

Introduction

Leiden Drug Development Symposium

Sep 19, 2024

Herman van Vlijmen

In Silico Discovery, Therapeutics Discovery, Johnson & Johnson Innovative Medicine
Beerse, Belgium

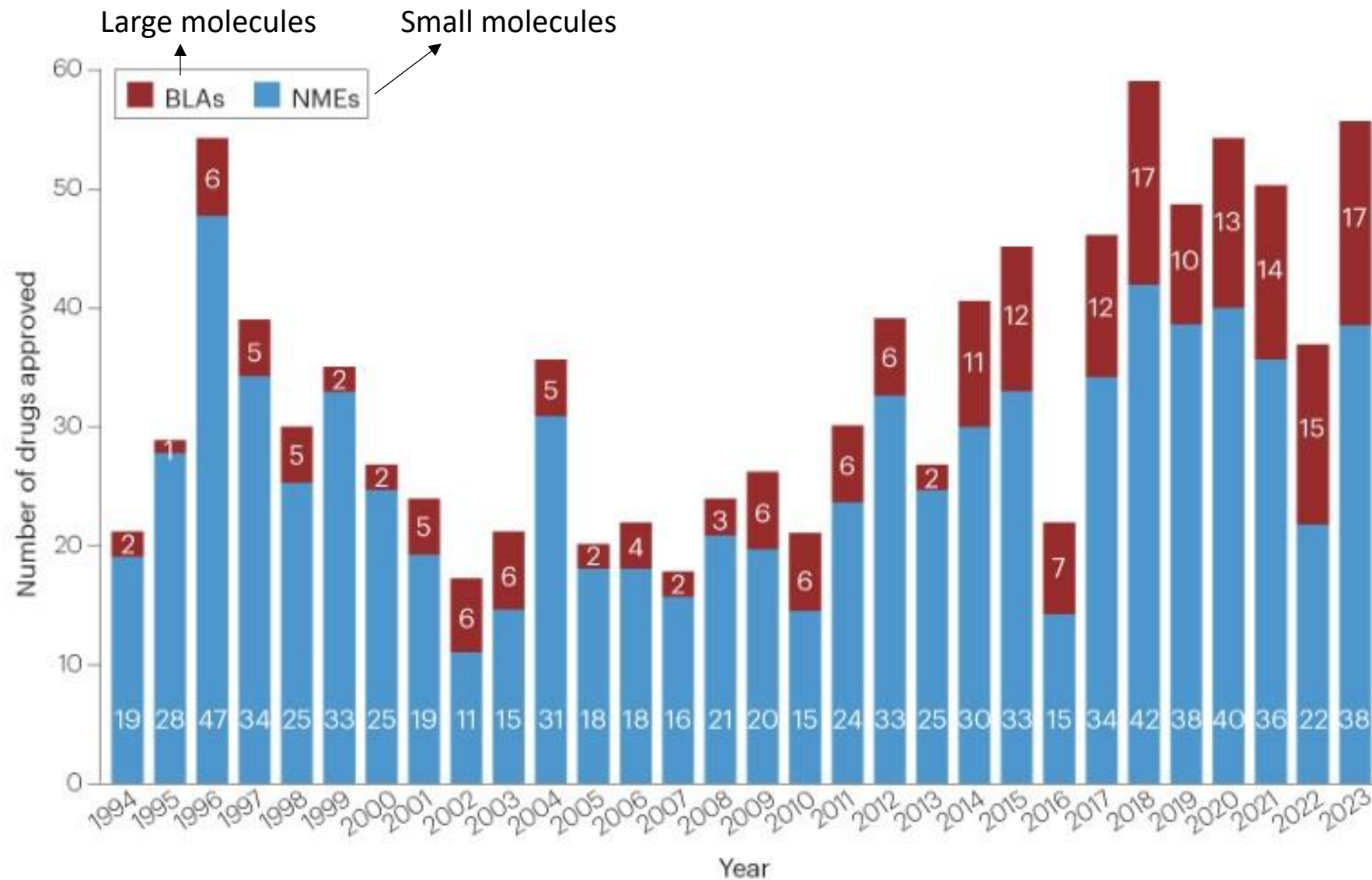
Adjunct Professor Computational Drug Discovery, LACDR

