



# Drug design with machine intelligence

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# Generative molecular design



©Jason Allen, "Théâtre D'opéra Spatial" (2022)

- The chemistry and pharma sectors **lag behind**
- **Rapidly growing field** (>1000 companies)
- "Big pharma" is developing **in-house A.I. capacities**

# The drug discovery cycle: The bots are coming!

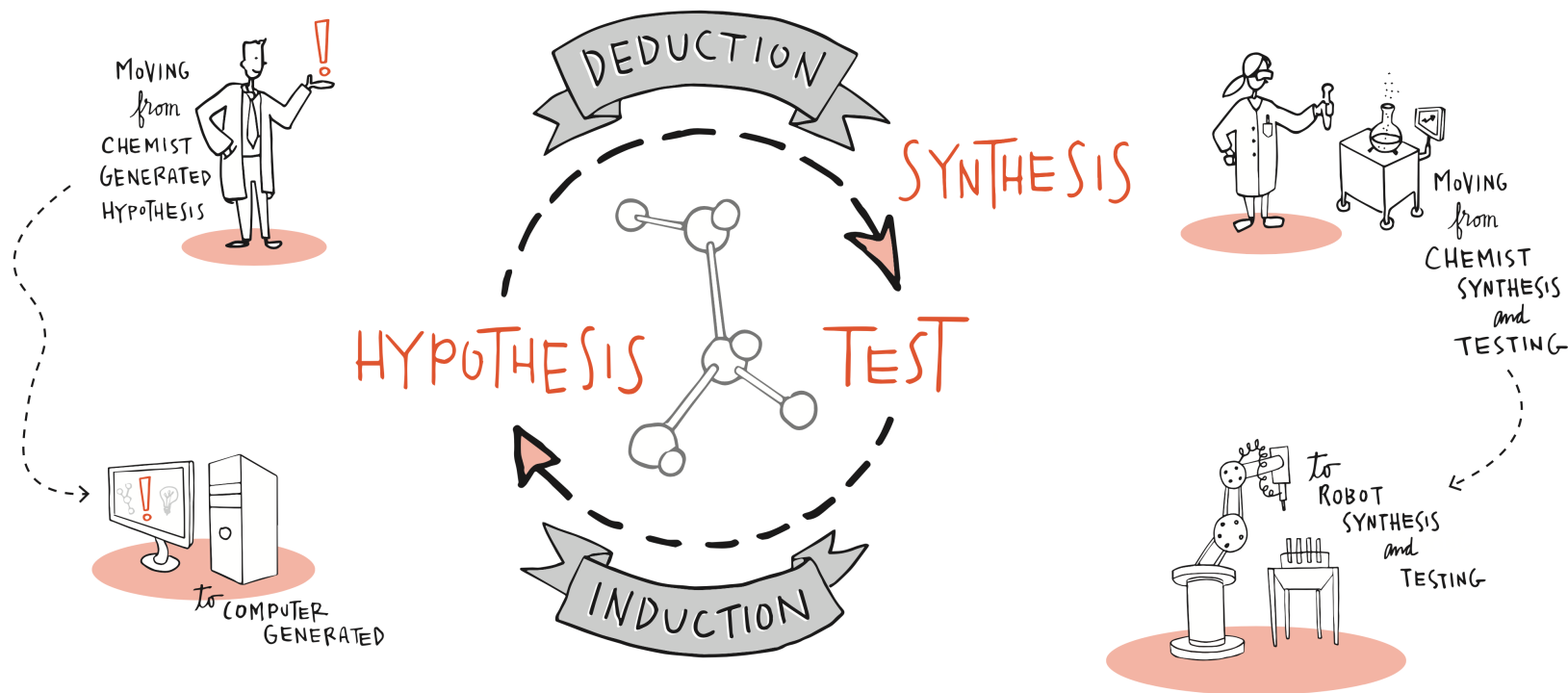
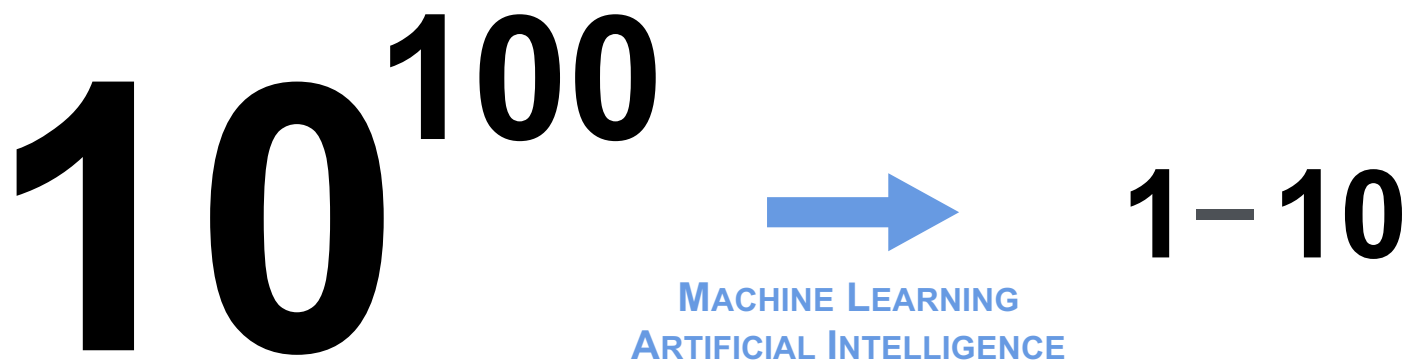


