

Success and Challenges of Artificial Intelligence in Drug Discovery

Dr Taravat Ghafourian
Nova Southeastern University

A brief biography

Experience in Academia

- **Oct 2022-Present:** Nova Southeastern University
- Director of Pharmacy Development and Reader in Pharmacy, University of Bedfordshire, **Aug 2020-2022**
- Senior Lecturer, School of Life Sciences, University of Sussex, **2015-2020**
- Lecturer, Medway School of Pharmacy, University of Kent, **2005-2015**
- Research Fellow, Liverpool John Moores University, **2003-2005**
- Visiting scientist at University College London **2001**
- Assistant/Associate Professor at Tabriz Faculty of Pharmacy, **1997-2003**

Education:

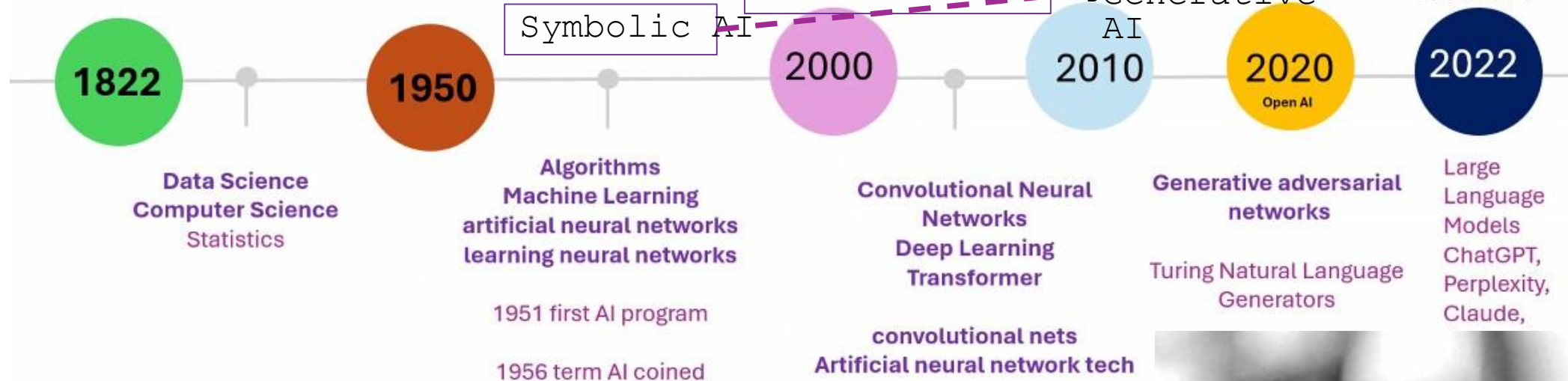
- Pharmacy Doctorate, Tabriz Faculty of Pharmacy, 1992
- PhD in Pharmaceutical sciences, Liverpool John Moores University, 1996
- Postgraduate Certificate in Higher Education, University of Kent, 2008



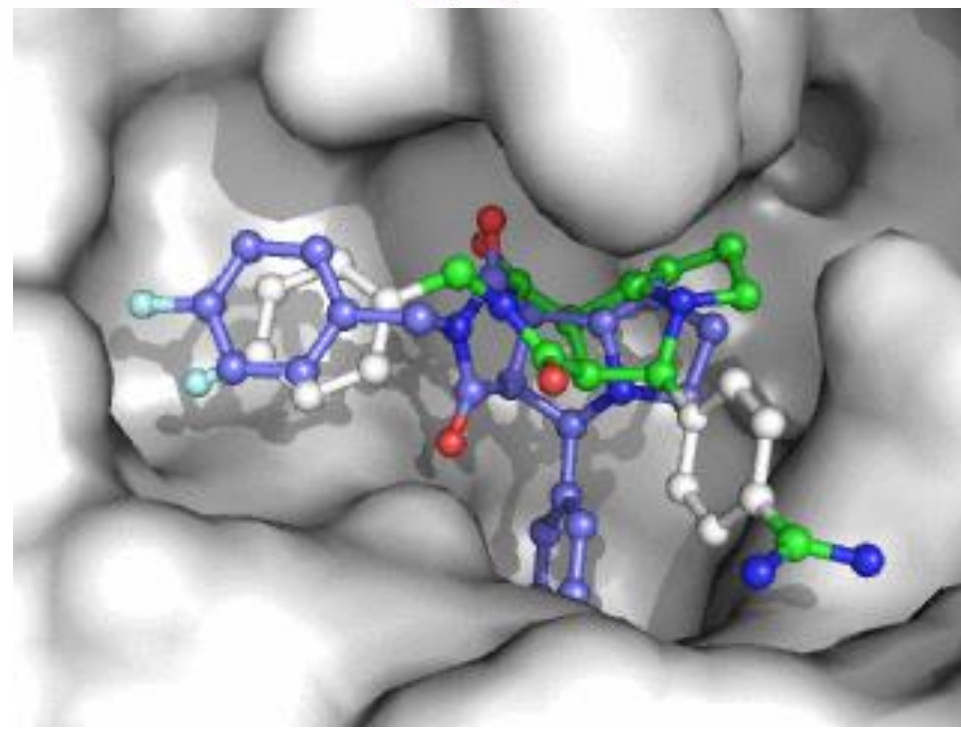
AI and Computational Modeling in Drug Discovery: History

Charles Babbage (1791-1871)
First analytical computer

Alan Turing (1912-1954)
father of computer science
and artificial intelligence



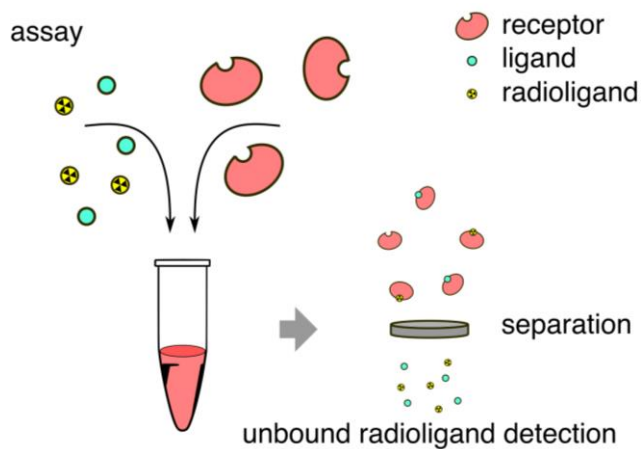
Corwin Hansch
QSAR paper 1953
& 1966



Computer-aided drug discovery has been around for decades
A recent surge in embracing computational technology

Scientific models in pharmaceutical sciences

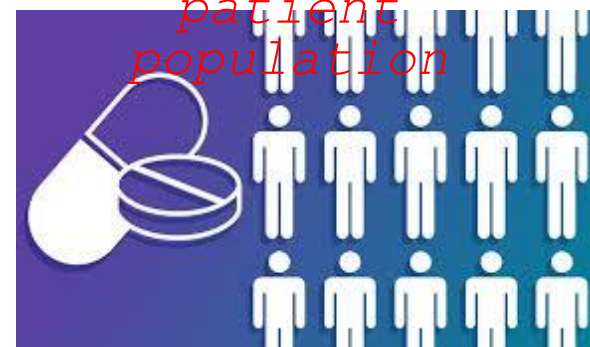
In vitro models



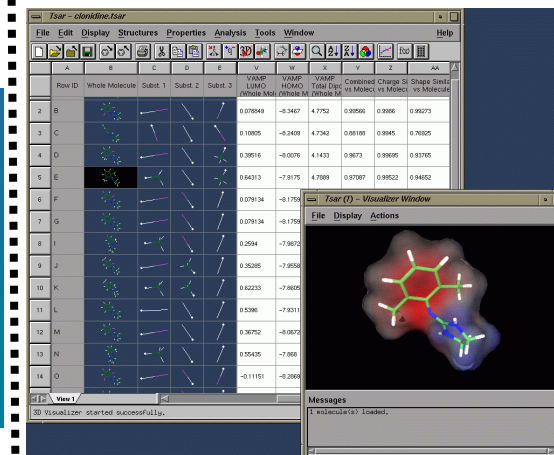
Animal models



*Clinical trials:
clinical models
of the real
patient
population*



Computational models



Hypothetical example: efficacy of an antidepressant in a tablet dosage form

All we do in science is modeling

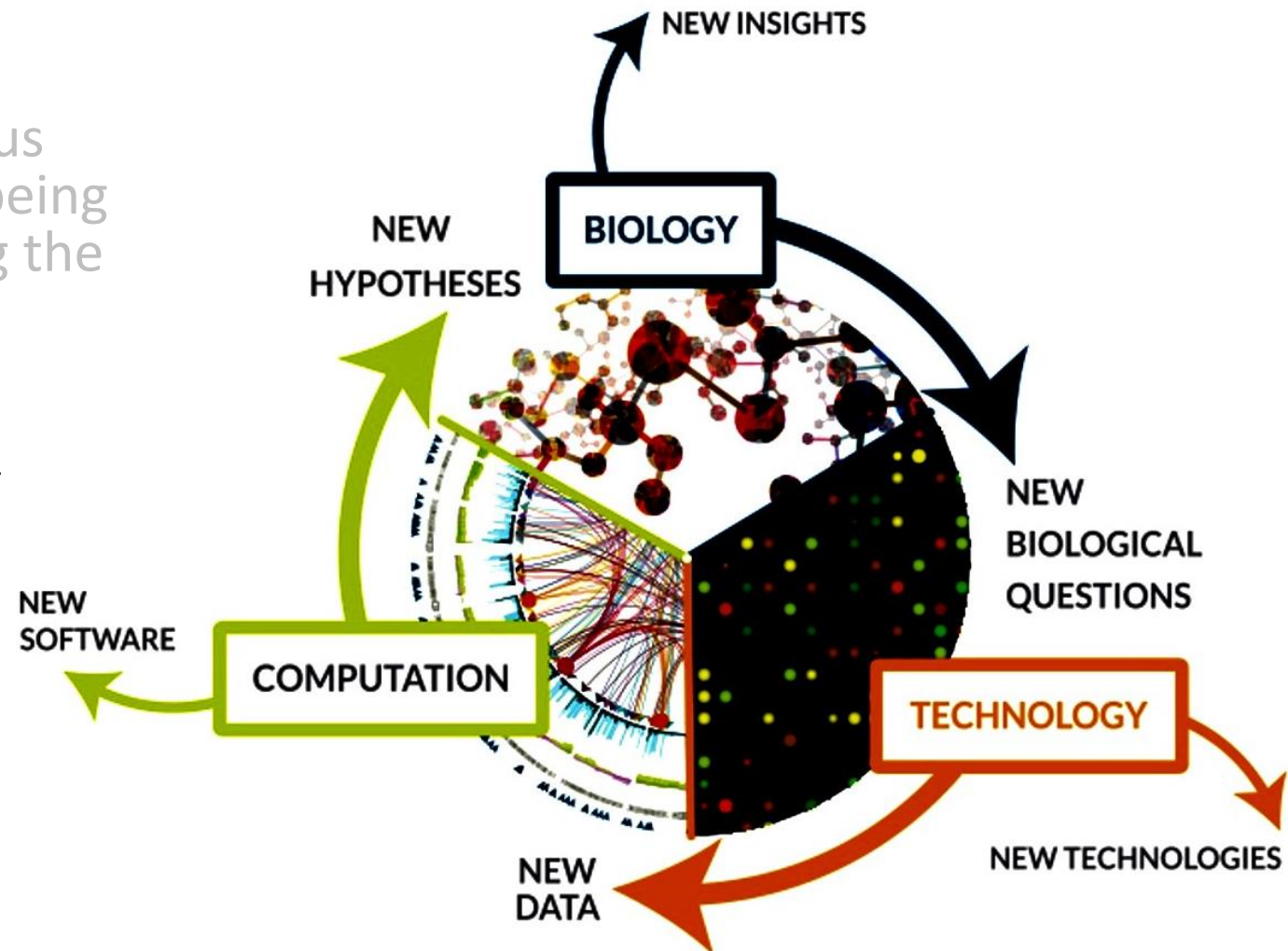
“... the sciences do not try to explain, they hardly even try to interpret, **they mainly make models**. By a model is meant a **mathematical construct** which, with the addition of certain **verbal interpretations**, describes observed phenomena. **The justification of such a mathematical construct is solely and precisely that it is expected to work—that is, correctly to describe phenomena from a reasonably wide area.**”

John von Neumann



Computational modelling:

The use of computers to simulate and study complex systems using mathematics, physics, and computer science. A computational model contains numerous variables that characterize the system being studied. Simulation is done by adjusting the variables alone or in combination and observing the outcomes. Computer modeling allows scientists to conduct thousands of simulated experiments by computer.



National Institute of
Biomedical Imaging
and Bioengineering

*Technologies to Shape
the Future of Health*

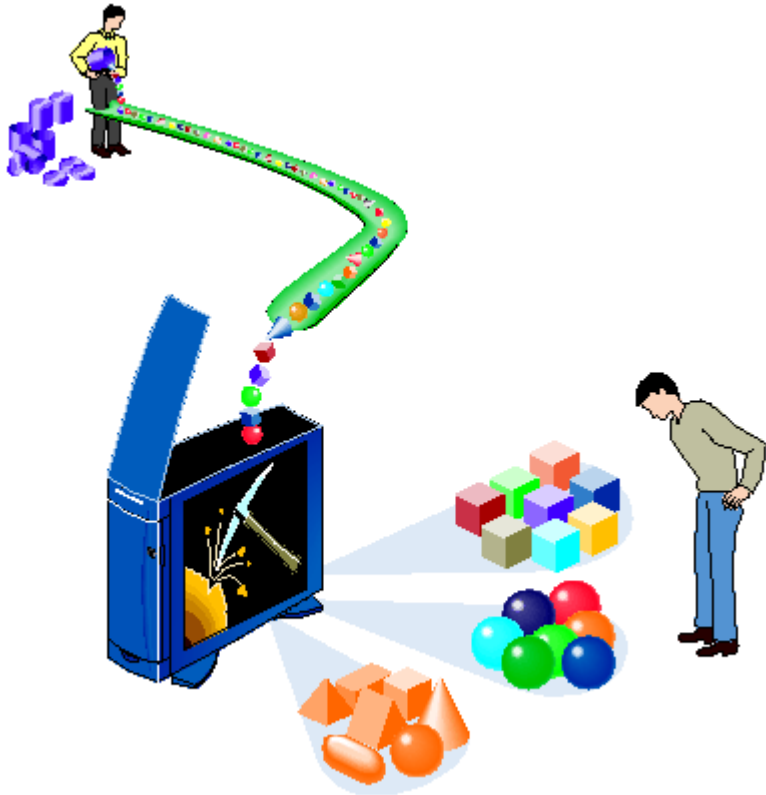
<https://www.nibib.nih.gov/science-education/science-topics/computational-modeling>

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College of Pharmacy
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AI and ML (Artificial Intelligence and Machine Learning)

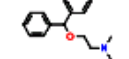
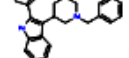
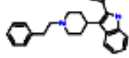
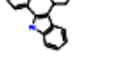
ML discovers patterns in data so that this knowledge can be applied to enable future predictions

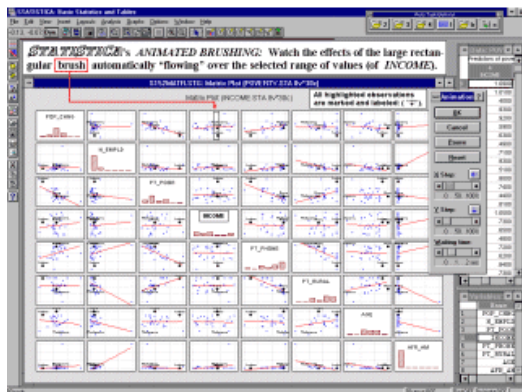


- Specific AI (weak AI) is engineered to execute a specific task, the most prevalent form of AI today
- Universal AI (strong AI) can comprehend, learn, and apply intelligence across a variety of tasks
- Superhuman AI: hypothetical, a topic of debate and research.
- ML is the tool used in AI: creating algorithms that learn from data and make predictions:
 - Supervised learning, Unsupervised learning, Reinforcement learning
 - Neural networks: an ML algorithm to identify patterns in data by simulating the brain's processing methods. Deep learning, employs complex, multilayered neural networks to perform these tasks.