Johnson & Johnson

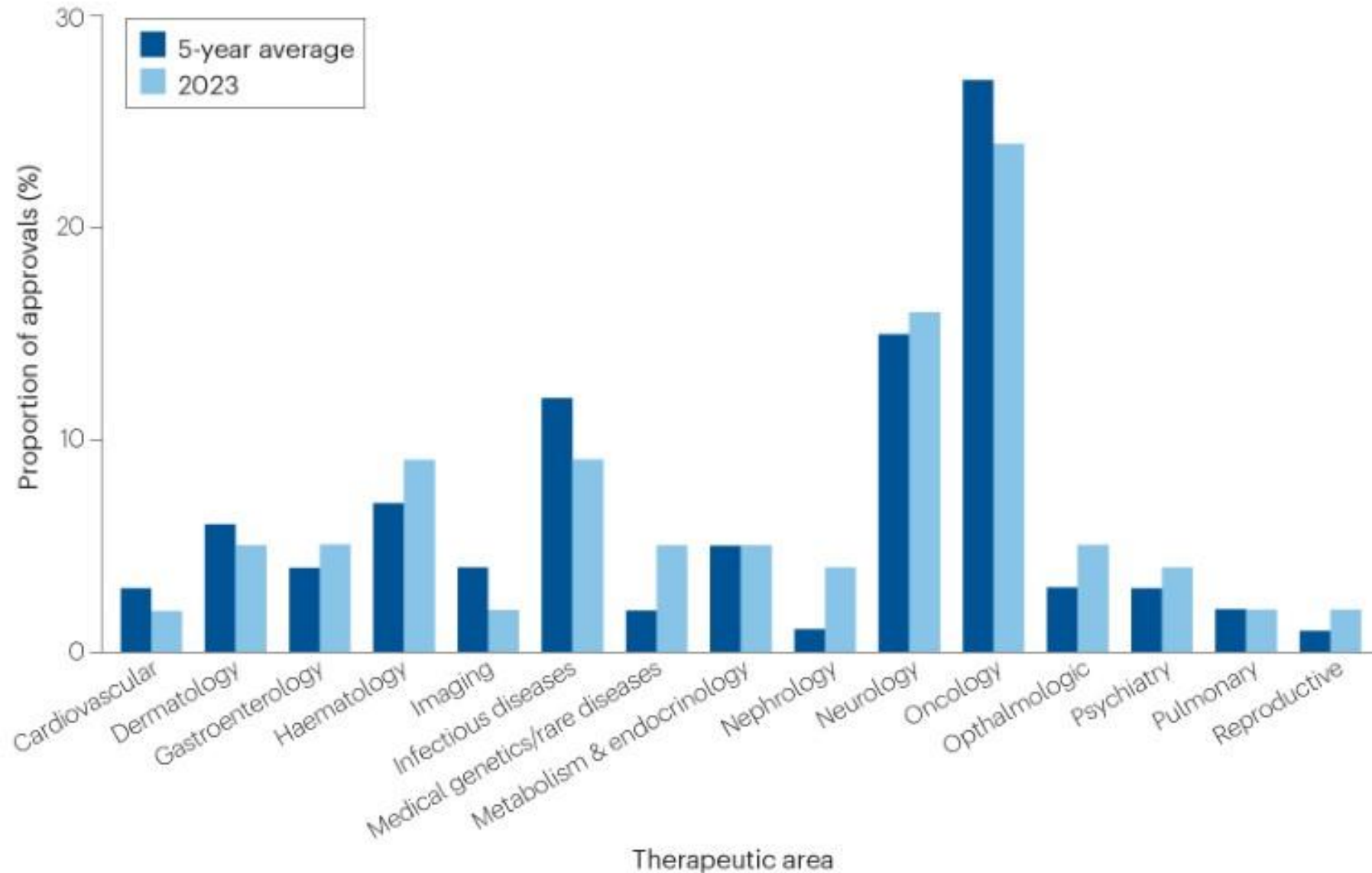


Universiteit Leiden

New Drug Approvals: Numbers



New Drug Approvals: Therapeutic Areas



Machine Learning and Artificial Intelligence in Drug Discovery A hot topic

SPOTLIGHT · 30 MAY 2018

How artificial intelligence is changing drug discovery

Machine learning and other technologies are new pharmaceuticals quicker, cheaper and more



Research Letter | Health Policy

Use of Artificial Intelligence in Drug Development

Louise C. Druedahl, PhD; W. Nicholson Price II, JD, PhD; Timo Minssen, Dipl Jur, LL.M., LL.Lic, LL.D.; Ameet Sarpatwari, PhD, JD

Nature 557, S55-S57 (2018)

15 AI Startups Accelerating Drug R&D For Big Pharma

August 2, 2018

Artificial Intelligence Client Intelligence Expert Intelligence Life Sciences/Healthcare