Image credit: Jack Burgess

*Nat. Mach. Intell.* **2019**, 1, 128.  
*Nat. Rev. Drug Discov.* **2020**, 19, 353.

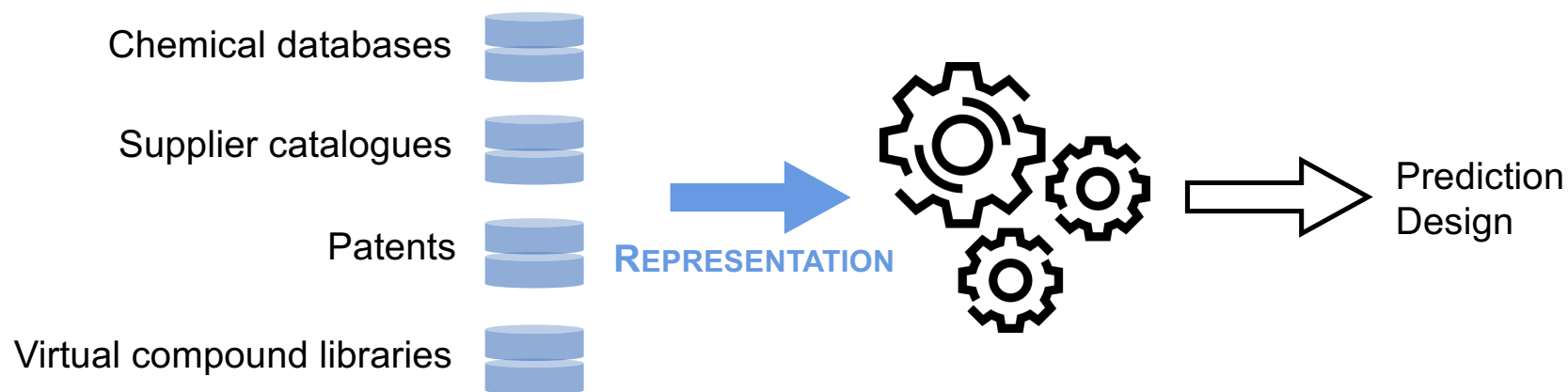
# Modern drug discovery: From screening to designing new molecules



