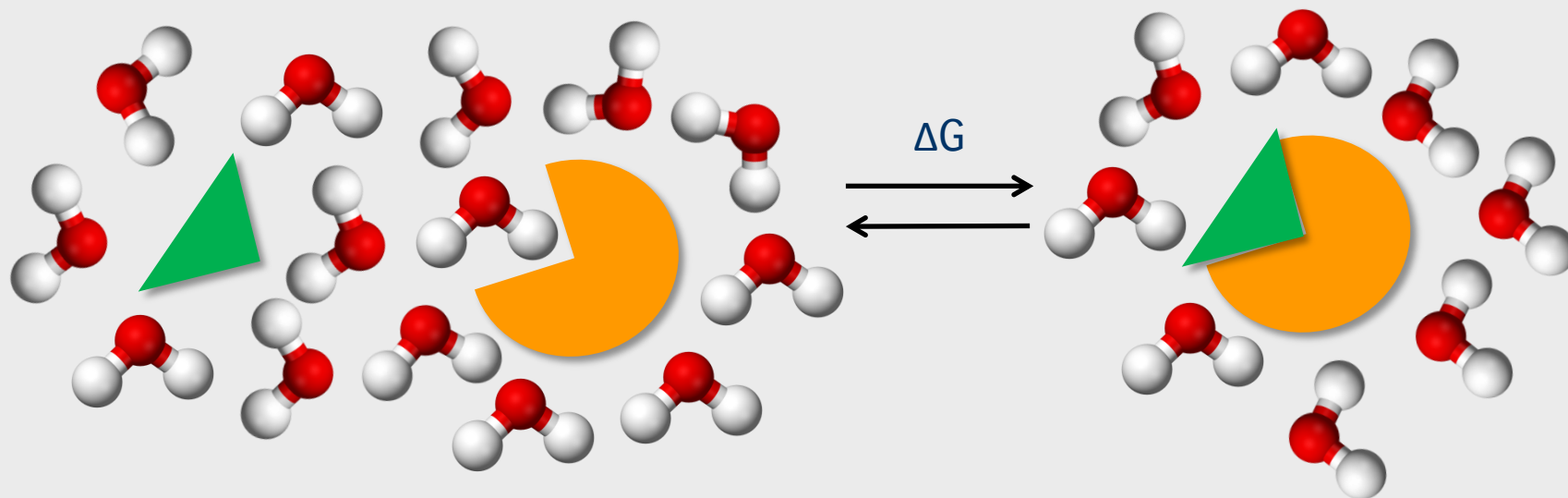
Xray Crystallography is a key technology for potency optimization, but....

Free Energy of Binding is an ensemble property -> Cannot be computed from a single structure



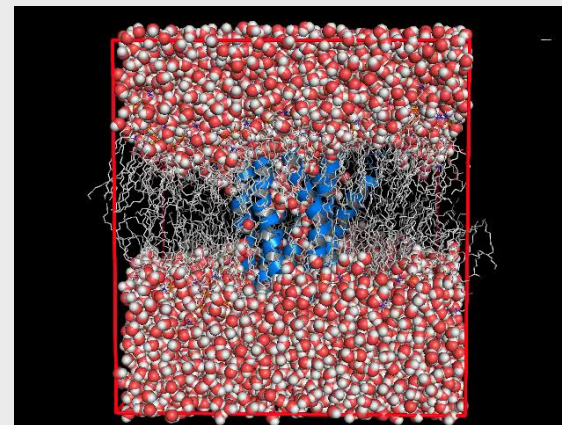
# Lead Optimization

## Computing Binding Free Energies

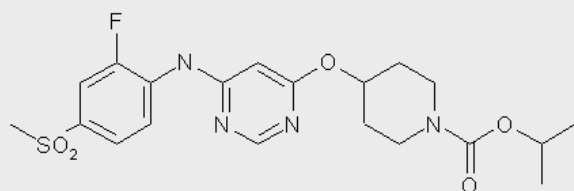


$$\Delta G = -RT \ln \left( \frac{1}{8\pi^2} \frac{C_P C_L}{C_{PL}} \frac{\int e^{-(U(r_{PL})+W(r_{PL}))/RT} dr_{PL}}{\left( \int e^{-(U(r_P)+W(r_P))/RT} dr_P \right) \left( \int e^{-(U(r_L)+W(r_L))/RT} dr_L \right)} \right)$$