Applying machine learning to challenges in the pharmaceutical industry

MIT researchers and industry form new consortium to aid the drug discovery process

AI for drug discovery is booming, but who owns the patents?

nature biotechnology

The rise of deep learning in drug discovery

AI in Drug Discovery: Challenges, Opportunities, and the Future

Diego Gomez-Cabrera^{1,2,3}, Alfonso Cabezon^{1,2}, Alejandro Seco-Gonzalez^{1,2}, Daniel Conde-Torres^{1,2}, Angel Piñeiro^{2,*} and Rebeca Garcia-Fandino^{1,*}

Review article

Artificial intelligence for natural product drug discovery

nature reviews drug discovery

Artificial intelligence in drug discovery and development

Debleena Paul[†], Gaurav Sanap[†], Snehal Sherkar[†], Dnyaneshwar Kalyane, Kiran Kalia and Rakesh K. Mishra

How A.I. Is Revolutionizing Drug Development

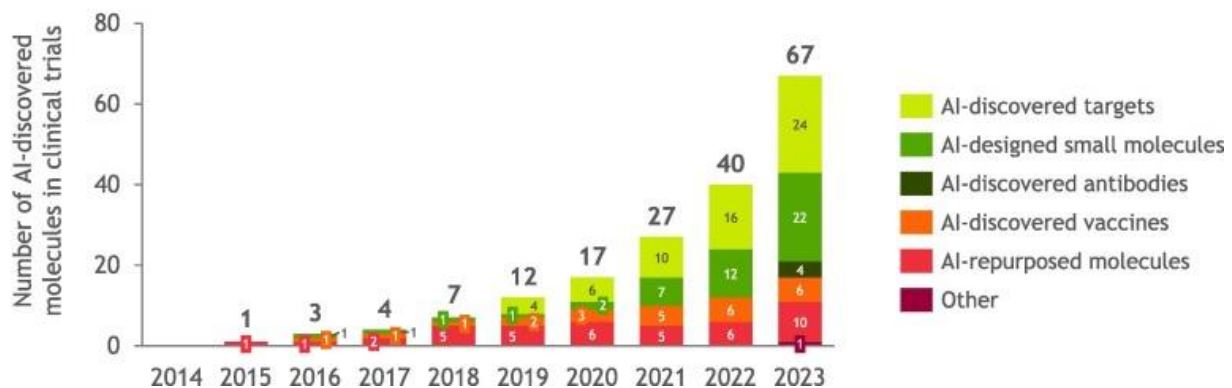
In high-tech labs, workers are generating data to train A.I. algorithms to design better medicine, faster. But the transformation is just getting underway.



Pubmed: "artificial intelligence" AND "drug discovery"