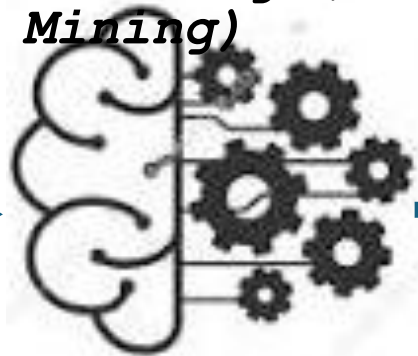
Data Modelling (Machine Learning)

Data Source

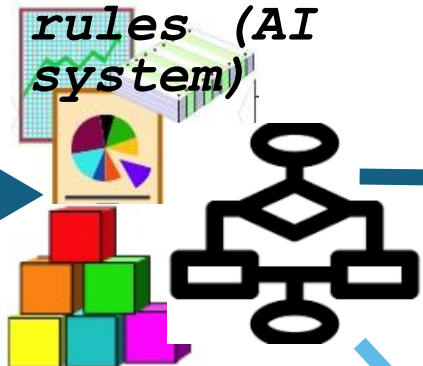
Structure	ID_NUM	logP	Polar surface area	'&LogS
	ID_000816	3.65	12.47	0.18144
	ID_000400	5.93	19.03	0.40616
	ID_000394	6.14	19.03	0.51136
	ID_000401	6.22	19.03	0.55696



Machine learning (Data Mining)



Learned Patterns or rules (AI system)



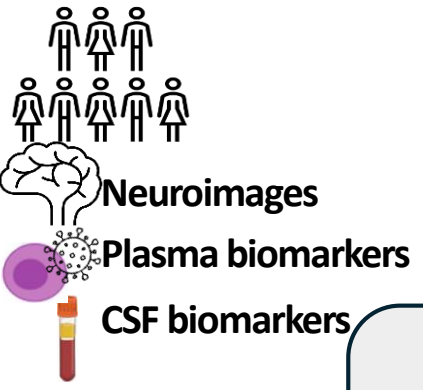
Predictions & Decisions for new molecules



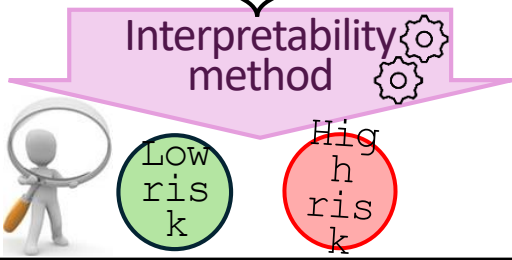
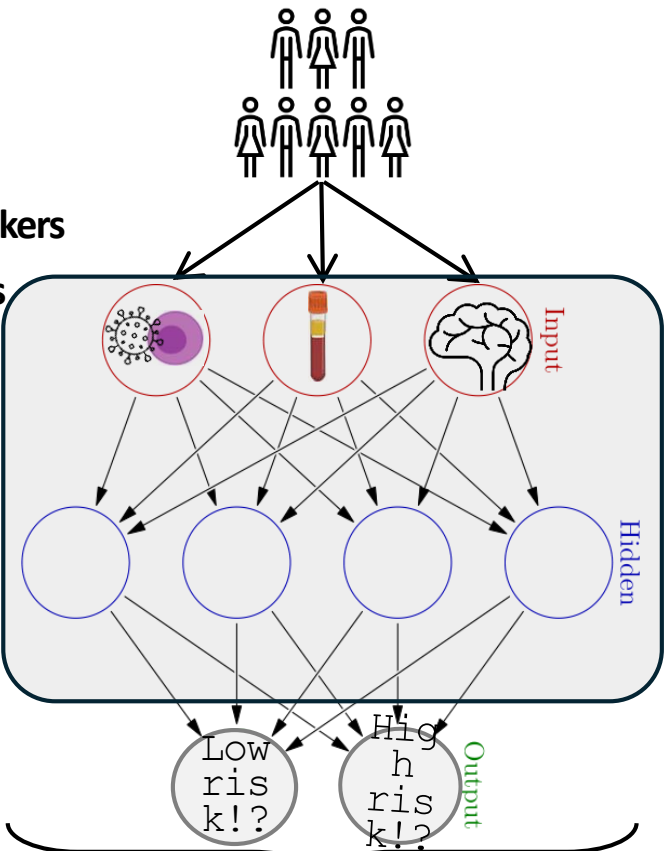
Knowledge



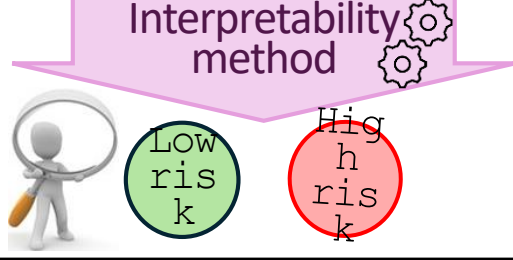
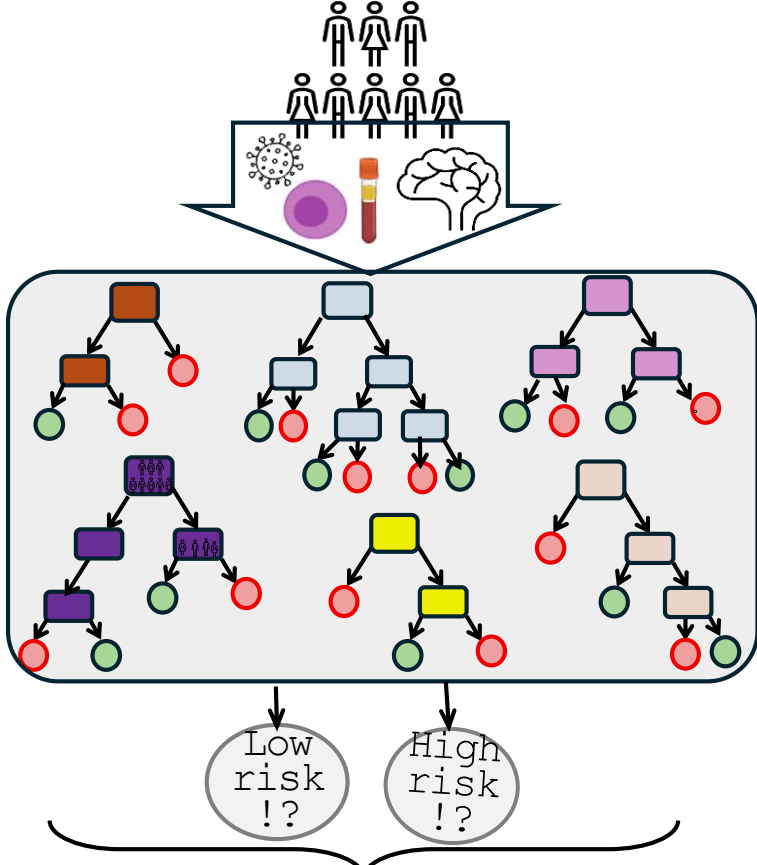
Patient dataset



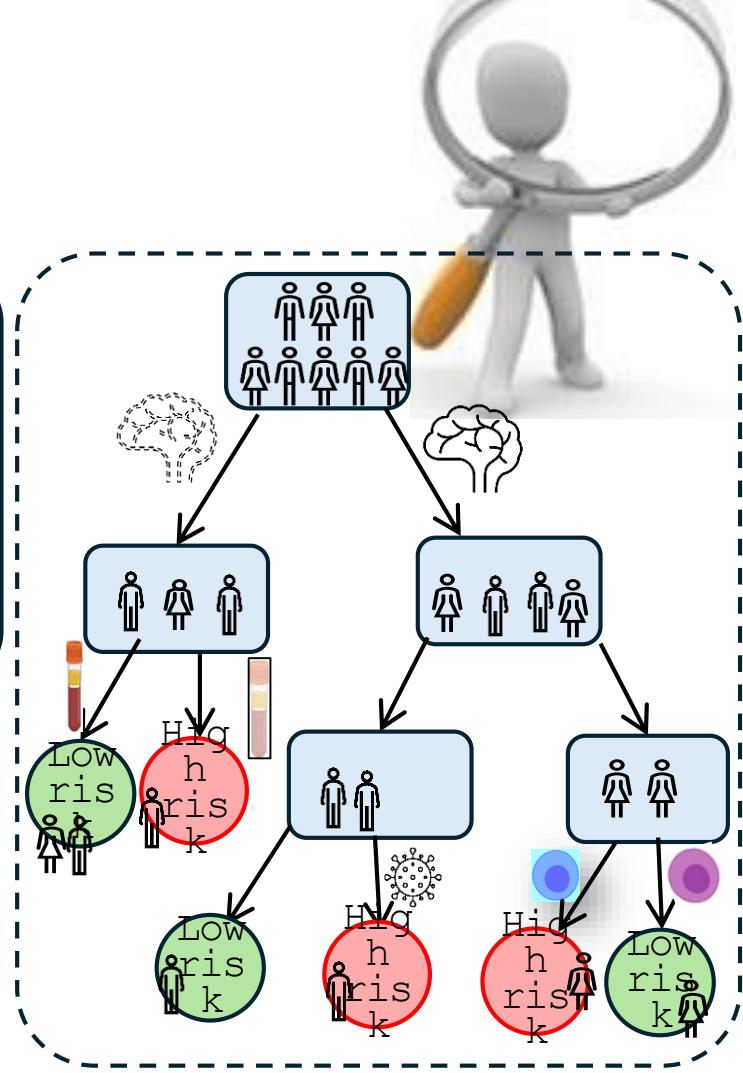
**Black box model
Neural Net**



**Black box model
Random Forest**

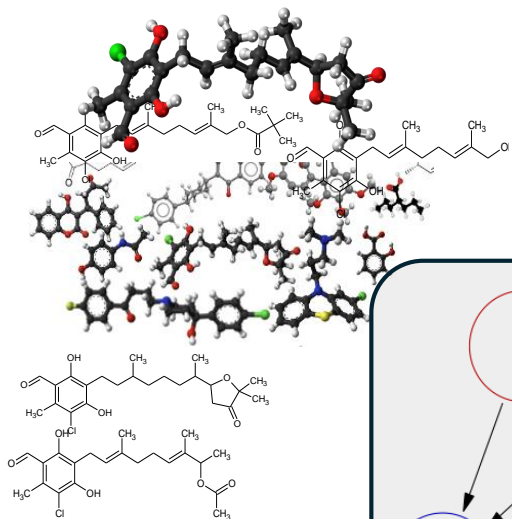


**White box model
Decision Tree**

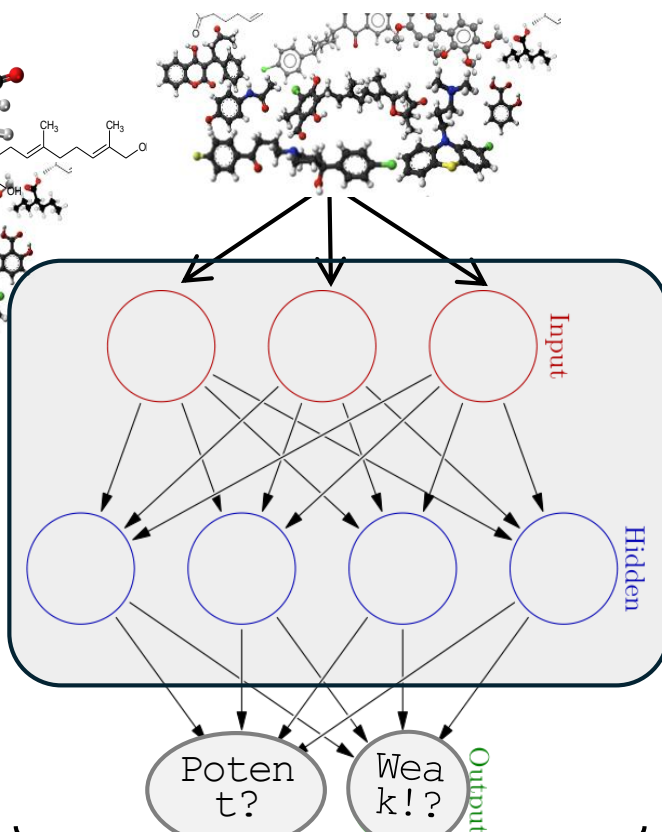


Prediction quality:
Accuracy, Generalizability, Reliability, Interpretability

Compound dataset



Black box model Neural Net

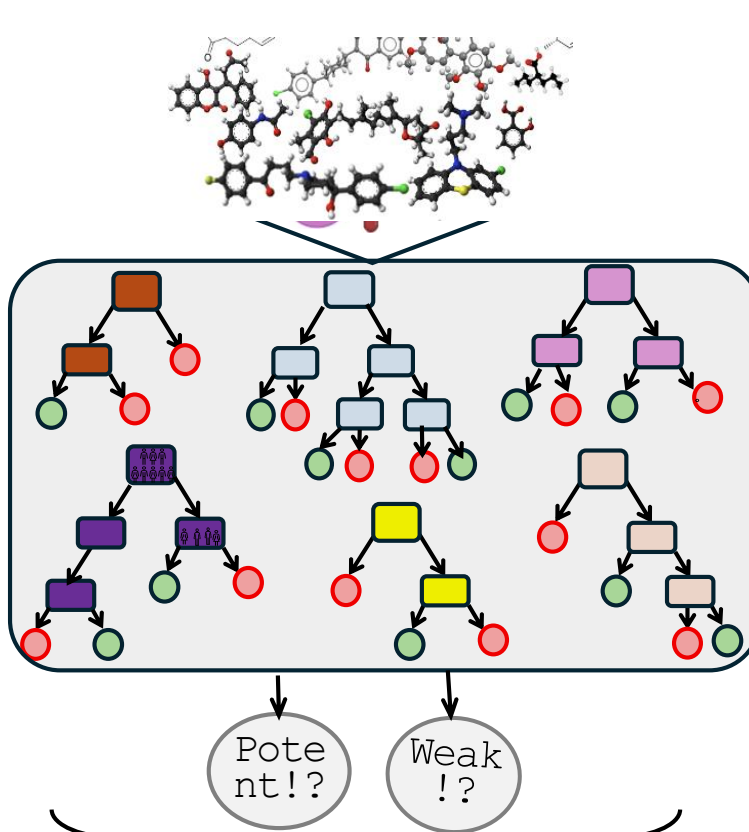


Interpretability method



Potent Weak

Black box model Random Forest

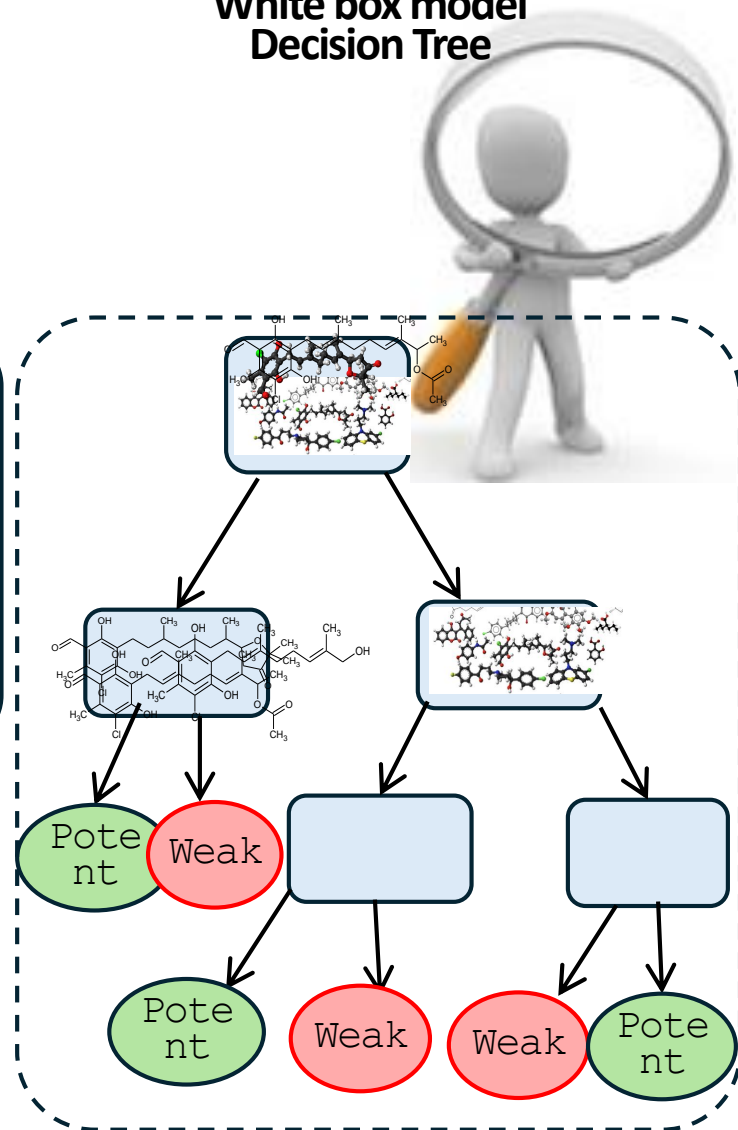


Interpretability method



Potent Weak

White box model Decision Tree



FDA Modernization Act 2.0

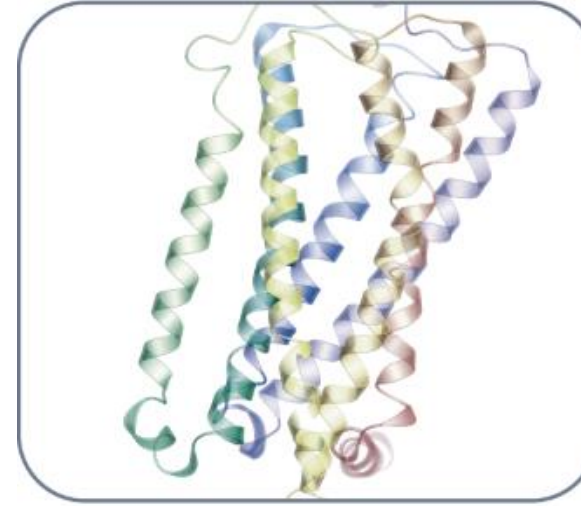
As part of the Omnibus Bill signed in Dec 2022 by President Biden, the act eliminates the requirement to conduct animal testing before human trials