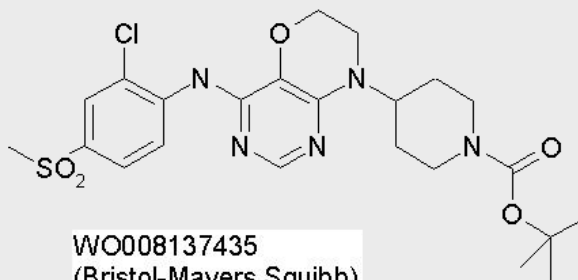
- Molecular Dynamics Simulations
- Alchemical Free-Energy calculations



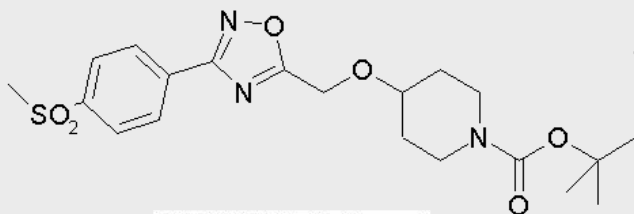
Activity of a molecule against a target is determined by their 3-dimensional structure



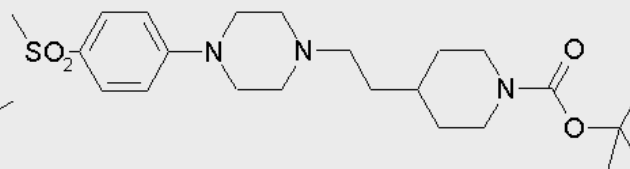
WO05121121 (Arena)



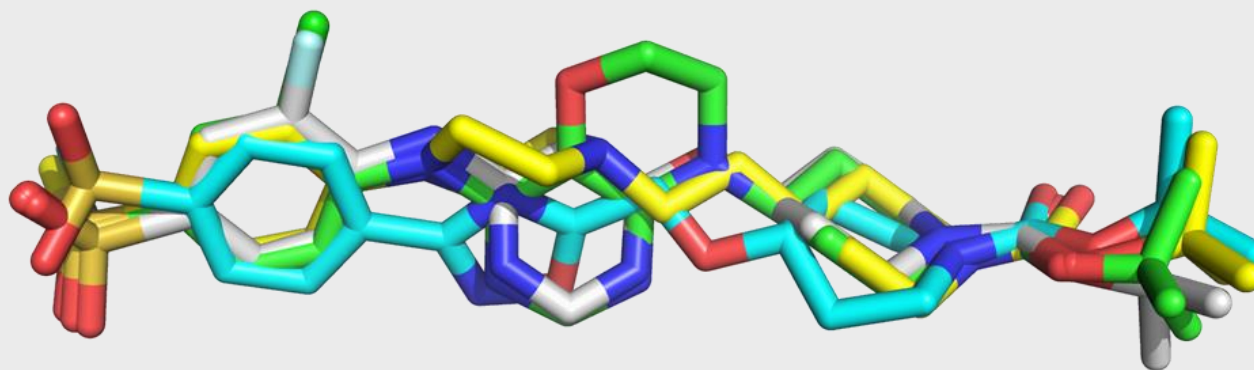
WO008137435  
(Bristol-Mayers Squibb)



WO08005576 (Arena)