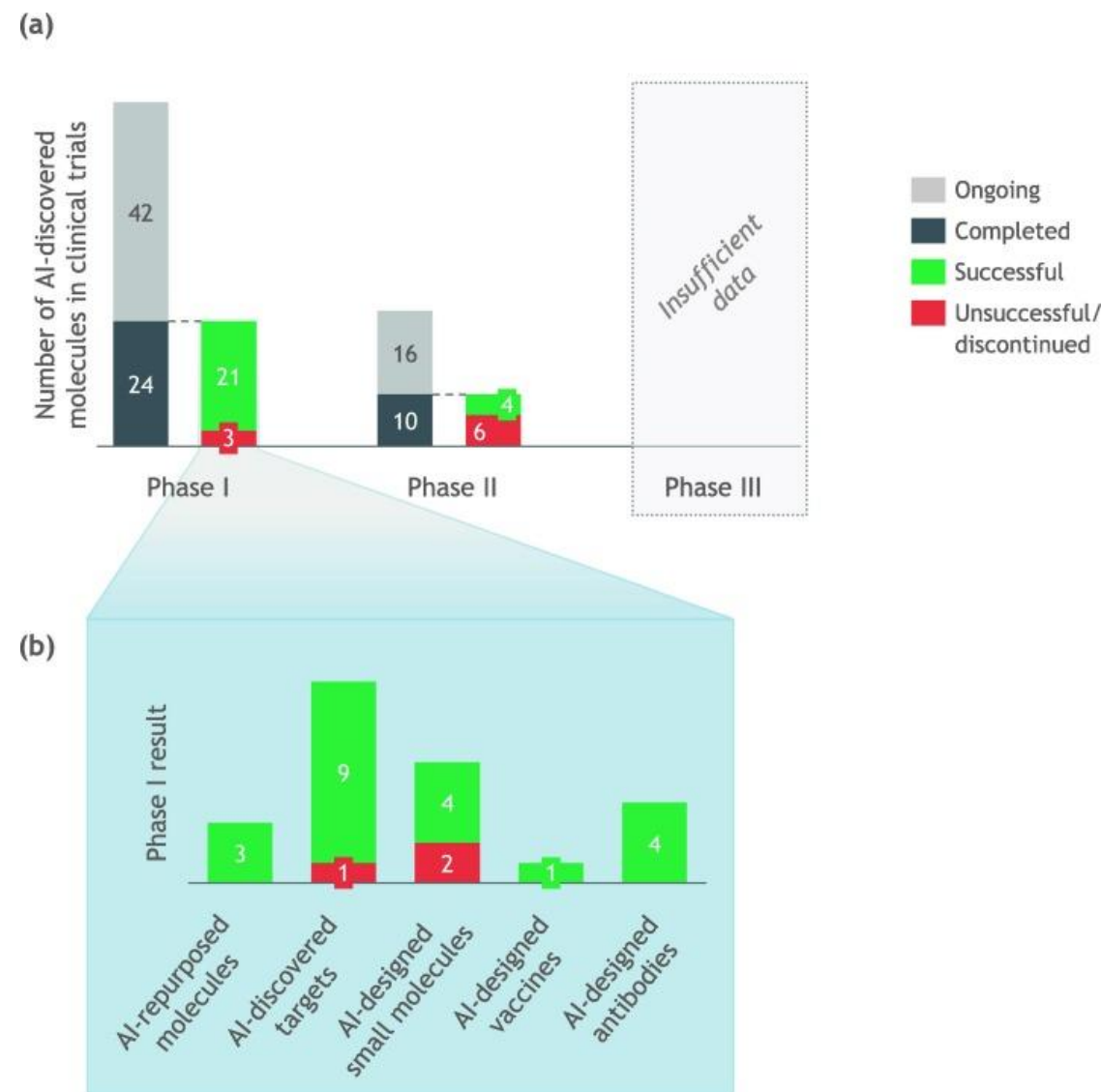
AI Discovered drugs in clinical trials: A first analysis



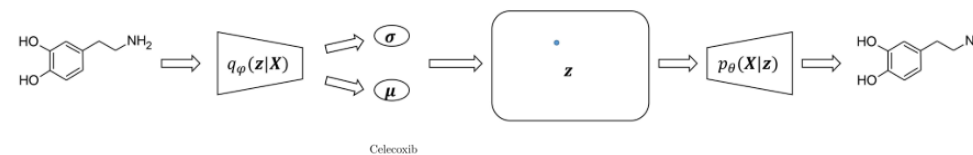
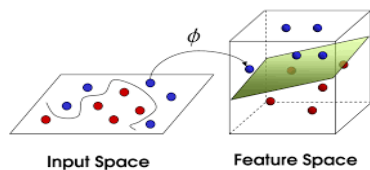
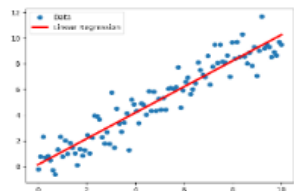
BUT:

OK, that's what I have from the table. I have linked to a relevant site for each drug candidate and then to a relevant site about the targets involved. The only one that I can't round up enough information to be sure about is ATH-63. What you will see is that in almost every case, these targets were already known to be implicated in the disease under investigation. In some of these examples, in fact there are several drugs already in the clinic targeting the same proteins, or even therapies that are already on the market working through the same mechanisms (*C. diff* toxin B, *e.g.*) I don't think any of these are bad targets, let me make that clear. There are some really interesting things on the list, but I do not see how any of them can be classified as "target discovered by AI". I really don't.

In the pipeline blog Derek Lowe, 13 May 2024

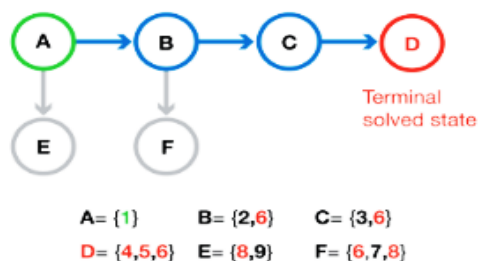
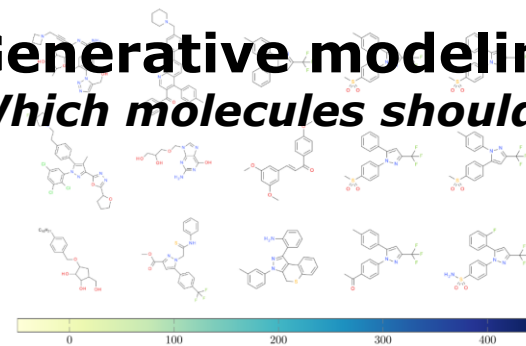


AI/ML in early discovery: Where does it make a difference?