- Opportunities for alternatives to animal testing

Progress in Computational modelling for Drug Discovery

- The flood of data on ligands and their binding to targets
- the 3D structures of proteins (PDB has 200K proteins, **AlphaFold** can predict the 3D model)
- abundant computing capacities
- on-demand virtual libraries of billions of drug-like molecules (3×10^{10} on-demand compounds in 2022)
- deep learning predictions of ligand properties and target activities

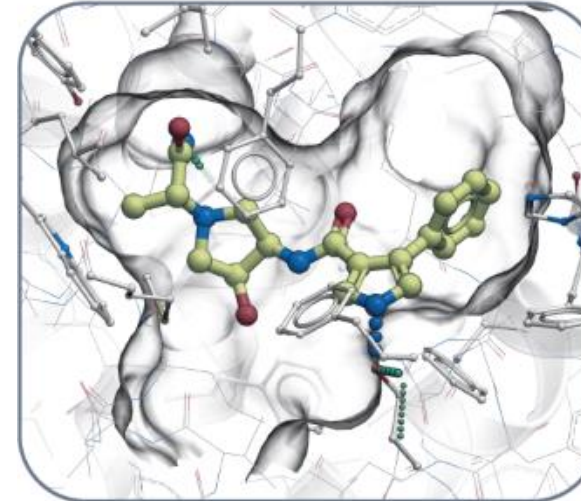
a Abundance of template 3D structures



b Growth of virtual chemical spaces



c Advanced computational methods



d Accessible computing power

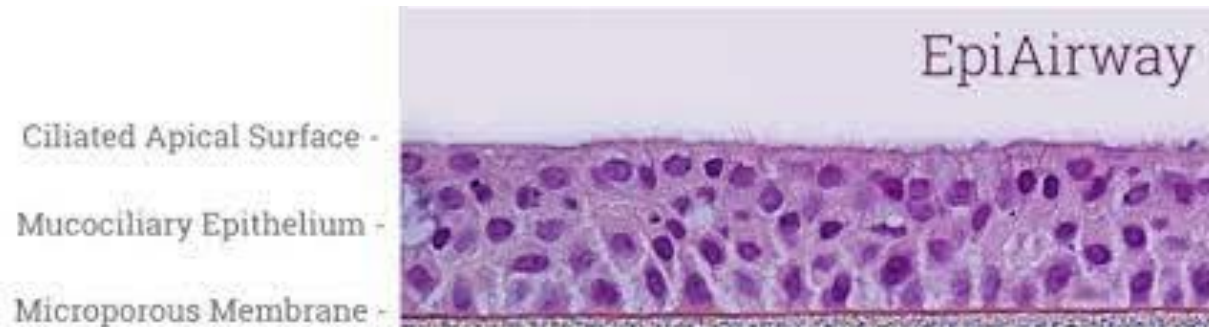
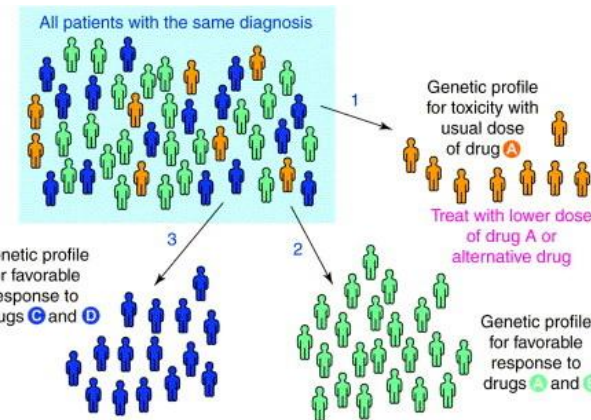
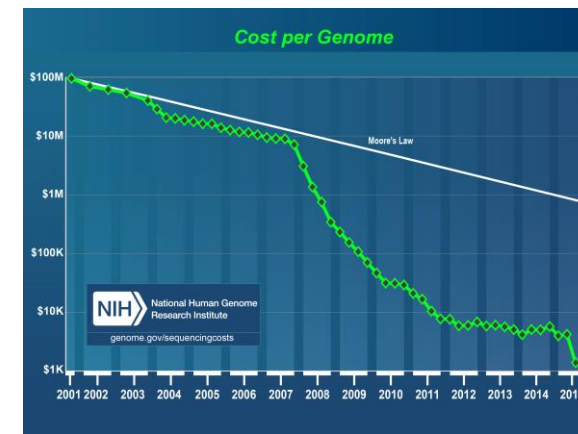


presenting new opportunities for the cost-effective development of drugs; democratizing the drug discovery

<https://www.nature.com/process/articles/s41586->

Impact of New "Revolutionary" Technologies on Drug Discovery and development

- High-throughput automated chemistry: microwave-assisted and flow chemistry, combinatorial chemistry
- Gene chips, genomics and sequencing and now CRISPR/Cas9 for gene editing
- Omics tools
- High-throughput screening & assays: 3D-cell cultures, Organ-on-Chip, in vitro ADME/Tox
- Progress in tissue engineering and organ on a chip
- Bioinformatics & Molecular biology tools
- Biomedical Databases: bioactivity, protein distribution, differential gene expression, network pharmacology
- Longitudinal observational data
- Virtual screening and library design and Docking
- and now AI



Databases: Big Data

- Chemical data and drug data

ChemSpider
Search and share chemistry

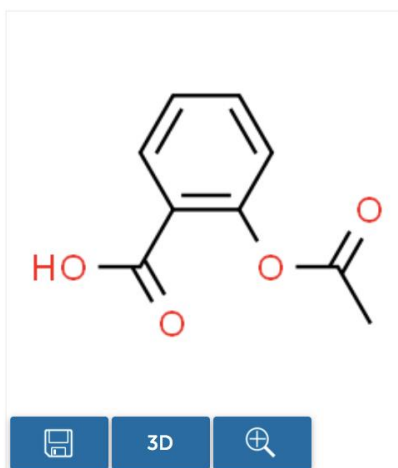
>114 million structures

For medical information relating to Covid-19, please consult the [World Health Organisation](#) or local health authorities.

[Simple](#) [Structure](#) [Advanced](#) [History](#)

Found 1 result

Search term: **aspirin** (Found by approved synonym)



Aspirin

Molecular Formula	C ₉ H ₈ O ₄
Average mass	180.157 Da
Monoisotopic mass	180.042252 Da
ChemSpider ID	2157



More details:

Systematic name	2-Acetoxybenzoic acid
SMILES	<chem>CC(OC1=C(C(=O)O)C=CC=C1)=O</chem> <chem>CC(=O)OC1=CC=CC=C1C(=O)O</chem>

DRUGBANK Online

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Aspirin

Identification

Pharmacology

Interactions

Products

Categories

Chemical Identifiers

References

Clinical Trials

Pharmacoeconomics

Properties

Spectra

Targets (19)

Enzymes (4)

Transporters (3)

Summary Aspirin is a salicylate used to treat pain, fever, inflammation, migraines and to prevent major adverse cardiovascular events.

Brand Names *Aggrenox, Alka-seltzer, Alka-seltzer Fruit Chews, Anacin, Arthriten Inflammation, Aspirin, Aspirin Low, Bayer Aspirin, Bayer Womens, Br Arthritis, Br Original Formula*

Generic Name Acetylsalicylic acid **DrugBank Accession Number**

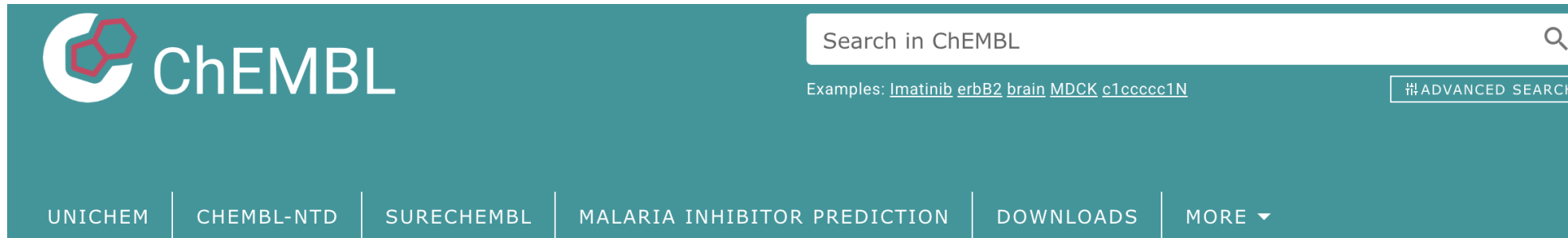
Background Also known as *Aspirin*, acetylsalicylic acid (ASA) is a commonly used drug to relieve pain and fever due to various causes. Acetylsalicylic acid has both anti-inflammatory and antipyretic effects. This drug also inhibits platelet aggregation and is used to prevent blood clots stroke, and myocardial infarction (MI) ^{Label}.

Interestingly, the results of various studies have demonstrated that low-dose acetylsalicylic acid may decrease the risk of various cancers, including colorectal, breast, and prostate cancer. ¹⁵ Aspirin is also used for

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Databases: bioactivity data



ChEMBL

Search in ChEMBL

Examples: [Imatinib](#) [erB2](#) [brain](#) [MDCK](#) [c1ccccc1N](#)

ADVANCED SEARCH

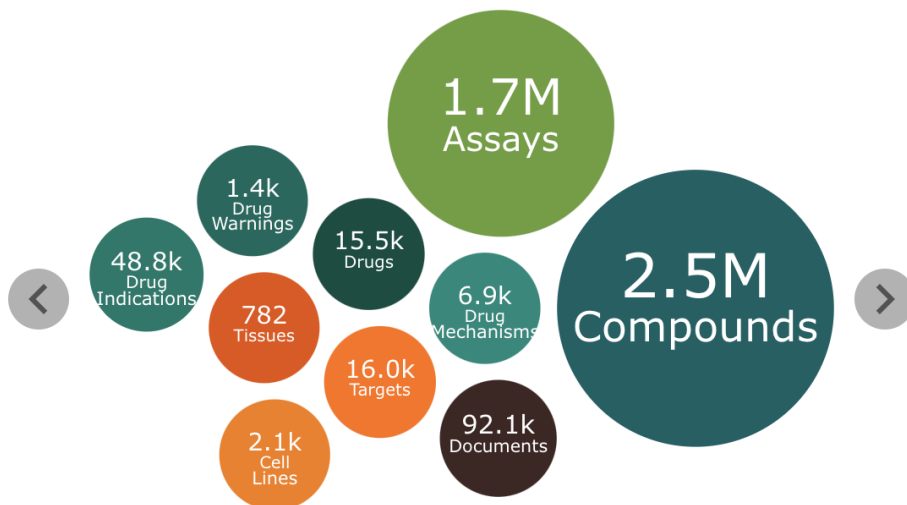
UNICHEM | CHEMBL-NTD | SURECHEMBL | MALARIA INHIBITOR PREDICTION | DOWNLOADS | MORE ▾

ChEMBL is a manually curated database of bioactive molecules with drug-like properties. It brings together chemical, bioactivity and genomic data to aid the translation of genomic information into effective new drugs.

Explore ChEMBL

Description: Shows a summary of the ChEMBL entities and quantities of data for each of them.

Instructions: Click on a bubble to explore a specific ChEMBL entity in more detail.



<https://www.ebi.ac.uk/chembl/>

Toxicogenomic Data



National Toxicology Program
U.S. Department of Health and Human Services

What We Study ▾

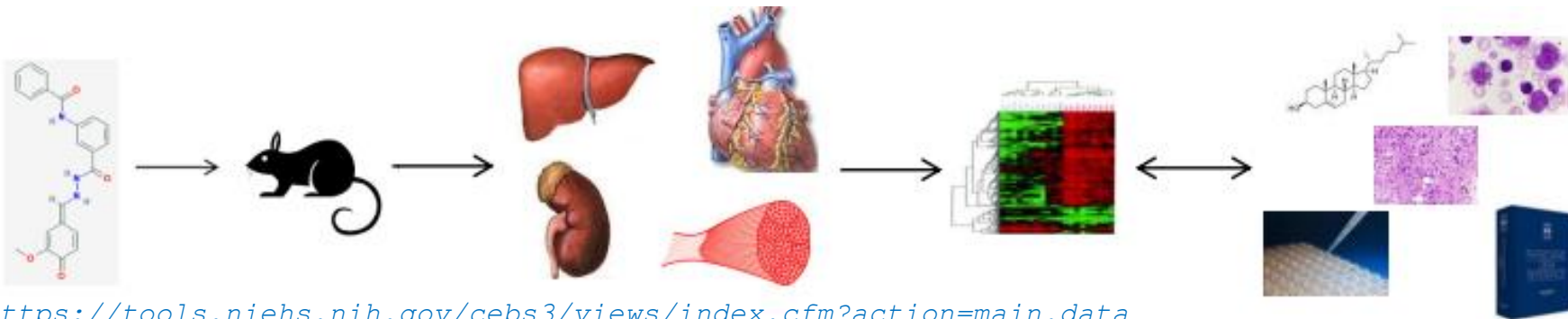
How We Work ▾

Data & Resources ↗

Publication

Home » Data & Resources » **DrugMatrix/ToxFX**

DrugMatrix/ToxFX

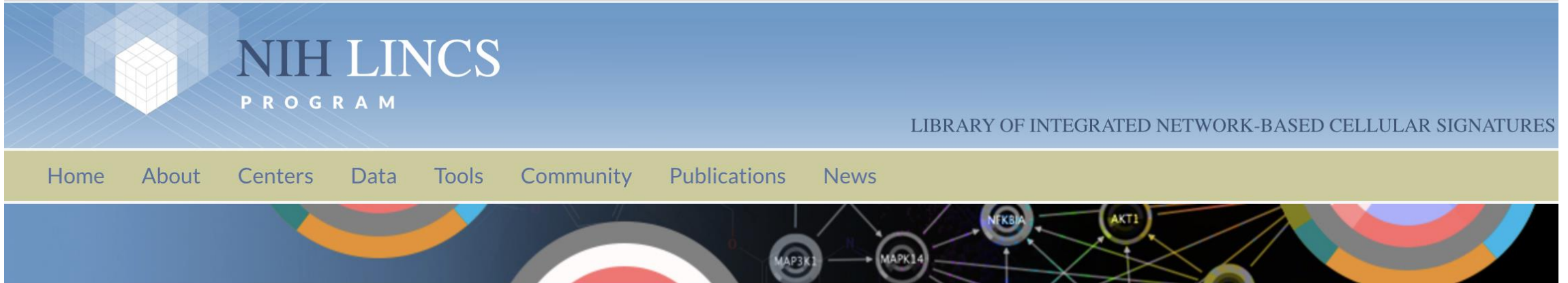


https://tools.niehs.nih.gov/cebs3/views/index.cfm?action=main.dataReview&bin_id=15670