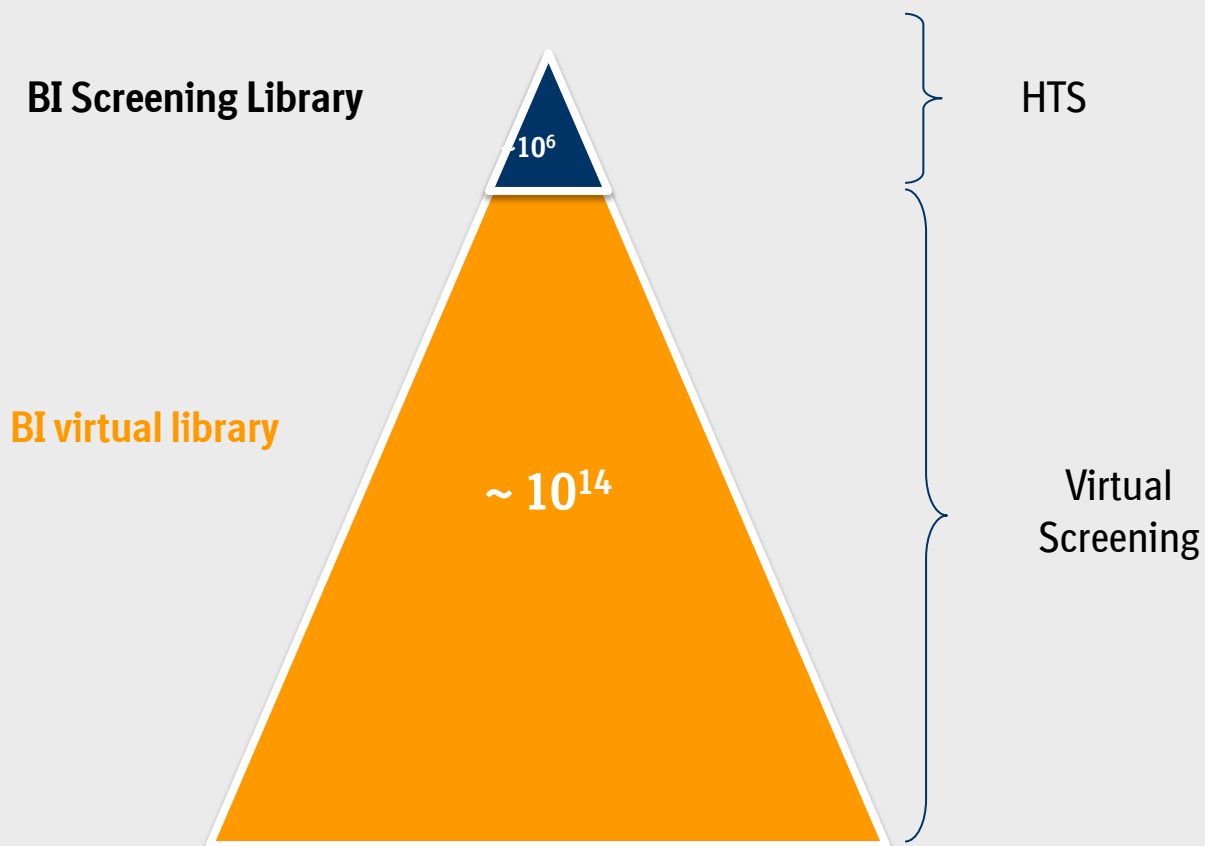


WO07003964 (Prosidion)



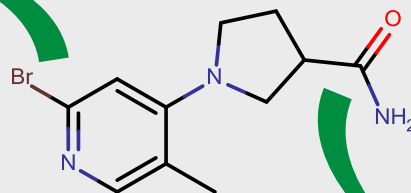
Ligand-based design: Search for molecules which are **similar** to a template molecule

Search for similar molecules in a virtual chemical space



BI's virtual library consist of molecules which can be easily synthesized

- Suzuki Coupling (boronic acids)
- Buchwald-Hartwig (anilines, amines)