- Generative design supports chemists by suggesting **surprising novel ideas**
- Examples: Chemical language model, graph neural network, transformer, GAN
- **Complements or replaces high-throughput screening**

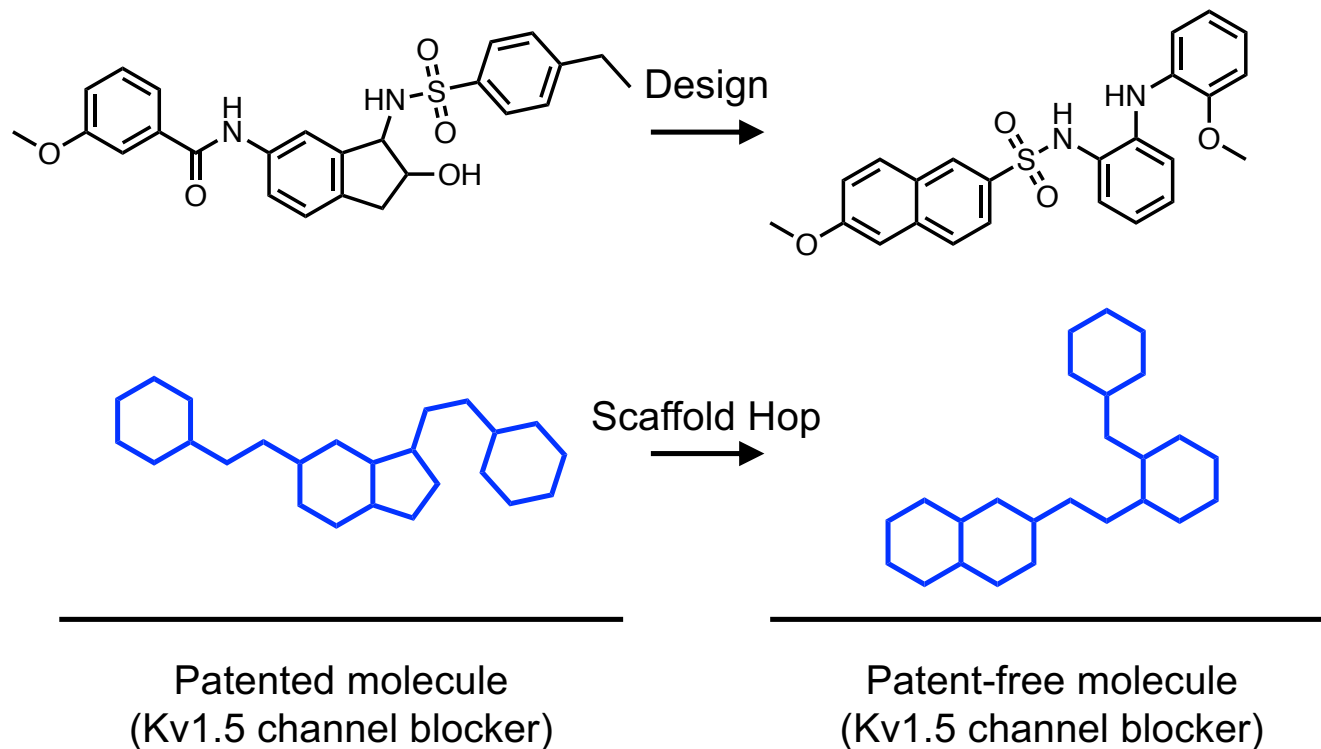
*Nat. Mach. Intell.* **2019**, 1, 128.  
*Nat. Rev. Drug Discov.* **2018**, 17, 97.  
*J. Med. Chem.* **2016**, 59, 4077.