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Differential Gene Expression due to many exogenous and endogenous perturbations



LINCS Data and Signature Generation Centers (DSGCs)

1. Drug Toxicity Signature Generation Center: cell signatures to predict adverse drug reactions
2. The HMS LINCS Center: normal and diseased human cells response to perturbation by drugs, mutations, environment
3. The LINCS Center for Transcriptomics is studying up to 50 cell types perturbed by a large number of compounds
4. The LINCS Proteomic Characterization Center for Signaling and Epigenetics studies phosphorylation-mediated signaling
5. Microenvironment Perturbagen (MEP) LINCS Center: impact on cellular phenotype, proteins, genes
6. The NeuroLINCS Center concentrates on human brain cells

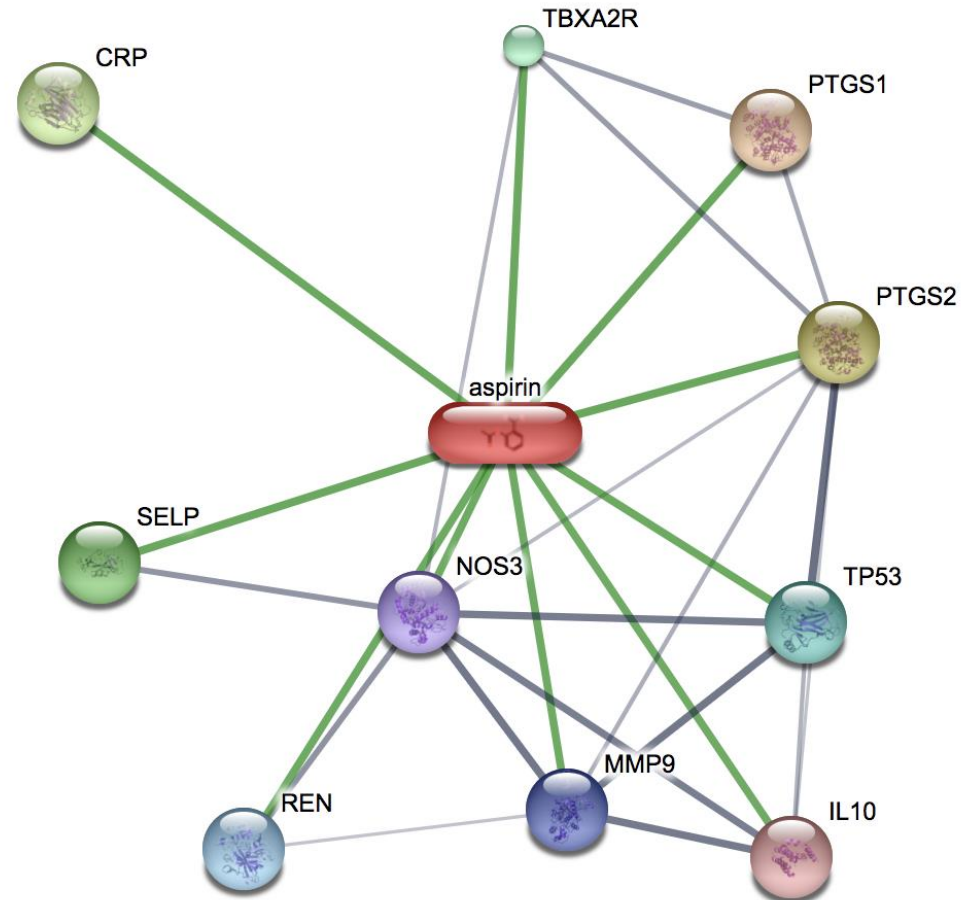
<https://lincsproject.org/LINCS/centers/data-and-signature-generating-centers>

STITCH: Chemical-Protein Interaction Networks

STITCH

Search

Download



<https://www.ebl.org>

Longitudinal Medical Data



Enable your research | Explore your participation | Learn more about UK Biobank

Enabling your vision to improve public health

Data drives discovery. We have curated a uniquely powerful biomedical database that can be accessed globally for public health research. Explore data from half a million UK Biobank participants to enable new discoveries to improve public health.

Data Showcase

Future data releases



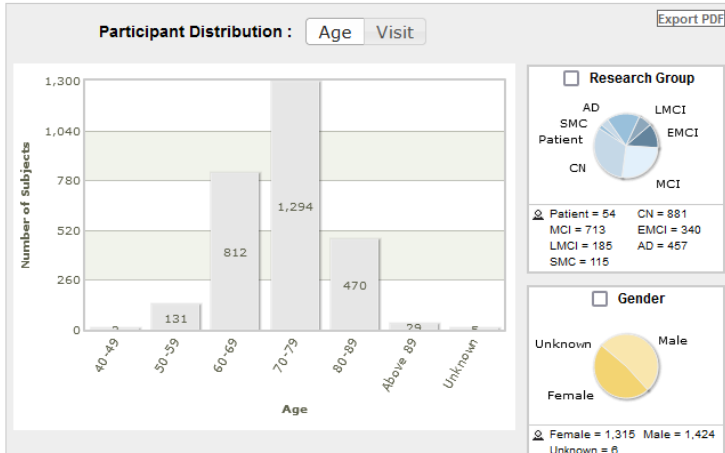
UK Biobank is a large-scale biomedical database and research resource, containing in-depth genetic and health information from half a million UK participants. The database is regularly augmented with additional data, and is globally accessible to approved researchers undertaking vital research into the most common and life-threatening diseases. It is a major contributor to the advancement of modern medicine and treatment and has enabled scientific discoveries that improve human health.

ADNI
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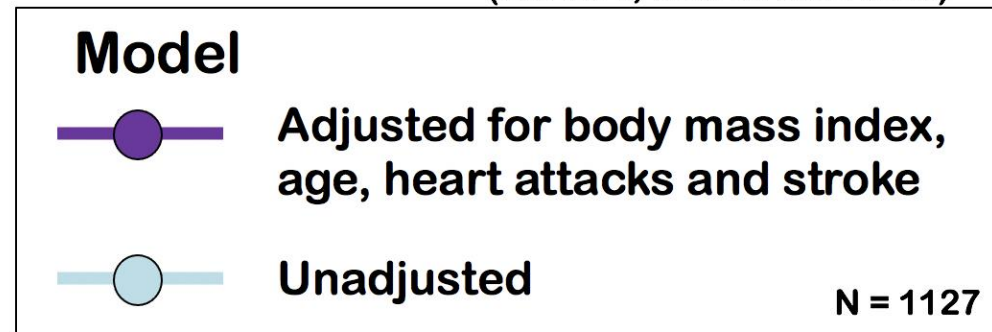
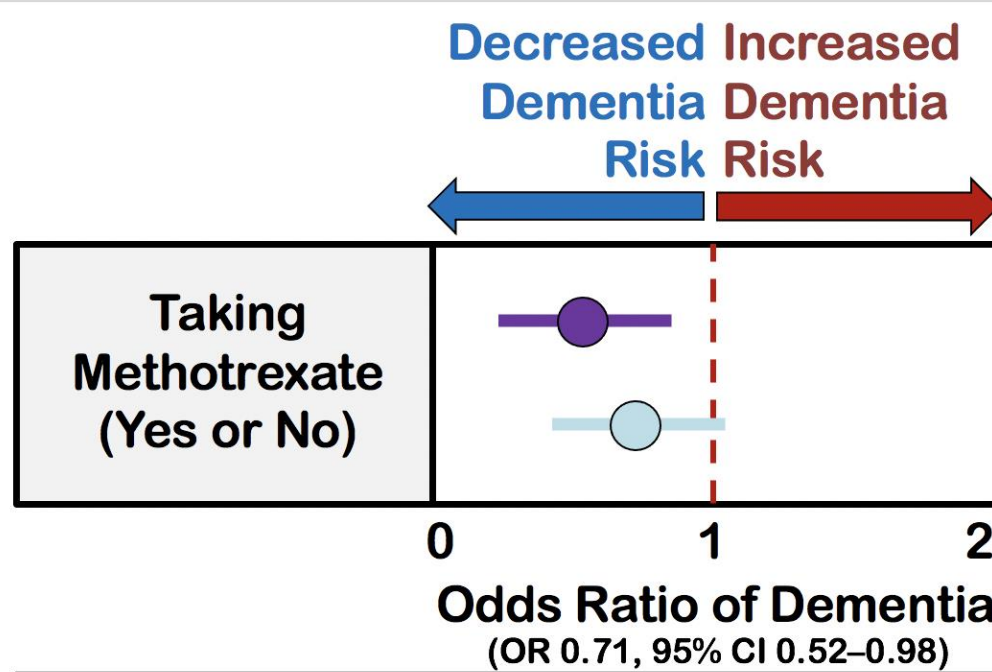
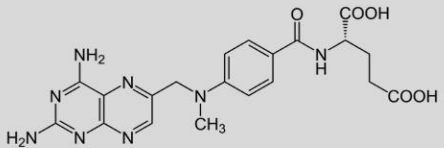
Alzheimer's Disease Neuroimaging Initiative

The Alzheimer's Disease Neuroimaging Initiative (ADNI) seeks to develop biomarkers of the disease and advance the understanding of AD pathophysiology, improve diagnostic methods for early detection of AD and improve clinical trial design. Additional goals are examining the rate of progress for both mild cognitive impairment and Alzheimer's disease, as well as building a large repository of clinical and imaging data.

- RELATED LINKS
- [NEWS AND ANNOUNCEMENTS](#)
 - [MRI RECALL NOTICES](#)
 - [SEARCHABLE DATA DICTIONARY](#)
 - [ADNI DATA USE AGREEMENT](#)



Methotrexate is associated with decreased dementia risk in people with rheumatoid arthritis



Newby et al (2020) *AlzResTher*

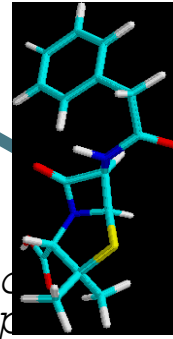


Drug Discovery & Development

Unmet medical need



Isolate protein involved in disease



Find a drug effective against disease pathogen



Preclinical testing

Formulation & Scale-up



Human clinical trials



File IND

File NDA

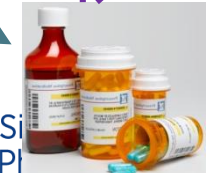
Profit decline/
withdrawal
from
market

Patent
expiration
and
competitor
products

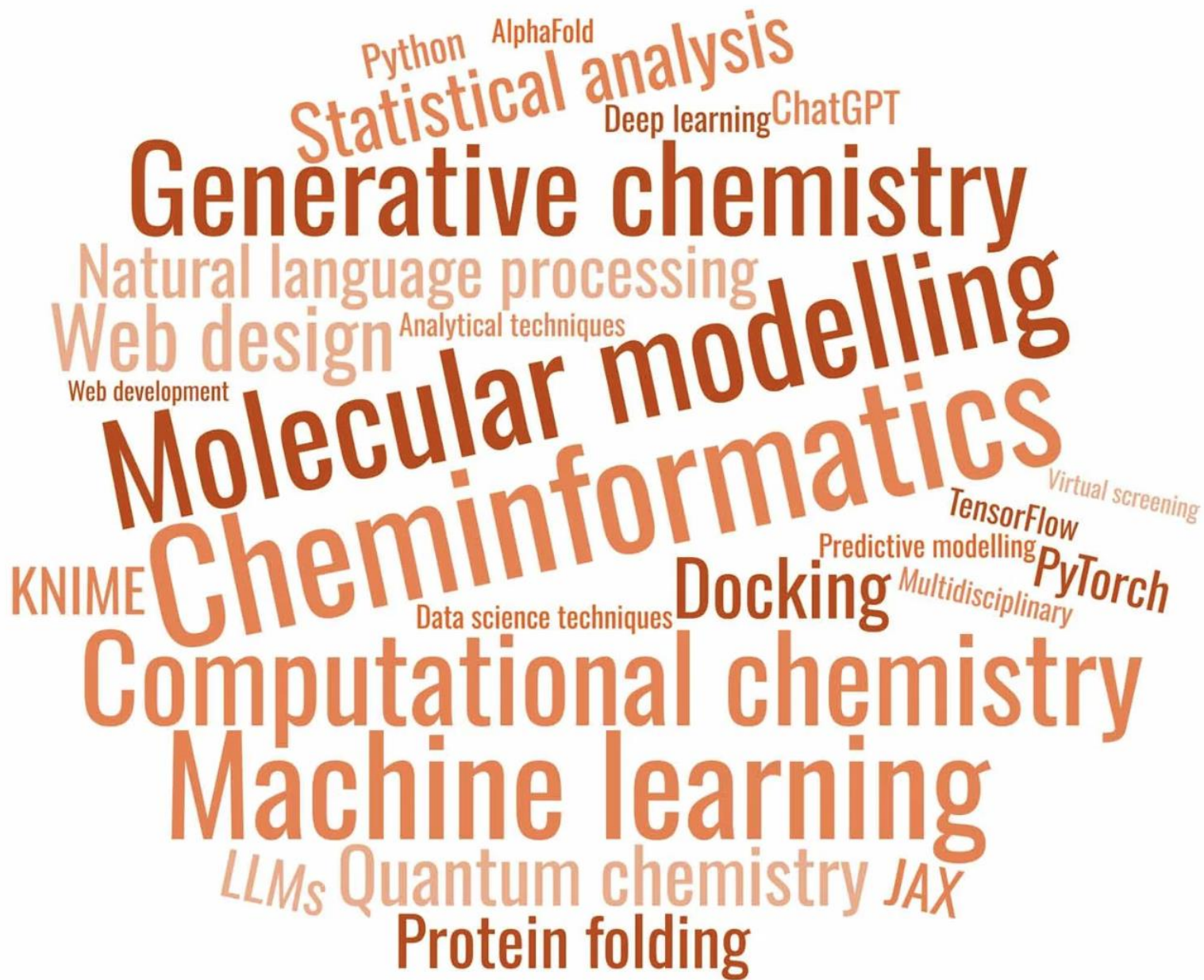
Post-
marketing
surveillance
for
safety
controls

Computer-based modelling
In vitro high-throughput testing

Regulatory Approval

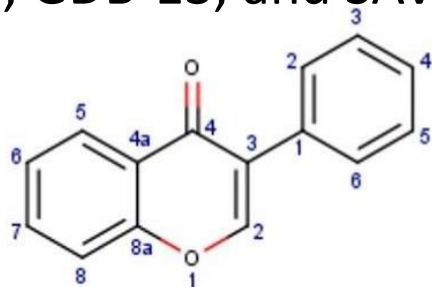


Skills for the AI-enabled chemist of the future



Molecular Representations in Chemical Librar: Used for virtual screening

- Large virtual chemical information generated by pharm, food, and agriculture industry with synthetic and stability feasibility
- Contain structural data, stereochemical information, physicochemical and spectroscopic properties
- PUBCHEM has 119m compounds
- ZINC, Enamine Real, GDB-13, and SAVI (10^9 compounds)