Core

Amid-coupling

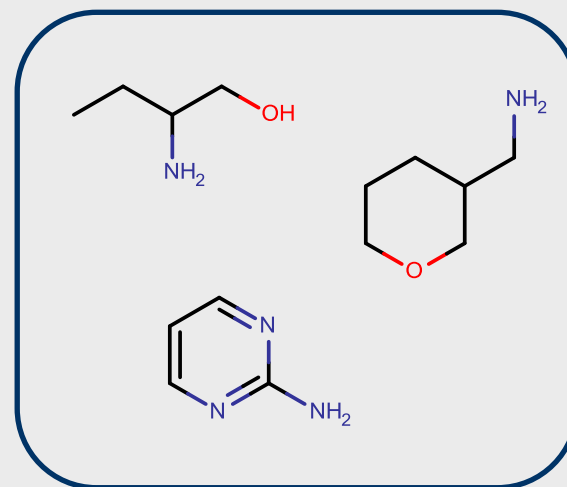
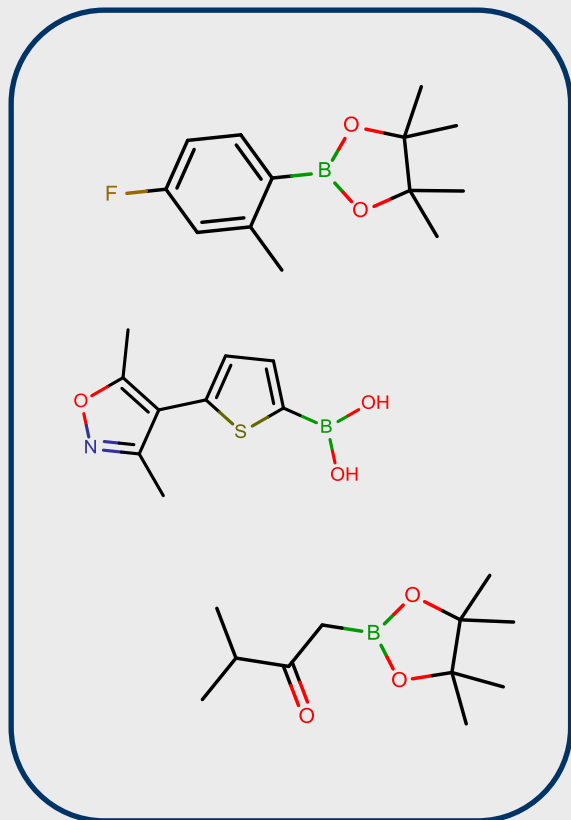
- amines
- anilines