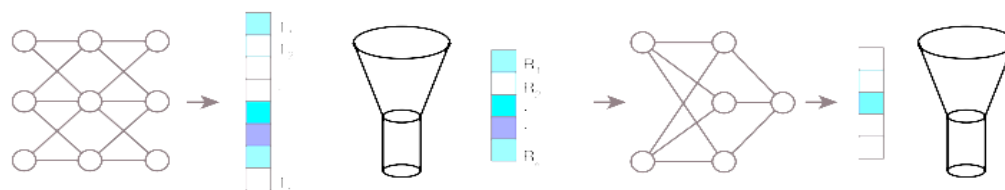


Improved activity and property modeling
Computationally assess molecular properties

Generative modeling
Which molecules should we make?



(Retro)synthesis Modeling
What is the best way to make this?
Which reactions are most likely to work?



Computer-Aided Drug Design Across Discovery (small mol)

Target Identification

Hit Identification

Hit to Lead

Lead Optimization

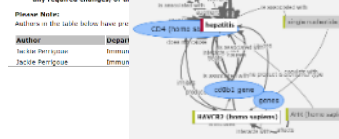
Late Lead Optimization

AI/ML

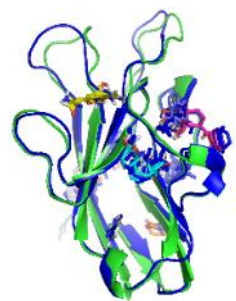
Home Summary Workflow Genes Transcripts Proteins Functions Designs

TARGET BROWSER -- SYSTEMATIC SEARCH FOR HAVCR2 INFORMATION
 Maria Van Dongen (Discovery Sciences), 30 January 2017

- This document is for exploratory purposes and contains only low information, based on simple databases, and is not appropriate for clinical use. This document is not intended to be used as a guide to the development of any drug.
- Links to the document are provided for your reference.
- If you need a manual, please refer to the manual.

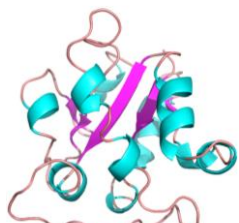


Information mining

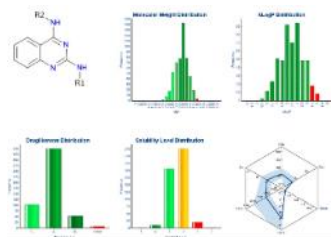


Ligandability assessment

Structure prediction



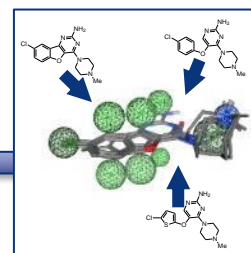
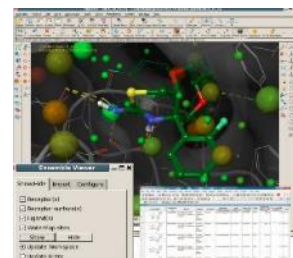
(uHT) Virtual screening



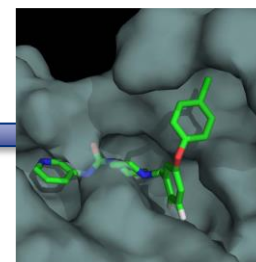
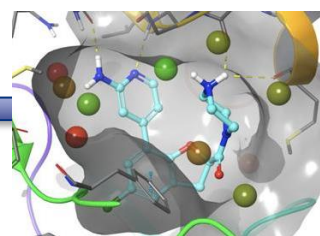
Library enrichment



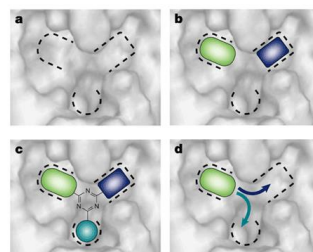
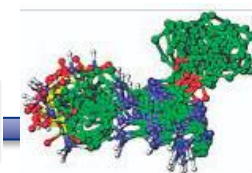
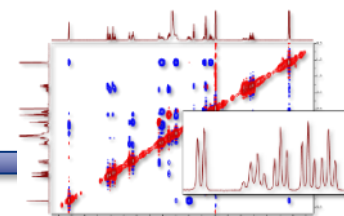
Hit triage