IUPAC Name

3-phenyl-4*H*-1-benzopyran-4-one

Smiles ACDChemSketch₁

O=C1c2ccccc2OC=C1c1ccccc1

Smiles ChemAxon₂

O=C1C(=COC2=C1C=CC=C2)C1=CC=CC=C1

Smiles JME editor₃

O=c2c(c1ccccc1)coc3ccccc23

Smiles JME editor₃

C=13(C(=CC=CC=1)C(C(C=2(C=CC=CC=2))=CO3)=O)

Smiles PubChem editor₄

C1=CC=CC2=C1C(C(=CO2)C3=CC=CC=C3)=O

SMART PubChem editor₄

c1cccc-2c1-[#6](-[#6])(=[#6]-[#8]-2)-c3ccccc3)=[#8]

InChI is the International Chemical Identifier developed by the IUPAC, a unique label for each compound

InChI=1S/C15H10O2/c16-13-10-15(11-6-2-1-3-7-11)17-14-9-5-4-8-12(13)14/h1-10H

Explore Chemistry

Quickly find chemical information from authoritative sources

Try aspirin EGFR C9H8O4 57-27-2 C1=CC=C(C=C1)C=O InChI=1S/C3H6O/c1-3(2)4/h1-2H3

Use Entrez Compounds Substances BioAssays

Draw Structure Upload ID List Browse Data Periodic Table

Molecular modelling software capabilities

Model or mimic the behavior of molecules using computational chemistry for drug design



Molecular graphics

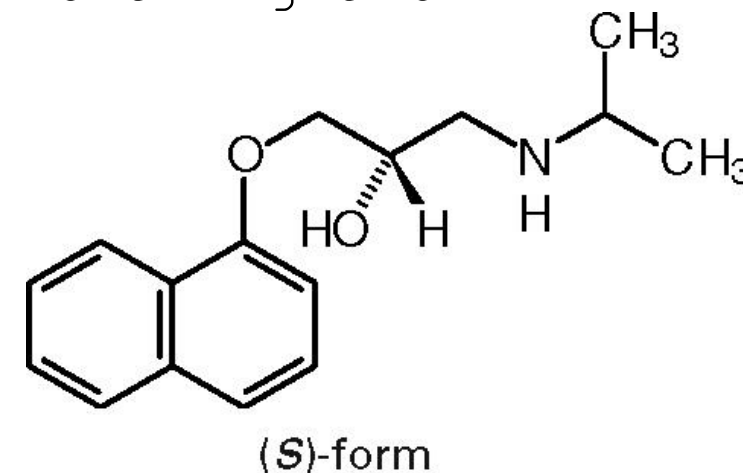


Perform theoretical chemistry calculations (forcefield or quantum mechanics)



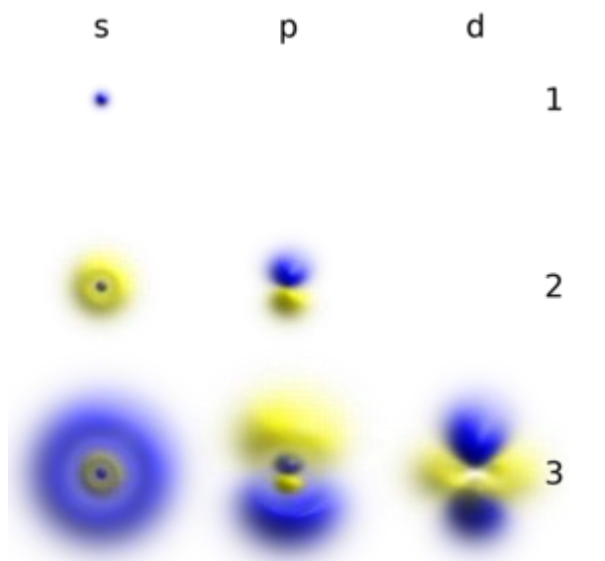
interactive molecular drawing and

The software recognizes the molecular structures in a chemically meaningful way, *i.e.*: Not just a graph, but a chemical entity



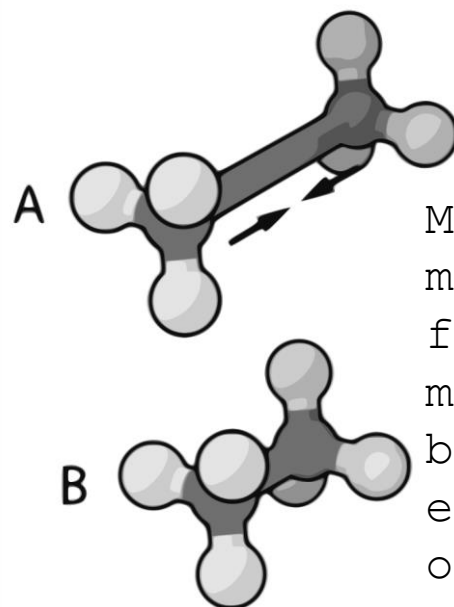
Molecular modelling

- They may treat atoms as the smallest unit (a **molecular mechanics** approach), or model protons, neutrons and electrons (a **quantum chemistry** approach)
- Methods that take advantage of data are winning as we get more data and more compute! Hence Machine Learning methods for molecular simulations ([Amin, Raja, Krishnapriyan, 2025](#))

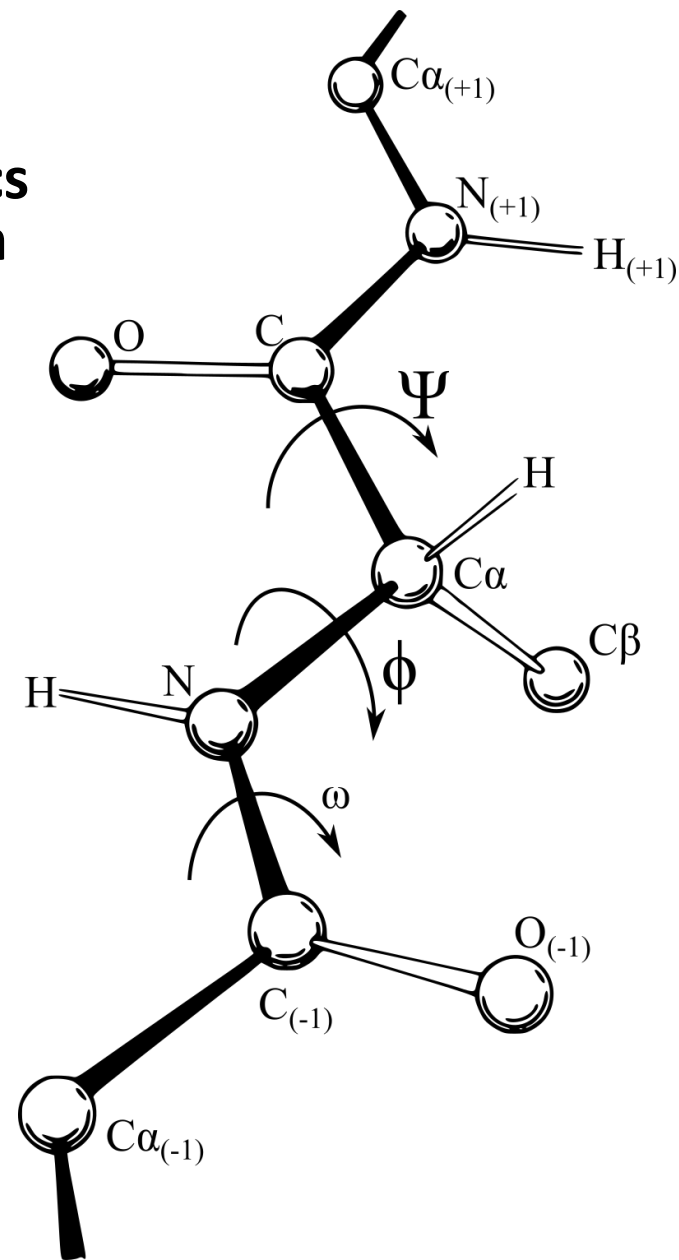


Probability densities of the wave functions of an electron in

hydrogen atom

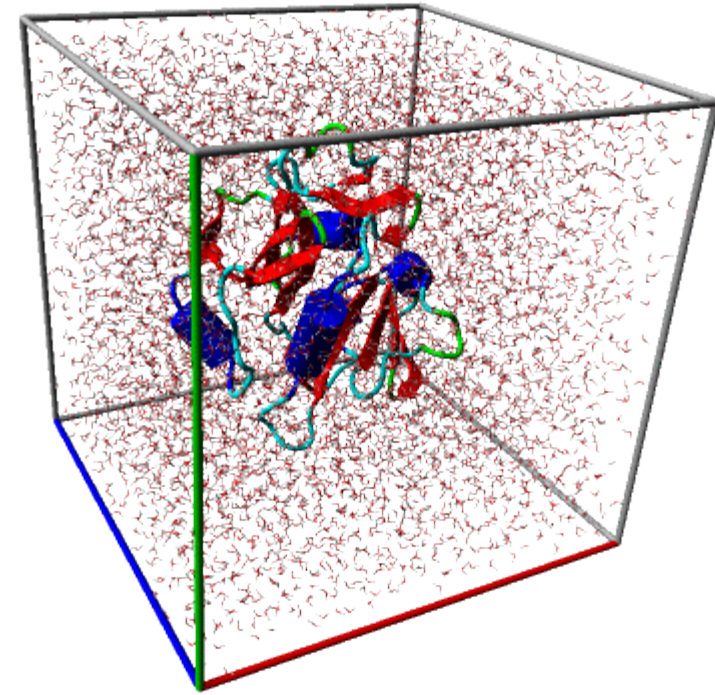


Molecular mechanics uses a force field to minimize the bond stretching energy and optimize angles.



Molecular modelling empowered by AI

- More accurate behavior is captured with:
 - Large scale simulations
 - Longer time scales
- Use available data to train AI models, one trained prediction cheap



Protein–ligand docking for virtual screening to identify hits

- Predict binding geometry of drugs to target proteins and interaction energy.
- Available software AutoDock and AutoDock Vina, rDock, FlexAID, Molecular Operating Environment, and Glide.
- Available compound libraries (10^9 compounds with fingerprints, molecular descriptors, etc)
- Accelerated docking protocols are necessary: the protein-ligand docking results between the prepared receptors and compounds are used to build ML data-frames for each binding site.

Babuji, Y. et al. Targeting sars-cov-2 with ai-and hpc-enabled lead generation: A first data release
<http://arxiv.org/abs/2006.02431>
2020

scientific reports


View

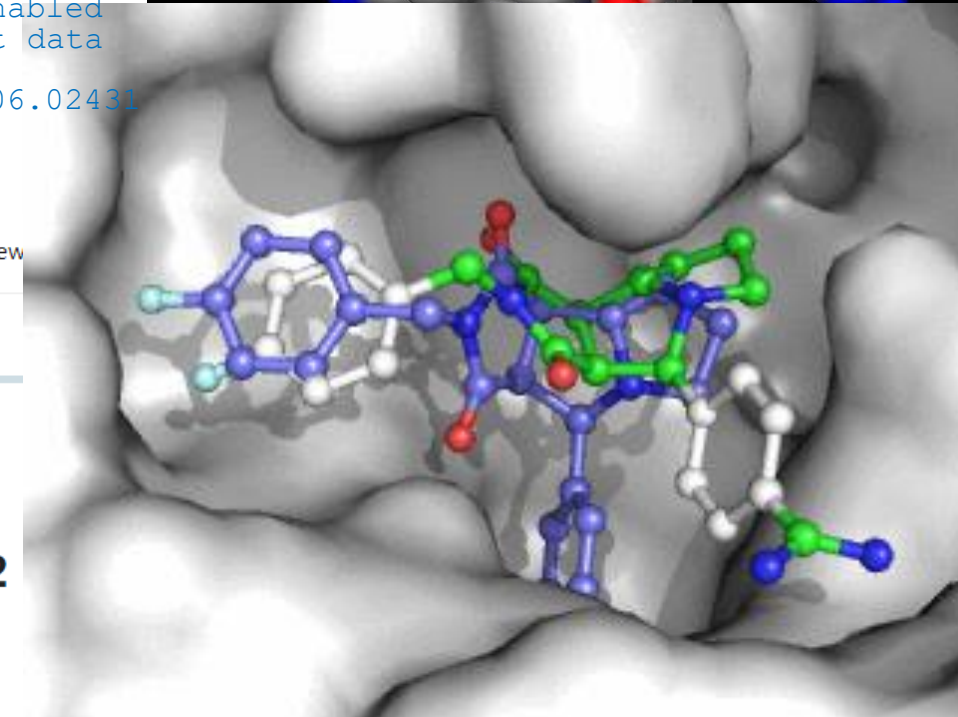
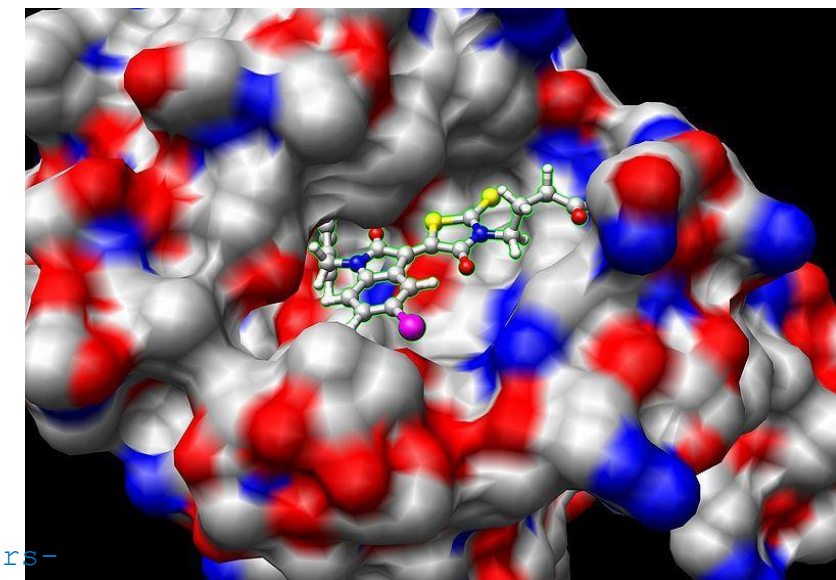
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Article | [Open access](#) | Published: 06 February 2023

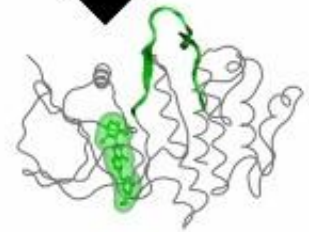
AI-accelerated protein-ligand docking for SARS-CoV-2 is 100-fold faster with no significant change in detection

[Austin Clyde](#) , [Xuefeng Liu](#), [Thomas Brettin](#), [Hyunseung Yoo](#), [Alexander Partin](#), [Yadu Babuji](#), [Ben Blaiszik](#), [Jamaludin Mohd-Yusof](#), [Andre Merzky](#), [Matteo Turilli](#), [Shantenu Jha](#), [Arvind Ramanathan](#) & [Rick Stevens](#)

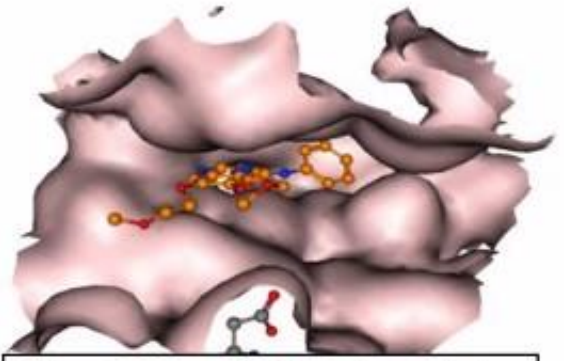


Typical Structure-Based Drug Design (SBDD) Workflows

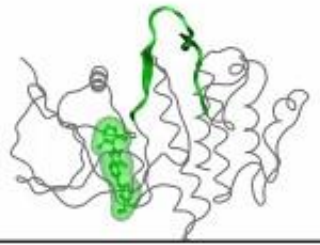
2D protein sequence



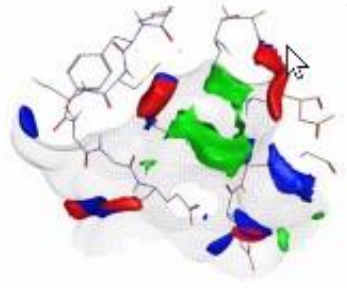
Protein Homology Model
3D structure



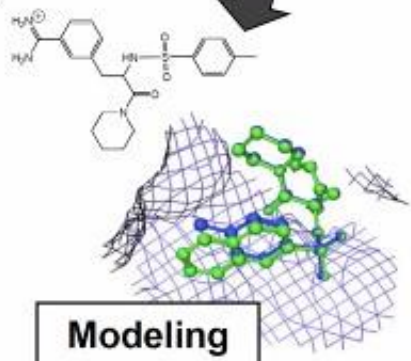
Binding pocket and protein-ligand
interaction analysis