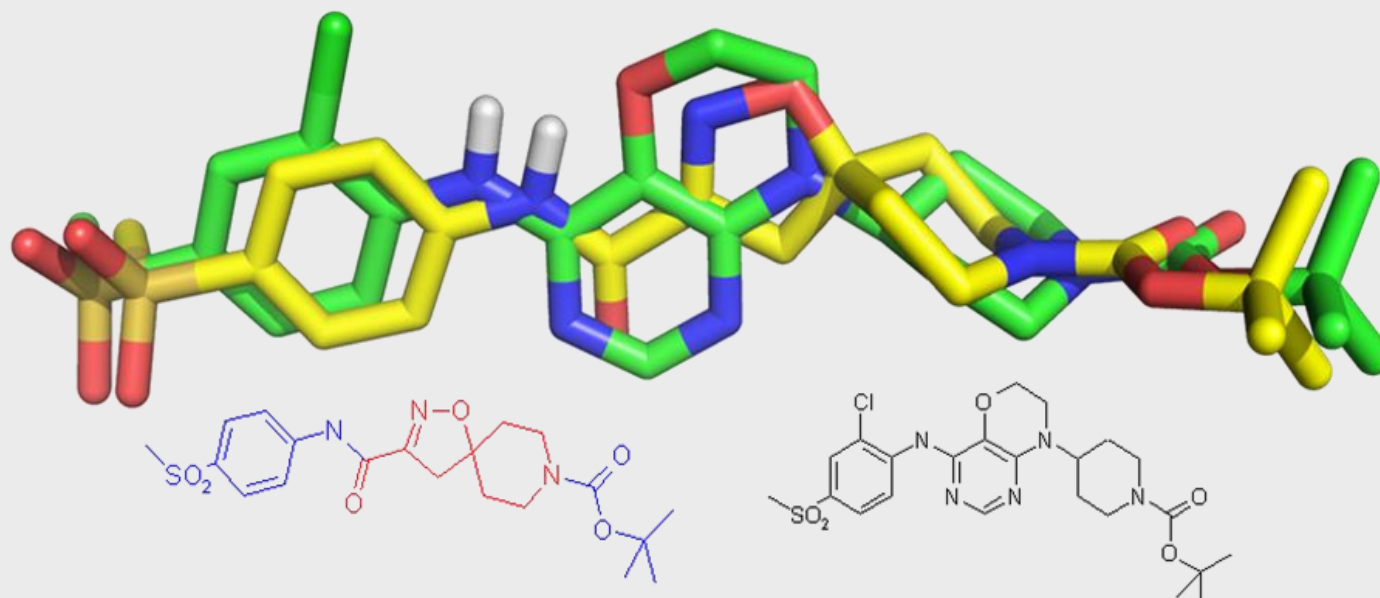
### BI in house

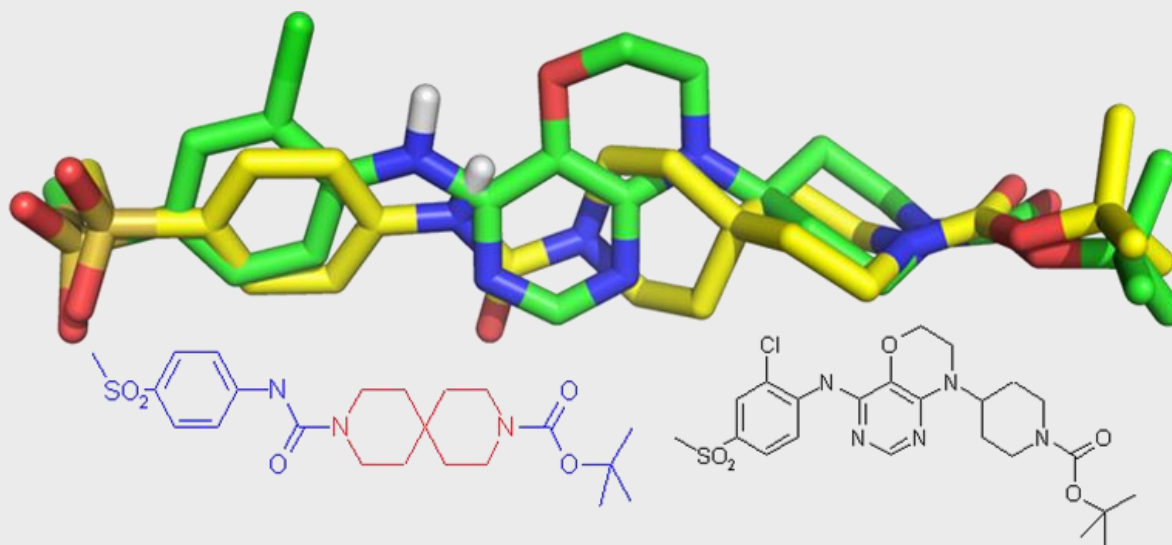
prim Amines (4000)  
prim. Anilines (3500)  
sec. Amines (6000)  
sec. Anilines (2000)  
boronic acids (2500)



Millions of possible combinations for each core.