# Sources of information for drug design with machine intelligence



- Computational drug design suffers from **scarce data**
- **Context-specific data representation** is essential

## “Patent busting” by automated “Scaffold Hopping”



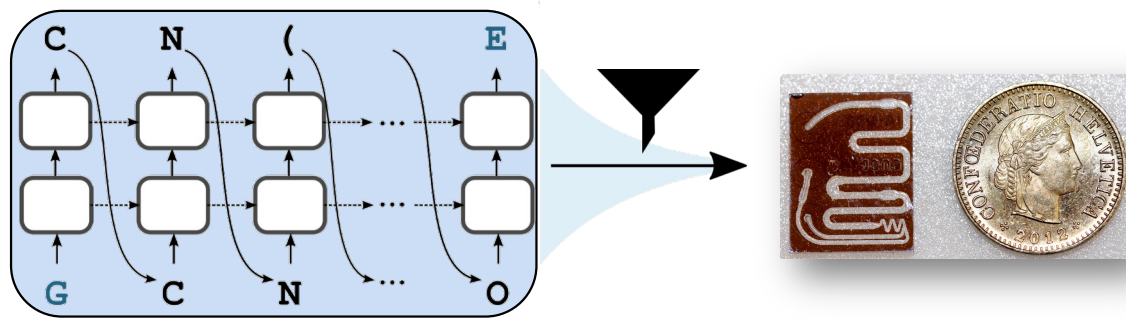
- **De novo design**  
generates new molecules
- **Fast and reliably**  
(>50% success)
- **Novel I.P.** and chemical  
scaffold classes

*Angew. Chem. Int. Ed.* **2000**, 39, 4130.

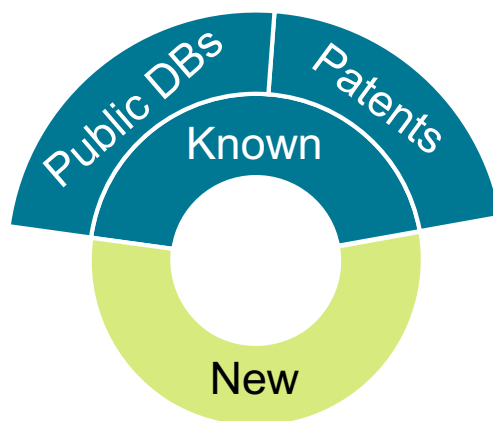
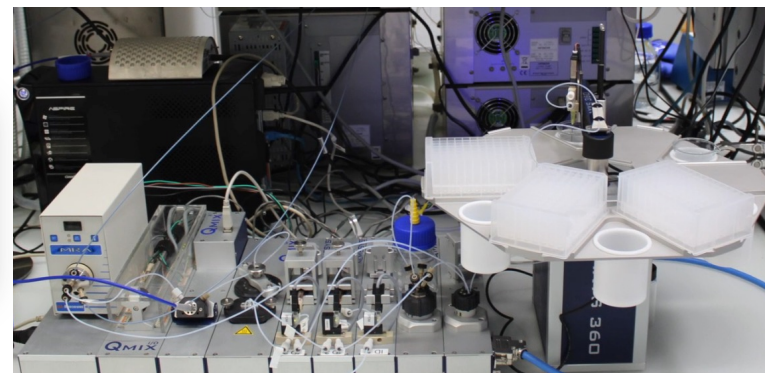


# Integrated drug discovery laboratory

## Chemical language model



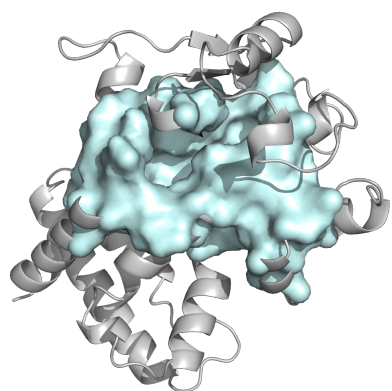
## Automated synthesis



- 55% novel chemical structures
- 21% recreated patented molecules
- 64% successfully synthesized
- 68% bioactive

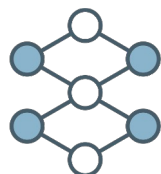
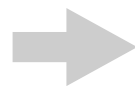
*Sci. Adv.* **2021**, *7*, eabg3338.