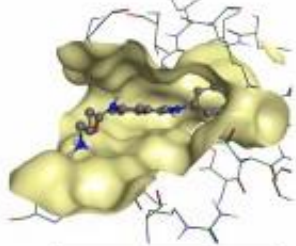
Loading and
preparing protein-ligand
complexes



Surfaces
and Maps



Modeling
ligands in
the pocket



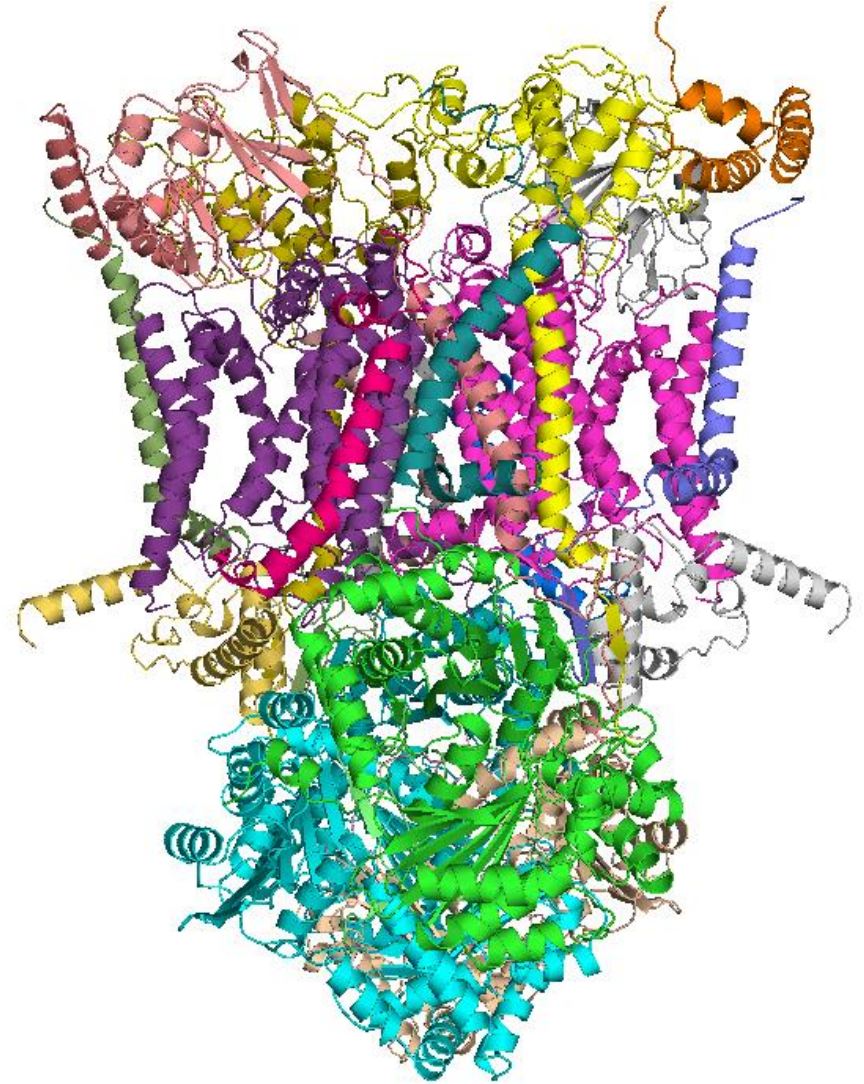
Docking



Aligning and
comparing
protein
complexes

Protein data bank

1. Protein Databank has the 3D structure of proteins
<https://www.rcsb.org>
2. Various resolutions and accuracy



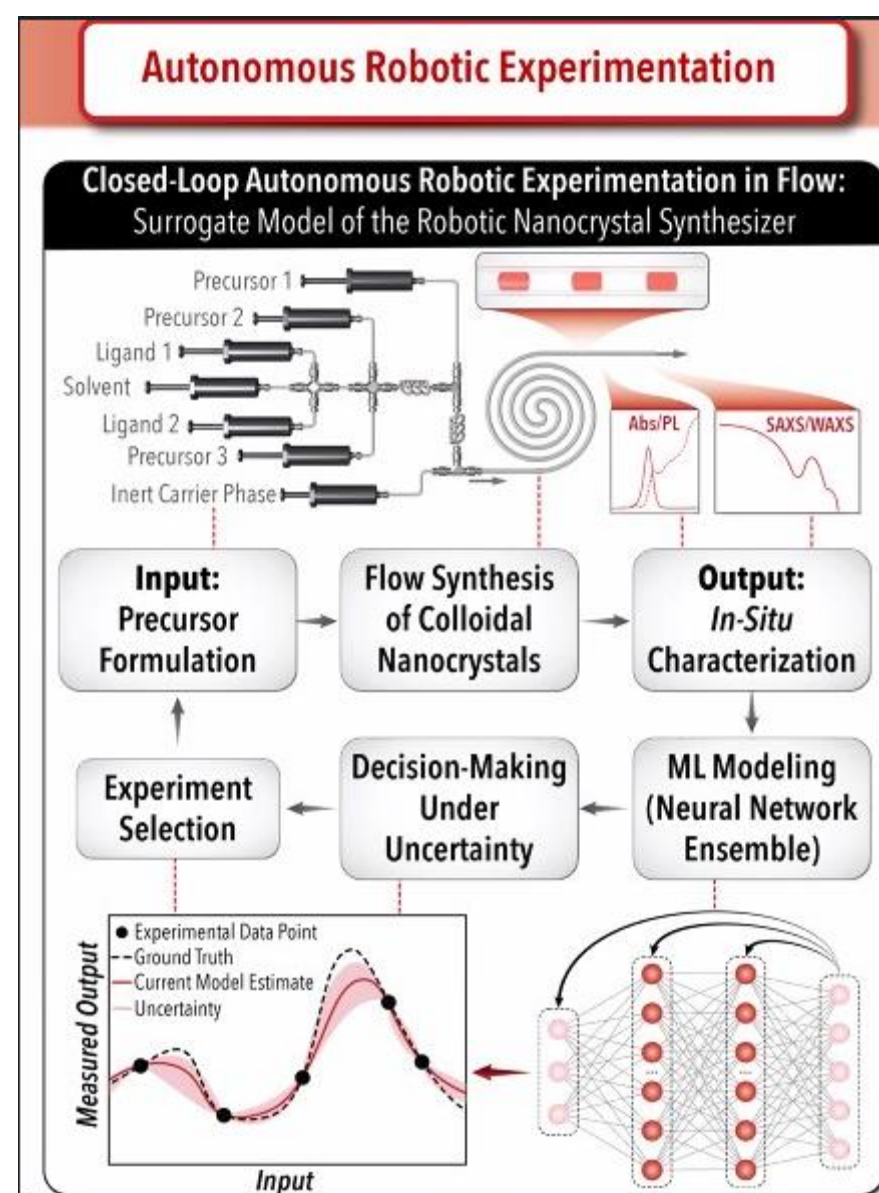
AI in Protein Folding: AlphaFold

- The problem of predicting protein folding from amino acid sequences a grand challenge (Nobel Laureate Christian Anfinsen in 1972)
- A biennial competition called Critical Assessment of Protein Structure Prediction (CASP) was launched in 1994 to encourage efforts around the protein folding problem
- DeepMind, a UK-based AI company now part of Alphabet Inc developed a neural network model named AlphaFold which was trained on known protein structures in the protein data bank (PDB) and won the 14th CASP competition with remarkably accurate predictions within error of experiments.

<https://youtu.be/cx719ZGFZkw?si=JvFNEcINqW-uuJjs>

Do we have enough data?

- No!
- Compare the amount of available human text that powers ChatGPT
- Complexity of systems requires complex data collection strategies
- High-throughput data collection is focused on specific research questions: (confirmation bias?)
- Phenotypic data is lagging behind



AlphaFlow is a self-driven fluidic lab capable of autonomously discovering complex multi-step chemistries.

Chen et al., Solhasani, et al, Nature Comm.

AlphaFlow, 2023,

[https://www.nature.com/articles/s41467-023](https://www.nature.com/articles/s41467-023-023)

A combined in vitro and in silico approach in the study of drug-induced mitochondrial dysfunction

Drug-Induced Mitochondrial Dysfunction related to organ toxicities

"Failures to predict adverse drug reactions have immense financial implications, result in adverse human suffering and erode in trust of regulatory and pharmaceutical processes"

Diwan, A., et al. Y. Hill. 2010. The High Financial Cost of Mitochondrial Toxicity Testing in drug development. Drug Discovery Today, 12(17): p. 777-785.

Examples of drugs with Black Box warnings

Drugs with mitochondrial liabilities in red

Hepatic toxicity		Cardiovascular toxicity		Renal toxicity
<u>Antivirals</u> Abacavir Didanosine Emtricitabine Entecavir Lamivudine Nevirapine Telbivudine Tenofovir Tipranavir Stavudine Zalcitabine Zidovudine	<u>CNS Drugs</u> Dandrolene Divalproex Sodium Felbamate Naltrexone Nefazodone Valproic acid	<u>NSAIDs</u> Celecoxib Diclofenac Diflunisal Etodolac Fenoprofen Ibuprofen Indomethacin Ketoprofen Mefenamic acid Meloxicam Naproxen Nabumetone	Oxaprozin Piroxicam Salsalate Sulindac Thioridazine Tolmetin	<u>Anti-cancer</u> Arsenic trioxide Cetuximab Denileukin diftitox Mitoxantrone Tamoxifen
<u>Anti-cancer</u> Flutamide Dacarbazine Gemtuzumab Methotrexate Pentostatin Tamoxifen	<u>Antibiotics</u> Isoniazid Ketoconazole Streptozocin Trovafloxacin	<u>Anthracyclines</u> Daunorubicin Doxorubicin Epirubicin Idarubicin	<u>Beta-blocker</u> Atenolol	<u>Immunosuppressants</u> Cyclosporin A
		<u>Anaesthetics</u> Bupivacaine	<u>Beta-blocker</u> Atenolol	<u>Antivirals</u> Tenofovir
		<u>Anti-diabetic</u> Pioglitazone Rosiglitazone	<u>CNS Depressants and Stimulants</u> Amphetamines Atomoxetine Droperidol Methamphetamine Pergolide	<u>Anti-cancer</u> Doxorubicin Cisplatin Ifosfamide

Of the 38 drugs withdrawn from the market between 1994 and 2006, the majority were hepatotoxic or cardiotoxic

Electron Transport Chain

Chain

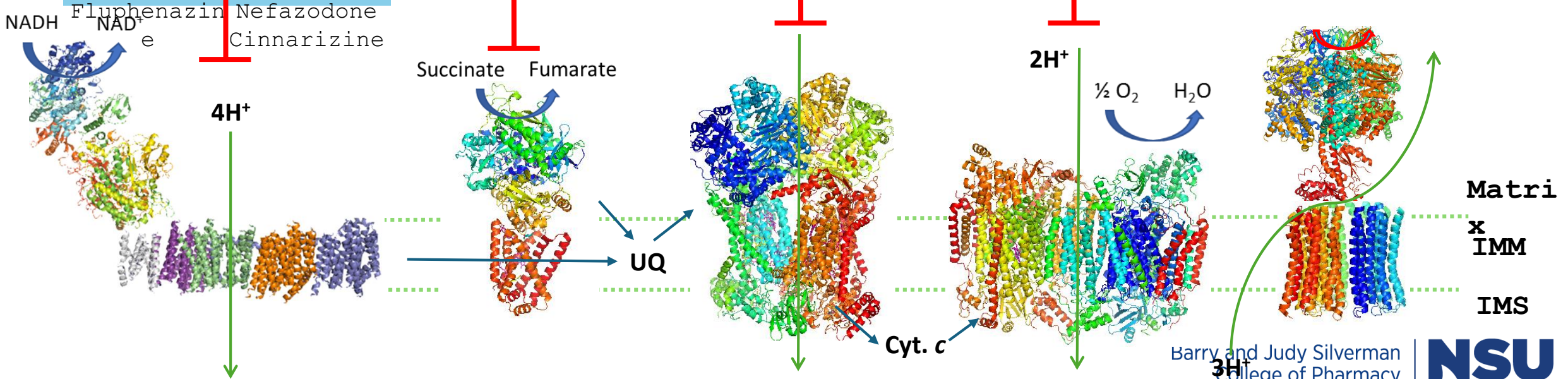
Amobarbital Buformin
 Haloperidol Phenformin
 Chlorpromazine Troglitazone
 Risperidone Rosiglitazone
 Clozapine
 Metformin Pioglitazone
 Articaine
 Bupivacaine Carvedilol
 Phenytoin Ifosfamide
 Meperidine Phenformin
 Clofibrate Canagliflozin
 Fenofibrate
 Fluphenazine Nefazodone
 Cinnarizine

Cyclophosphamide
 Isoniazid
 Clozapine
 Olanzapine
 Ketoconazole
 Carboxin
 Fenfuram
 Methfuroxam
 Thifluzamide

Atovaquone
 Isoflurane
 Sevoflurane
 Simvastatin
 Lovastatin
 Darglitazone
 Ciglitazone
 Troglitazone
 British Anti-Lewisite

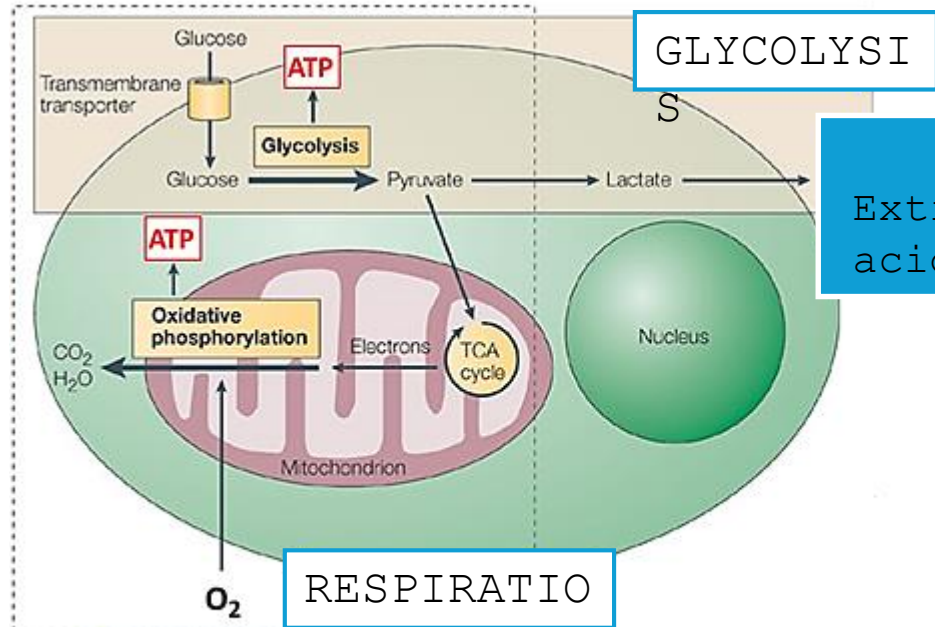
Cephaloridine
 Tamoxifen
 Cefazolin
 Hydrocortisone
 Cefalotin
 Azide
 Cyanide
 Tamoxifen

Oligomycin
 Lidocaine
 Paraquat
 Propranolol
 Aurovertin A



Figured adapted from Ashton, T.M., et al., *Oxidative Phosphorylation as an Emerging Target in Cancer Therapy*. Clin Cancer Res, 2018. 24(11): p. 2482-2490.