### Drug Design is a Multi-Parameter Optimization

- Potency
- Selectivity

**Structure/Ligand-based Design (target-specific)**

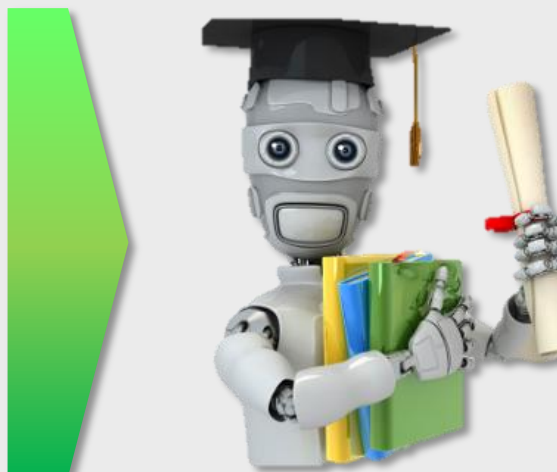
- Bioavailability
- Solubility
- Metabolic Stability
- Plasma Protein Binding
- Cytochrome Inhibition (Drug/Drug Interactions)
- Brain Permeation
- Toxicity
- Pharmacokinetic
- .....

**Data-driven Design  
(often target-independent)**

What is Machine Learning?



Data (Big Data)