# Protein structure-based drug design

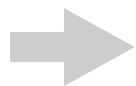


PPAR $\gamma$   
Ligand binding pocket

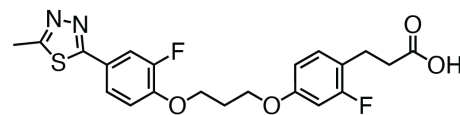
DESIGN



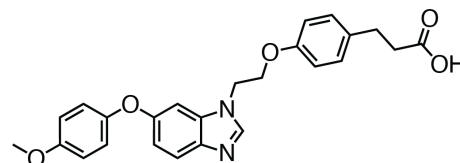
SYNTHESIS



3D graph network  
Message passing network  
Transformer network  
Chemical language model



De novo molecule 1



De novo molecule 2

## TESTING

$$EC_{50} = 1.5 \pm 0.2 \mu\text{M}$$

14.6  $\pm$  0.6-fold activation

$$EC_{50} = 2.3 \pm 0.7 \mu\text{M}$$

4.4  $\pm$  0.4-fold activation

- ✓ Novel chemical structures
- ✓ LXR $\alpha$ , RAR $\alpha$ , RXR $\alpha$ : inactive
- ✓ CYP panel: inactive
- ✓ Anti-target panel: inactive

*Nat. Commun.* **2024**, *15*, 3408.



# Automated A.I.-driven design of selective anticancer peptides

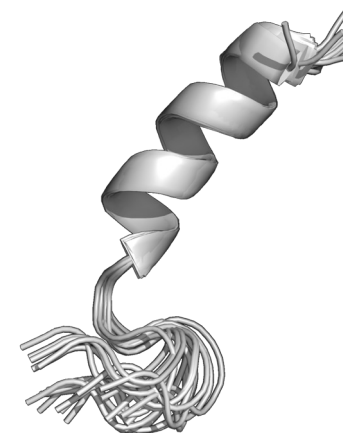
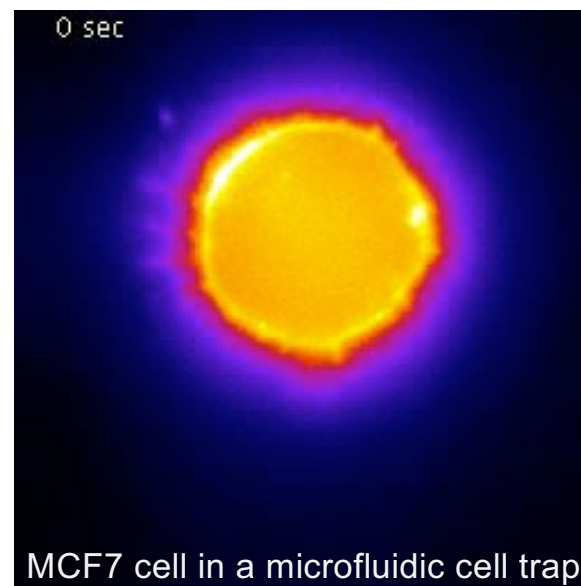
Known peptide sequences



$P(X, Y)$



New sequence(s)



KVWKIKKNIRLLHGKRGWKG

Video: Petra Dittrich, Lukas Armbrechter

KLWKKIEKLIKLLTSIR  
YIWARAERVWLWWGKFLSL  
ELAKKLTCLKRQLHRIW  
DLFKQLQRLFLGILYCLYKIW  
KLIDQWKKVLYHVE  
...

- **Chemical language model** for peptide design
- Novel amino acid **sequences not found in nature**

*Angew. Chem. Int. Ed.* **2019**, 58, 1674.

*J. Chem. Inf. Model.* **2018**, 58, 472.

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