Seahorse Bioscience
XF96

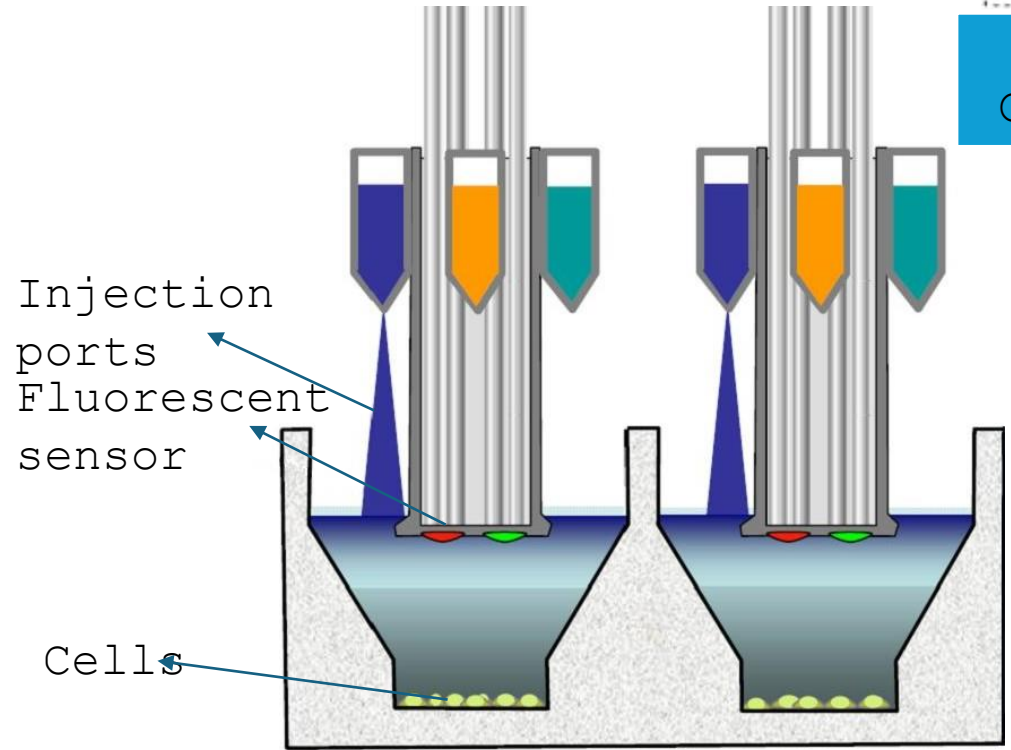


GLYCOLYSIS

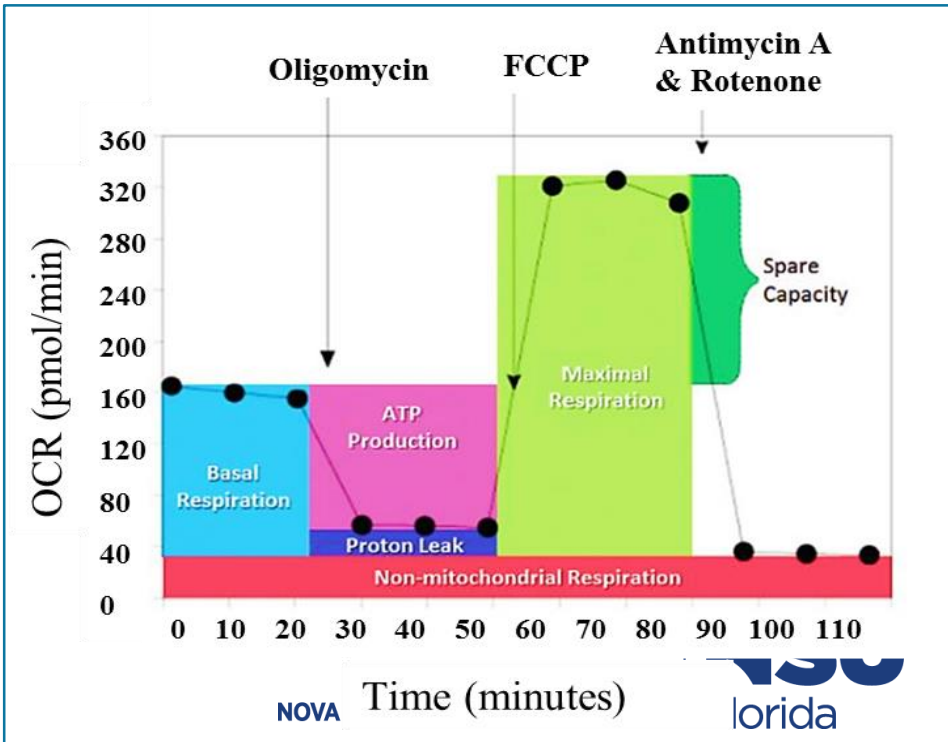
ECAR
Extracellular acidification rate

RESPIRATION

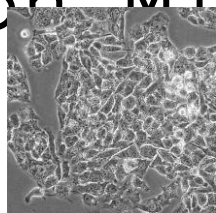
OCR
Oxygen consumption rate



Injection ports
Fluorescent sensor
Cells



The Acute Extracellular Flux Assay to Investigate Real-Time Effects of Fungicides on Mitochondrial Function

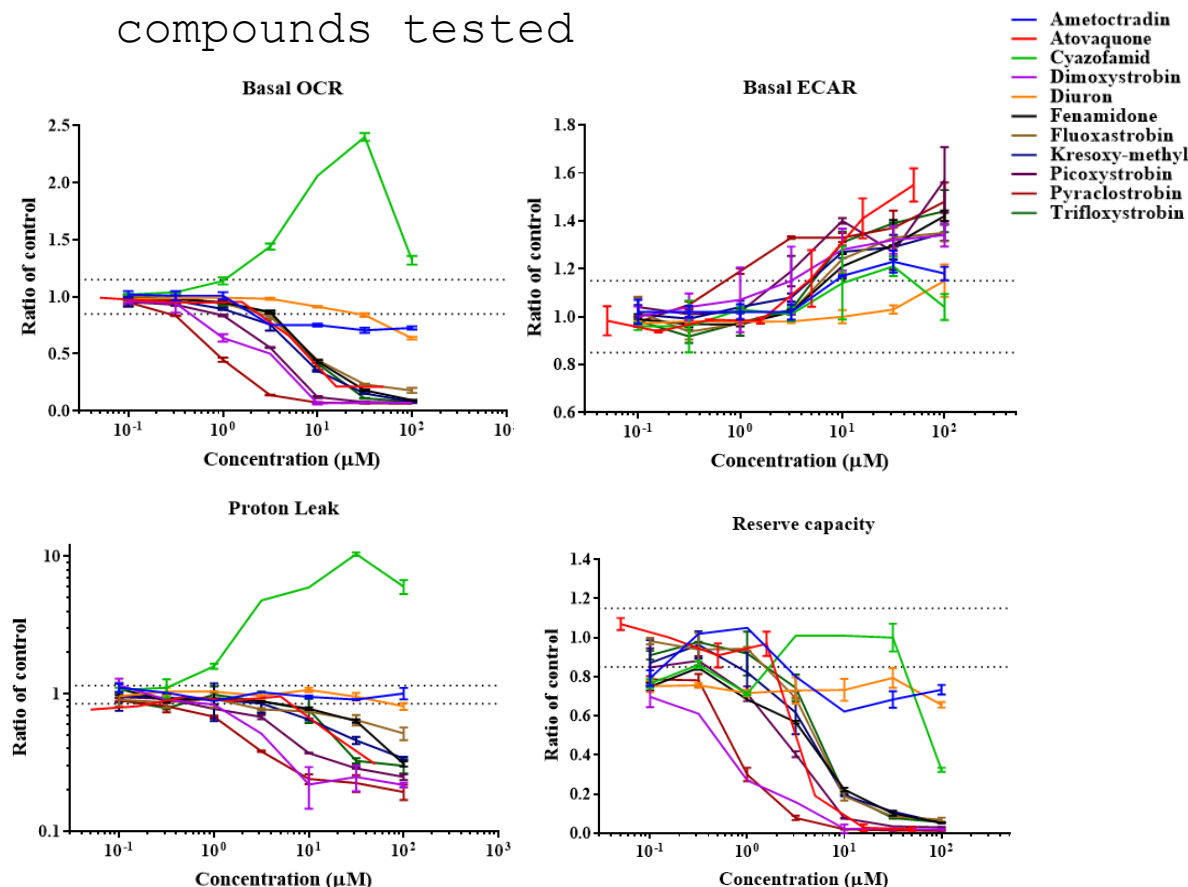


Intact HepG2 cells



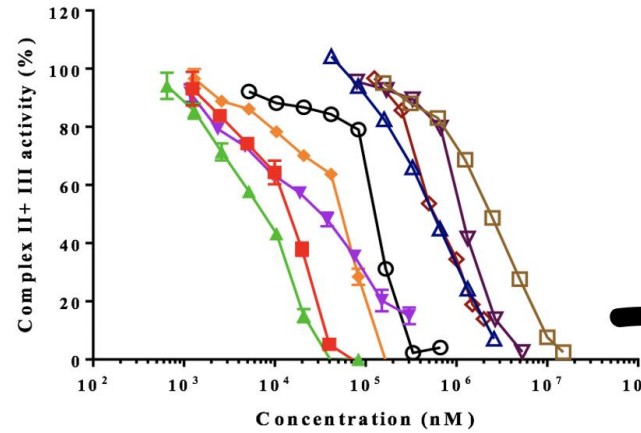
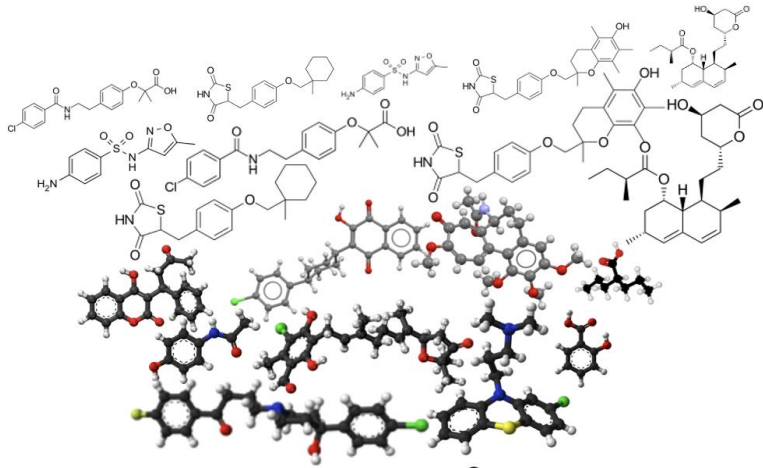
Seahorse Bioscience
XF96

Bioenergetic profile of compounds tested

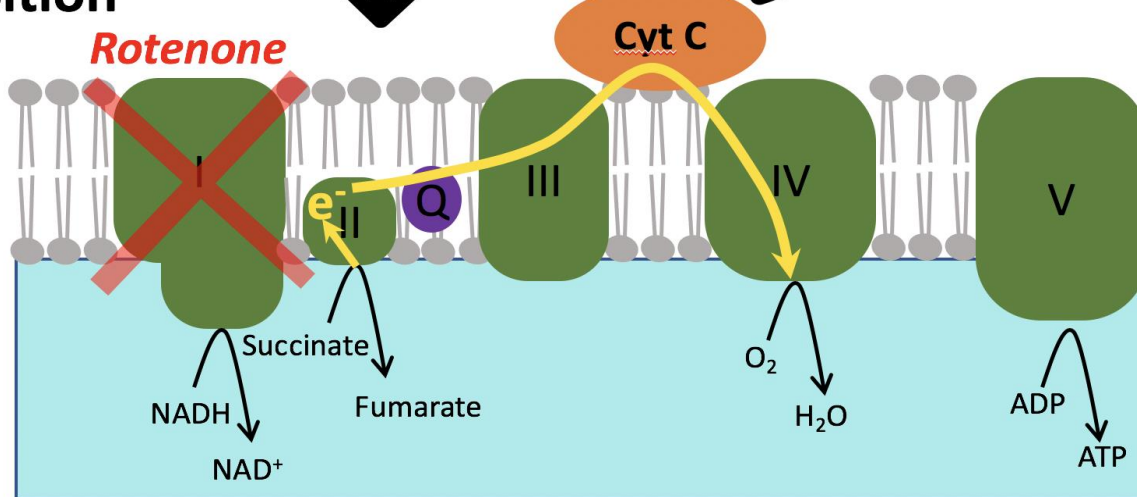


Compound	Concentration range (µM)	Direction of change					Summary mechanism
		OCR	Reserve capacity	ECAR	ATP	Proton leak	
Ametoctradin	0.1 – 100	↓	↓	↑	↓	NR	ETC inhibitor
Atovaquone	0.05 – 50	↓	↓	↑	↓	↓	ETC inhibitor
Cyazofamid	0.1 – 100	↑	↓	↑	↓	↑	Uncoupler
Dimoxystrobin	0.1 – 100	↓	↓	↑	↓	↓	ETC inhibitor
Diuron	0.1 – 100	↓	↓	↑	↓	↓	ETC inhibitor
Fenamidone	0.1 – 100	↓	↓	↑	↓	↓	ETC inhibitor
Fluoxastrobin	0.1 – 100	↓	↓	↑	↓	↓	ETC inhibitor
Kresoxim-methyl	0.1 – 100	↓	↓	↑	↓	↓	ETC inhibitor
Picoxystrobin	0.1 – 100	↓	↓	↑	↓	↓	ETC inhibitor
Pyraclostrobin	0.1 – 100	↓	↓	↑	↓	↓	ETC inhibitor
Trifloxystrobin	0.1 – 100	↓	↓	↑	↓	↓	ETC inhibitor
Rotenone	0.003 – 1	↓	↓	↑	↓	↓	ETC inhibitor

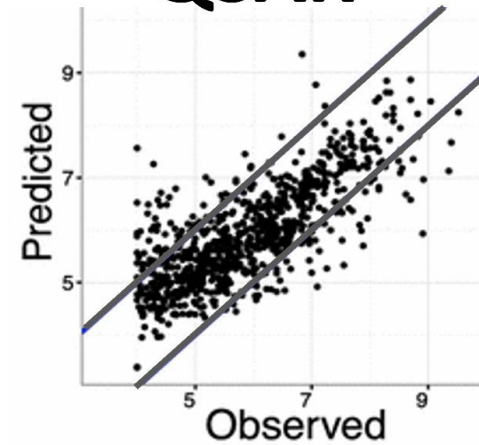
Succinate-cytochrome *c* reductase activity followed by Computer-based modelling



Mitochondrial Succinate-Cytochrome-C Inhibition



QSAR

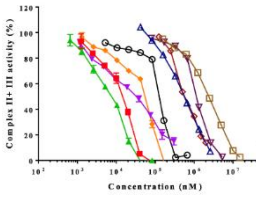
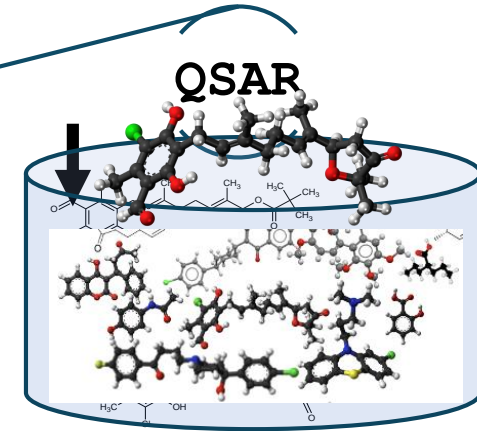


A combined in vitro and in silico approach in the study of drug-induced mitochondrial dysfunction