Artificial Intelligence



Prediction



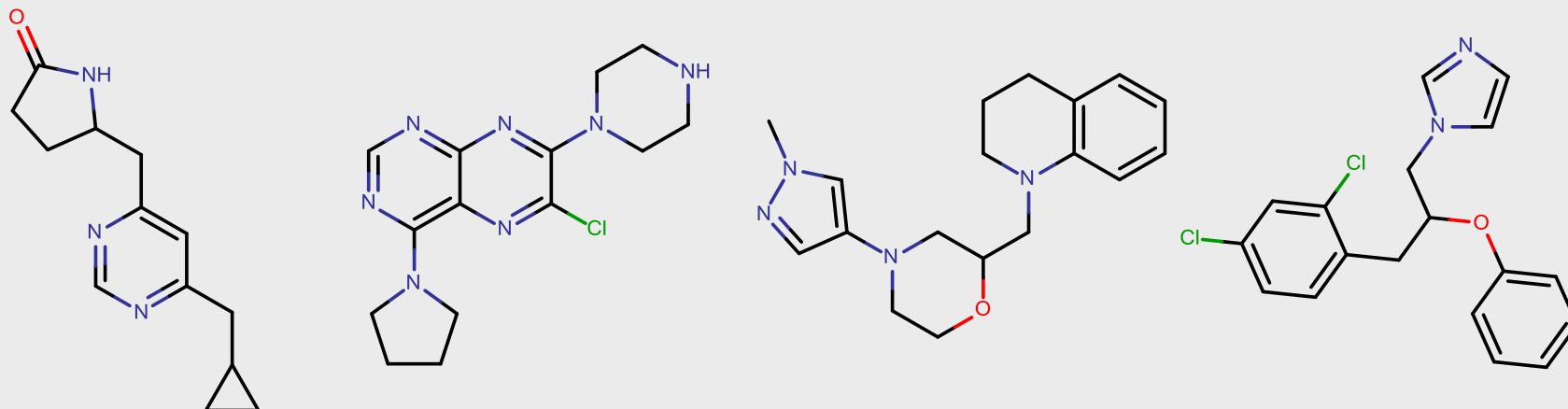
# Prediction of Molecule Properties

## Machine Learning

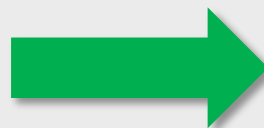


# Prediction of Molecule Properties

## Machine Learning



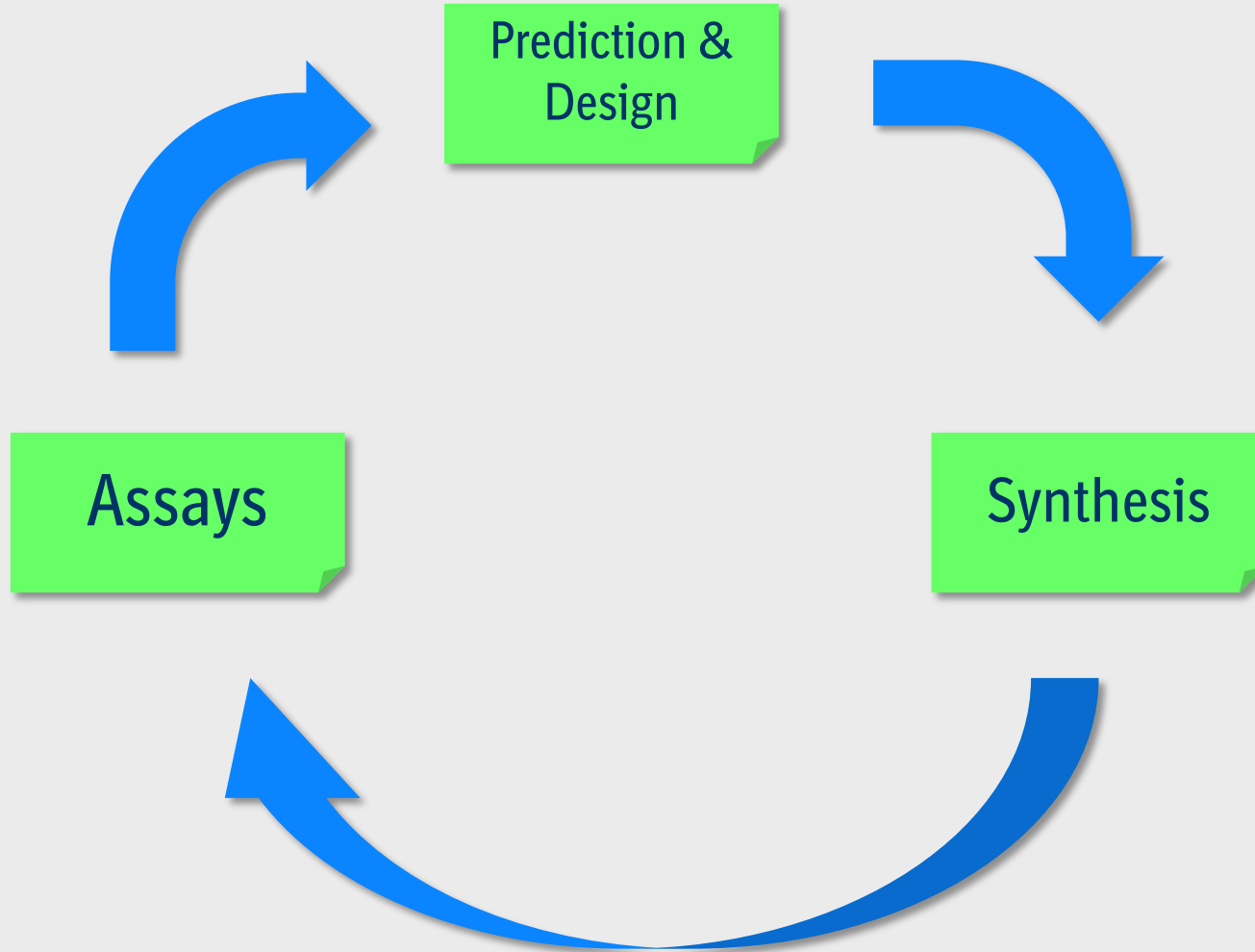
- Solubility?
- Metabolic Stability?
- hERG inhibition?
- CYP inhibition?
- Plasma Protein Binding?