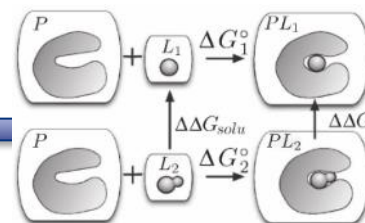
Ligand based design



Structure-Based Design



FBLD



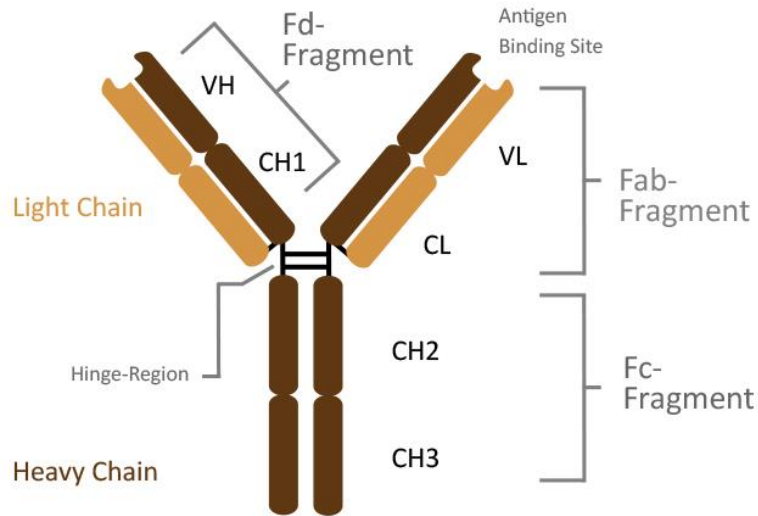
Free Energy of Binding



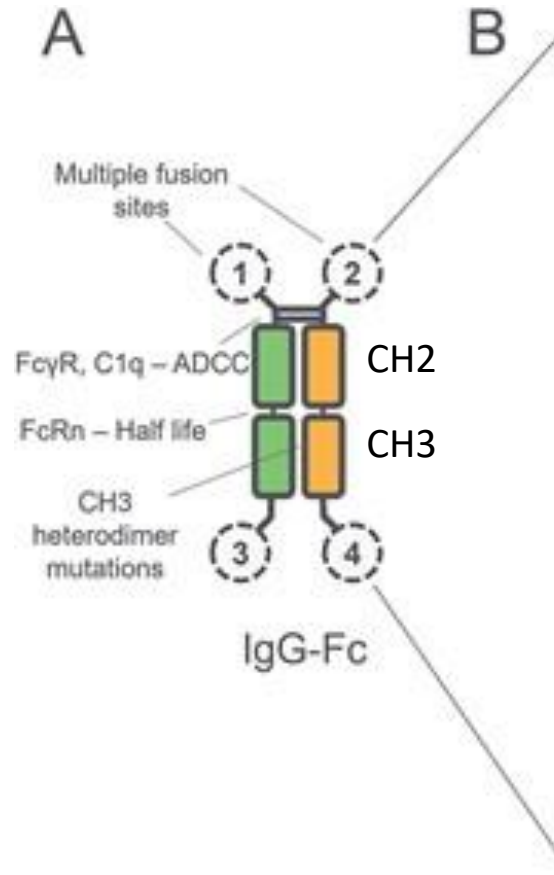
Cheminformatics







Antibodies: the main type of biologics

Standard antibody structure



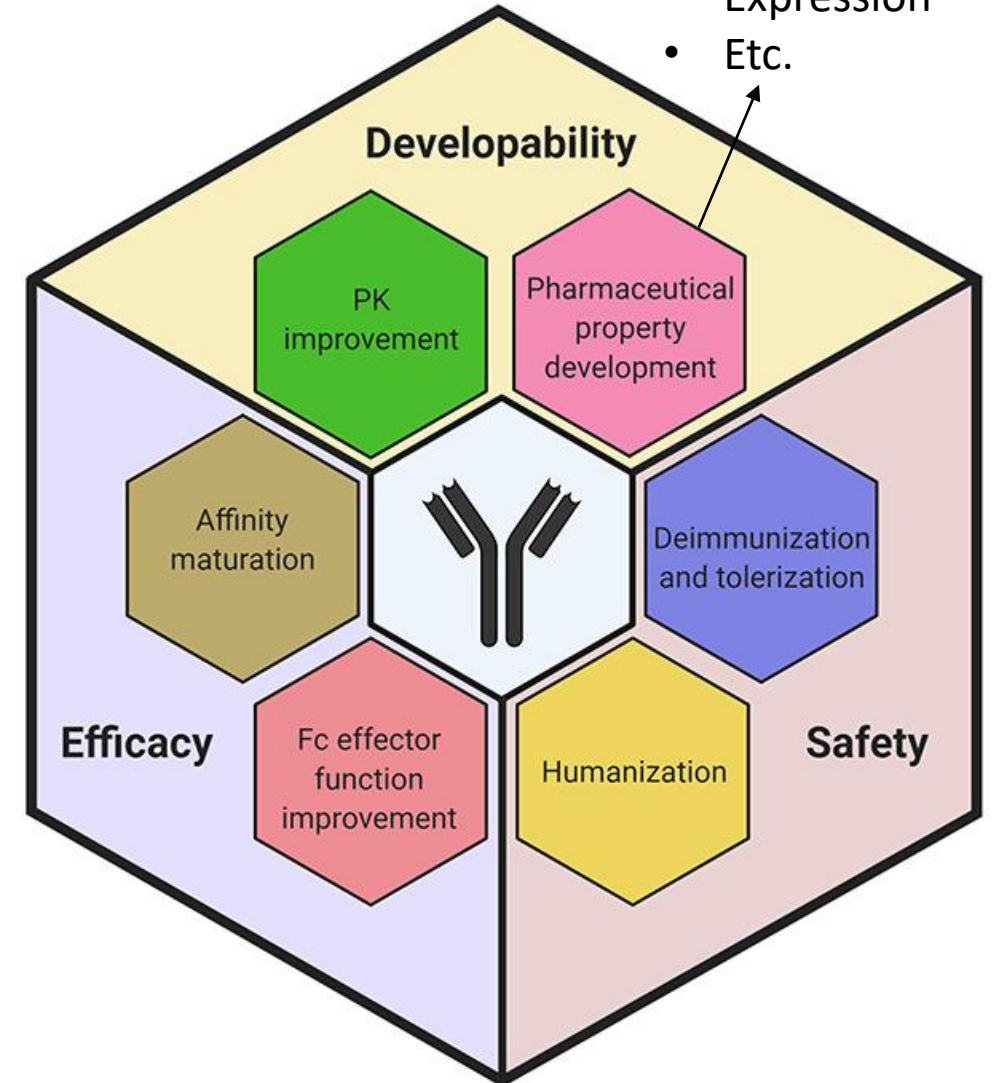
Large variety of genetically engineered antibodies



Building Blocks	Folding Domain	MW (kDa)	Binding SASA (Å ²) / Total SASA (Å ²)
 Fab	Immunoglobulin	45-55	5-7%
 scFv	Immunoglobulin	20-30	9-11%
 VHH	Immunoglobulin	15-20	20-29%
 Cytokine	IL2: Helical bundle IL18: β-trefoil fold IL23-p19: Helical bundle IL23-p40: Fibronectin type-III	10-30	19-56%
 Miniprotein	DARPin: Ankyrin repeat Anticalin: β-barrel, attached helix Knottin: Cysteine knot	3-20	14-43%
 De novo miniprotein	CTC-445.2: Alpha-beta motif IL7Rα Binder: Helical bundle HB1.6928.2.3: Alpha-beta motif	3-20	14-39%

Property Optimization of biologics

- Thermostability
- Solubility
- Chemical stability
- Expression
- Etc.