Molecular docking + PLIF analysis

In silico methodologies

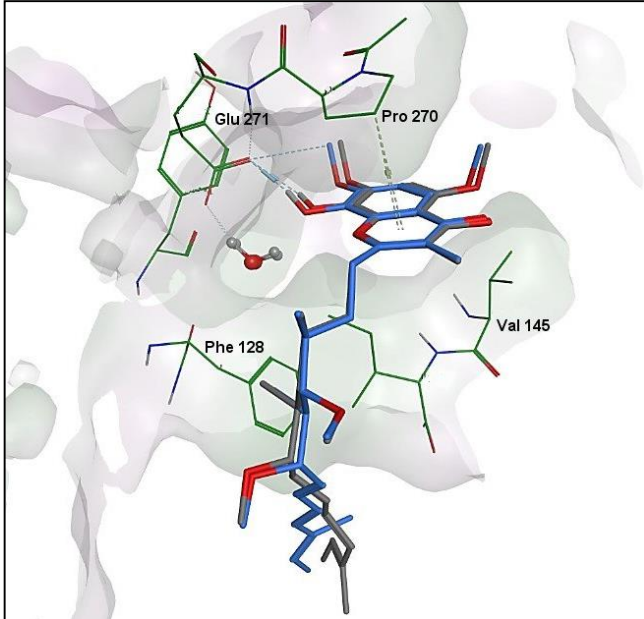
To predict future inhibitors



Molecular Modelling

Molecular Descriptors

Machine Learning Model



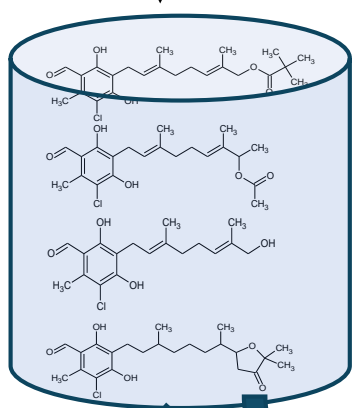
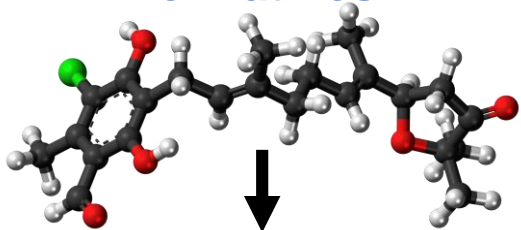
mol	mol	pKa(uM)	5-HT1A pKa(uM)	5-HT1B pKa(uM)		
16		3 8 28	1064	-1.0000	-1.0000	-1.0000
17		3 3 26	1069	-1.0000	-1.0000	-1.0000
18		3 7 29	1071	-1.0000	-1.0000	-1.0000
19		3 16 24	1156	-1.0000	-1.0000	-1.0000

- Investigate the interaction mechanisms between the mitochondria and its inhibitors
- Calculate binding energies to mt Enzymes

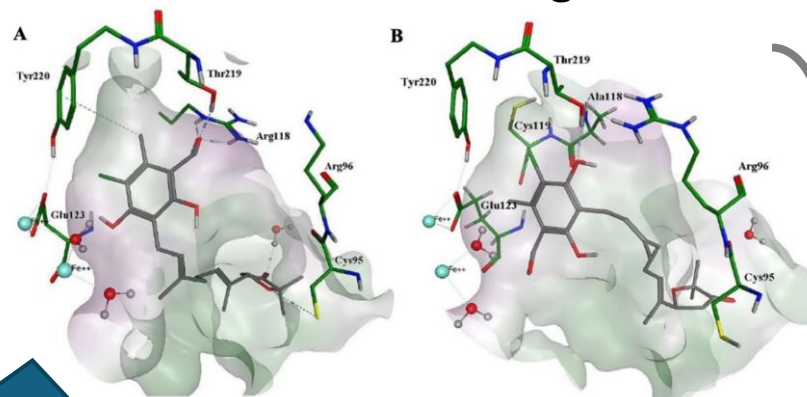
- Identify the molecular features responsible for the inhibitory activity of compounds
- Calculate IC₅₀s

Prediction of AOX inhibitors as antifungals

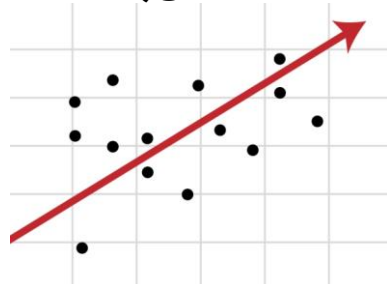
Derivatives



Molecular Docking



QSAR



Molecular Descriptors

High-resolution respirometry to experimentally determine the IC_{50} values of AOX inhibitors (recording Oxygen Consumption Rates) using an Oroboros® Oxygraph-2K and



Predicted AOX Inhibitors

Journal of Computer-Aided Molecular Design
<https://doi.org/10.1007/s10822-020-00360-8>



1 QSAR and molecular docking for the search of AOX inhibitors:
2 a rational drug discovery approach

3 Alicia Rosell-Hidalgo¹ · Luke Young¹ · Anthony L. Moore¹ · Taravat Ghafourian^{1,2}

4 Received: 21 January 2020 / Accepted: 12 November 2020
5 © The Author(s) 2020

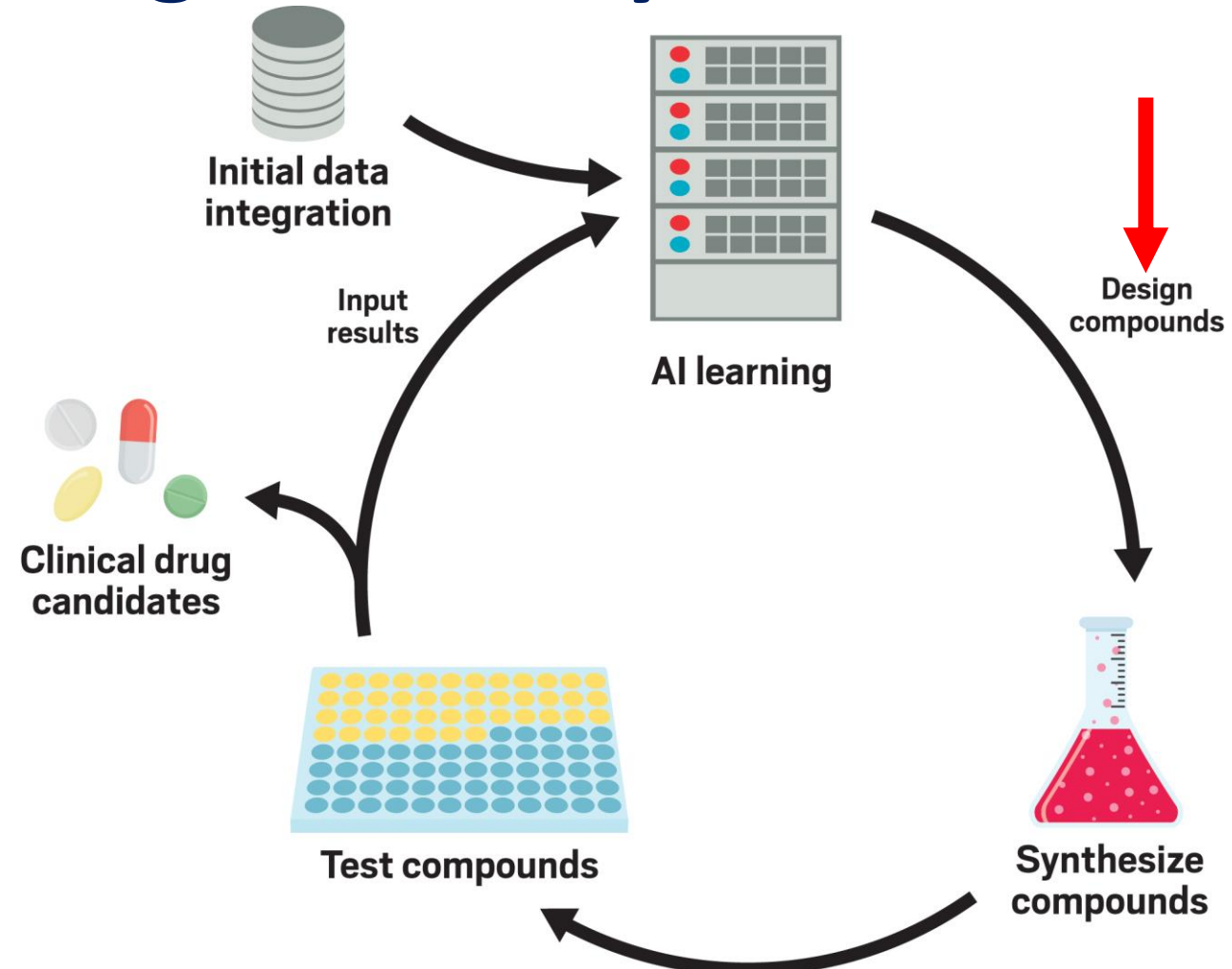
Rosell-Hidalgo A, Young L, Moore AL, Ghafourian T, QSAR and molecular docking for the search of AOX inhibitors: a rational drug discovery approach *J Comput Aided Mol Des* (2020)

Barry and Judy Silverman
College of Pharmacy
NOVA SOUTHEASTERN UNIVERSITY



AI in the Pharmaceutical Industry: artificial intelligence (AI)-based drug-discovery

- Design-Build-Test model
- The entire decision-making and design process is driven by algorithms
- **Exscientia** (Andrew Hopkins): collaborations with other drug companies—including Evotec, GlaxoSmithKline, Roche, and Sanofi
- **Insilico Medicine** (Zhavoronkov, 2013)
- **BenevolentAI** (Bryn Williams-Jones): Partnered with AstraZeneca and Merck



Treatment	Organization	Description	Phase	Lead indication
REC-2282	Recursion	Small molecule pan-HDAC inhibitor	2/3	Neurofibromatosis type 2
REC-994	Recursion	Small molecule superoxide scavenger	2	Cerebral cavernous malformation
REC-4881	Recursion	Small molecule inhibitor of MEK1 and MEK2	2	Familial adenomatous polyposis
INS018_055	InSilico Medicine	Small molecule inhibitor	2	Idiopathic pulmonary fibrosis
BEN-2293	BenevolentAI	Topical pan-tyrosine kinase inhibitor	2a	Atopic dermatitis
EXS-21546	Exscientia and Evotec	A _{2A} receptor antagonist	1b/2	Solid tumors carrying high adenosine signatures.
RLY-4008	Relay Therapeutics	Inhibitor of FGFR2	1/2	FGFR2-altered cholangiocarcinoma
EXS-4318	Exscientia	PKC-θ inhibitor	1/2	Inflammatory and autoimmune conditions
BEN-8744	BenevolentAI	Small molecule PDE10 inhibitor	1	Ulcerative colitis
Undisclosed	Recursion	Small molecular inhibitor of RBM39, a CDK12-associated protein	Pre-clinical	HRD-negative ovarian cancer

C. Arnold, Nature Medicine (2023) pp.1292-1295 <https://www.nature.com/articles/s41591-023-02361-0/tables/1>

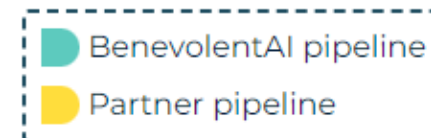
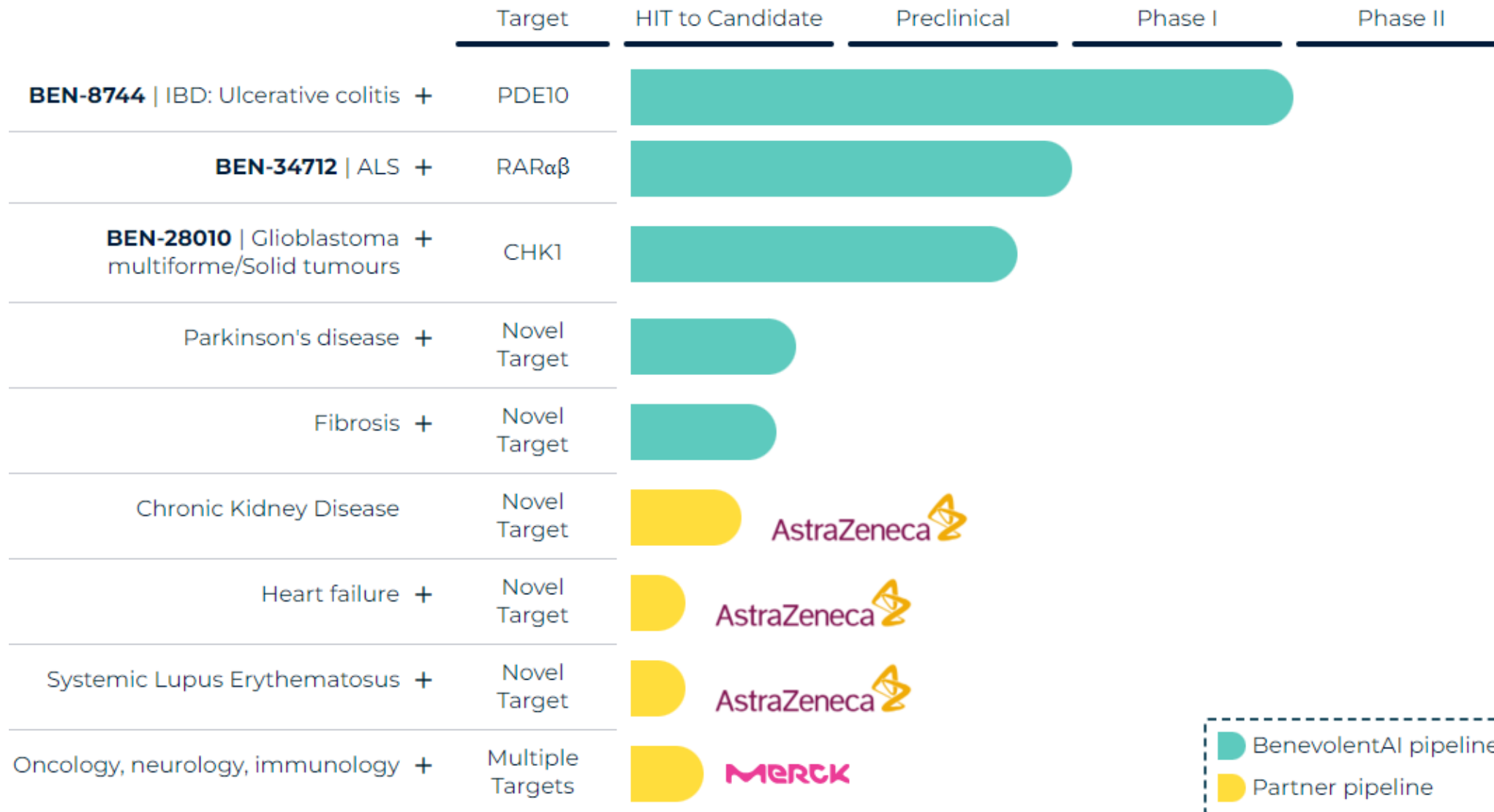
Aug 2024: Merger of Exscientia with Recursion:

Dec 2024: Recursion Reports Interim Phase 1 Clinical Data for REC-617 Monotherapy, a CDK7 Inhibitor

REC-3565 is a potential best-in-class MALT1 inhibitor for multiple hematology indications, designed to reduce the risk of hyperbilirubinemia, a common side effect of other MALT1 inhibitors

REC-4539, an LSD1 inhibitor, is the first designed to be reversible and CNS penetrant for small-cell lung cancer

BenevolentAI drug pipeline



Retrieved: Feb, 2025

Example AI system in the Pharmaceutical Industry

- R2E (Retrieve to Explain) system combines AI-driven information retrieval (scientific literature, genomics, and clinical information) with explainable predictions to prioritize drug targets

Conclusion

- AI can enable wider accessibility of drug discovery to smaller, minimally funded entities (democratization of drug discovery)
- Researchers and start-ups can benefit greatly within the competitive market of the pharmaceutical industry.
- A scientist and a health professional of the future will need to be able to operate the AI systems (prompt engineering etc), if not build them!
- Complex machine-learning algorithms may grow in the future, for example, by incorporating biological/clinical data into AI models for personalized dosing and precision medicine.
- The prediction quality of AI models, including their accuracy, generalizability, reliability, and interpretability, is a major consideration, especially when used for regulatory purposes (e.g., FDA submissions) and clinical decision-making.
- The black-box nature of AI systems hinders their