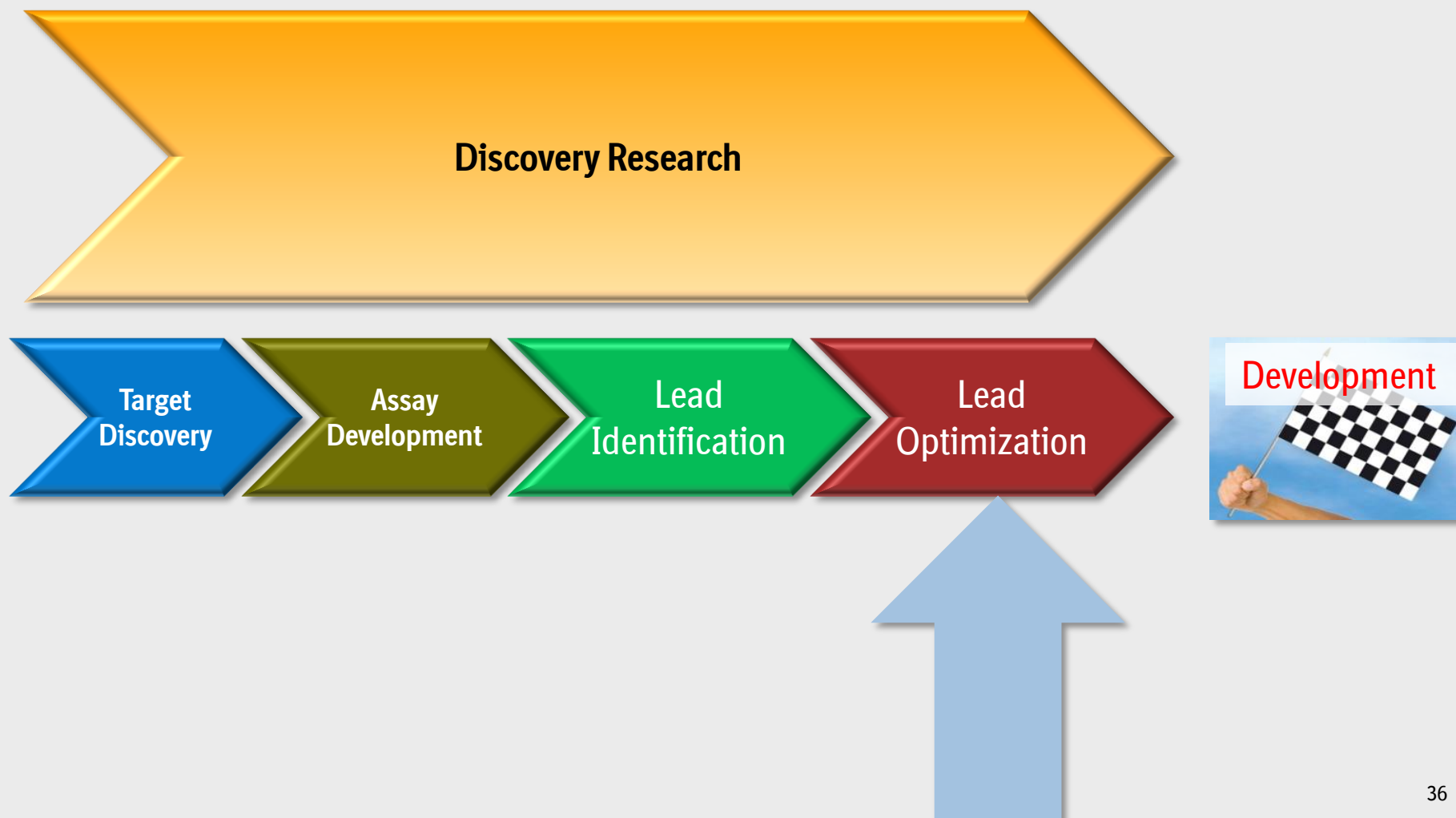


- Solubility: > 50 000 data points
- Metabolic Stability: > 80 000 data points
- hERG inhibition > 8 000 data points
- CYP inhibition > 40 000 data points
- Plasma Protein Binding > 4 000 data points

**Project (Target)-independent properties**

**Large data sets assembled over years and different research projects**





- The paradigm of modern drug discovery is to connect diseases and symptoms to molecular mechanisms
- Drug discovery programs are target centric
- Drug design is a multi-parameter optimization
- Modern computational technologies and hardware developments allow reasonable predictions of activity and other molecular properties
- Drug discovery is a very interdisciplinary field of science