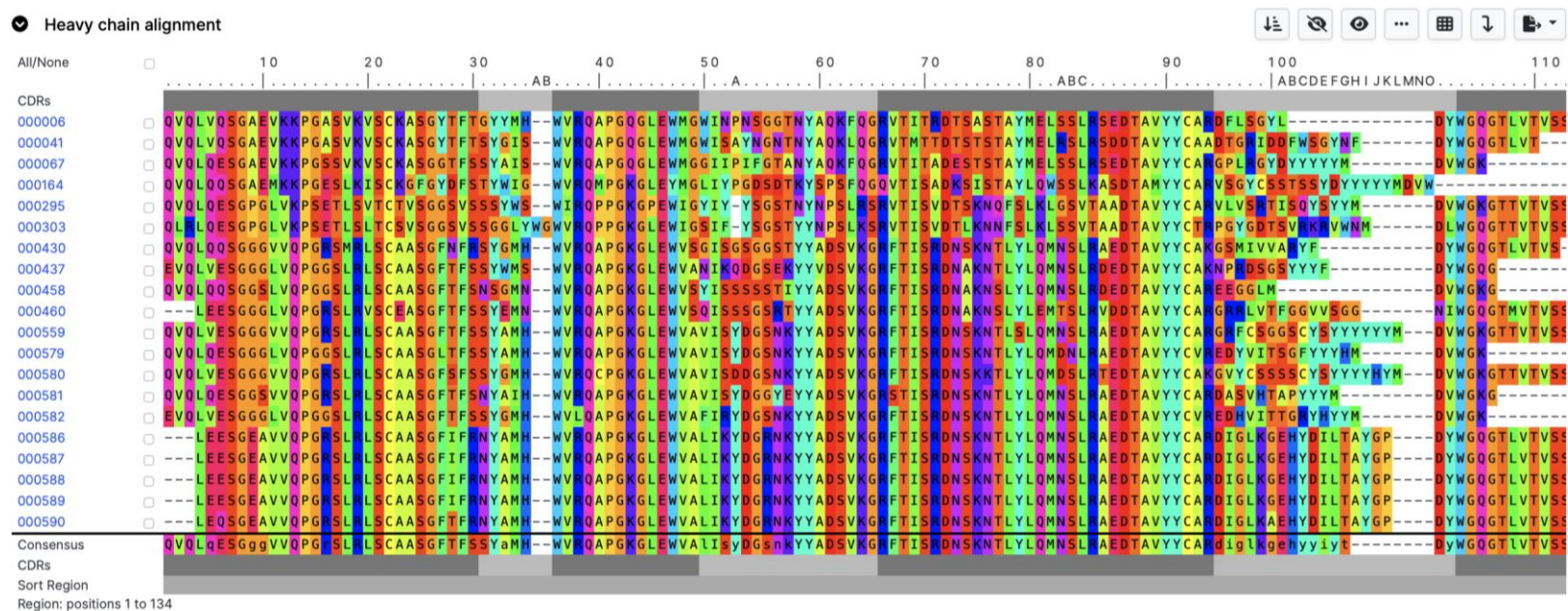


Large Language Models in molecular optimization

```
OC [C@H] 1O [C@H] ([C@H] (O) [C@@H] 1O) n2cnc3c2ncnc3CSc4cccc4I
C#Cc1nc (nc2 [nH] cnc12) Nc3cccc (c3) C (N) =O
O= [N+] ([O-]) c1cccc (c1) SCc2ncnc3c2ncn3 [C@@H] 4O [C@H] (CO) [C@@H] (O) [C@H] 4O
CCN(CC) c1nc2c (nc (SCC (=O) NCCCN) n2CCc3c [nH] c4cccc34) c (C) n1
O=C (O) CSCc1ncnc2c1ncn2 [C@@H] 3O [C@H] (CO) [C@@H] (O) [C@H] 3O
C [C@] 1 (O) C (O [C@H] (CO) [C@H] 1O) n2cnc3c2ncnc3C (=N) N
OC [C@H] 1O [C@H] ([C@H] (O) [C@@H] 1O) n2cnc3c2ncnc3/C=C/N4CCOCC4
CCN(CC) c1nc2c (nc (SCC (=O) NCCCN) n2CCNc3nc (N) nc4 [nH] cnc34) c (C) n1
COC (=O) c1ccc (cc1) SCc2ncnc3c2ncn3 [C@@H] 4O [C@H] (CO) [C@@H] (O) [C@H] 4O
Cc1cc (C) c (SCc2ncnc3c2ncn3 [C@@H] 4O [C@H] (CO) [C@@H] (O) [C@H] 4O) c (C) c1
CC (=O) OCCSC [C@H] 1O [C@H] ([C@H] (OC (C) =O) [C@@H] 1OC (C) =O) n2cnc3c2ncnc3C
C (#Cc1ncnc2c1ncn2C3CCOCC3) c4cccc4
CCc1ccc (cc1) c2nc3c (nc (O) n3c4cccc4OC) c (n2) C (N) =O
NS (=O) (=O) OC [C@H] 1O [C@H] ([C@H] (O) [C@@H] 1O) n2cnc3c2ncnc3C#Cc4cccc4F
CCCCC#Cc1ncnc2c1ncn2C3O [C@H] (CO) [C@@H] (O) [C@H] 3O
CCOc1cccc1c2nc3c (nc (O) n3c4cccc4) c (n2) C (N) =O
```

SMILES: language of small molecules

Amino acid sequence:
language of biologics



Thank you!