

The OMICS Approach

The Buzz that makes the World go round

Gerhard F. Ecker

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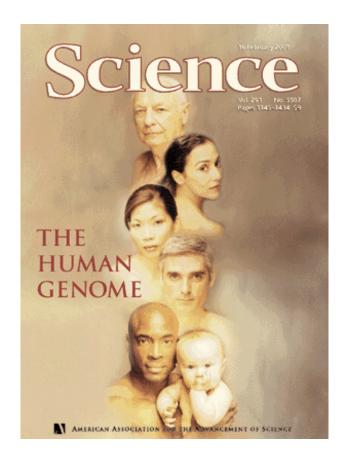
Disclosure



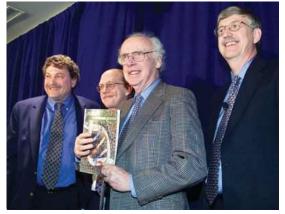
G. Ecker is co-founder of Phenaris GmbH

The Human Genome









2001: 10 Years, 2,7 bio USD

Now: a few days, a few 100 USD

2003: ENCODE Project (ENcyclopedia

Of DNA Elements)

2008: 1.000 Genomes Project

2010: UK10K study; 4.000 healthy people, 6.000 with genetic disease

2012: 100.000 Genomes Project; status Aug 7, 2017: 32.642 genomes sequenced

2017: Chinese province is sequencing 1.000.000 genomes

100.000 Genomes Project





"Genomics has the potential to improve outcome through appropriate **stratification of medicines**, and pharmacists should be part of this exciting development"

"The sequencing part is relatively easy and fast. The challenge lies in data analysis and interpretation!"

May also **link genomic data** with **additional health data** from general practitioners, hospitals, national disease registries, but also other sources such as smart devices

Robinson, The Pharmaceutical Journal 2017

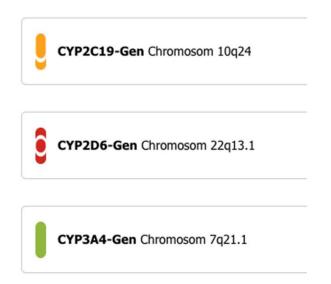
100.000 Genomes – Why?

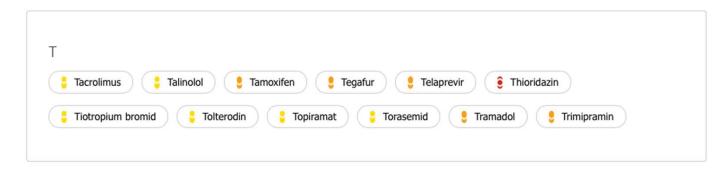


- Differences in our DNA determine our unique characteristics
- can also be the basis for certain diseases
- Sequencing the genomes of many individuals enables researchers
 - to gain better understanding of these diseases
 - to develop treatments
 - to make new diagnoses
- Variations in person's genome can affect their individual response to a drug
- Genome sequencing can
 - help match patients to the most appropriate drug
 - work out the best dose
 - predict whether they are likely to suffer adverse effects (pharmacogenomics)

Individual Genetic Profiles



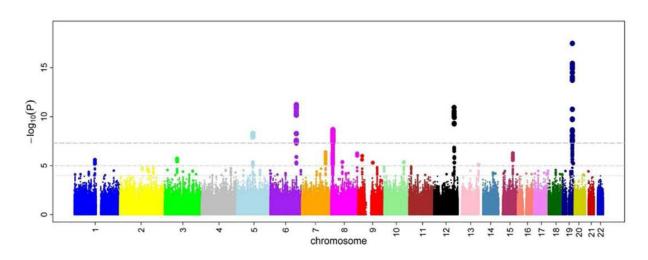




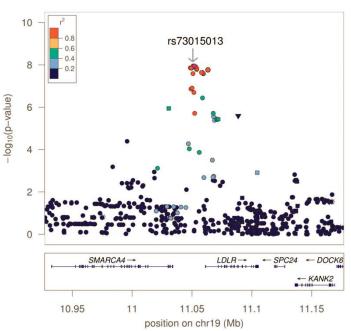


Genome Wide Association (GWA)





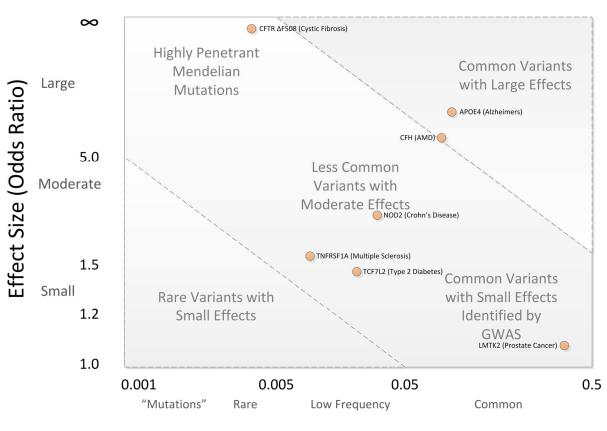
Ikram MK et al (2010) Four Novel Loci (19q13, 6q24, 12q24, and 5q14) Influence the Microcirculation In Vivo. PLoS Genet. 2010; https://commons.wikimedia.org

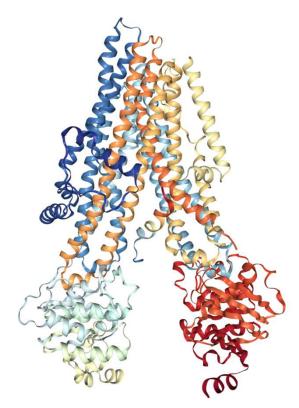


By Sanna S et al - Sanna S (2011) Fine mapping of five loci associated with low-density lipoprotein cholesterol detects variants that double the explained heritability. PLoS Genet. 2011 https://commons.wikimedia.org

GWAS and Causality







Allele Frequency

CFTR (pdb: 5UAK)

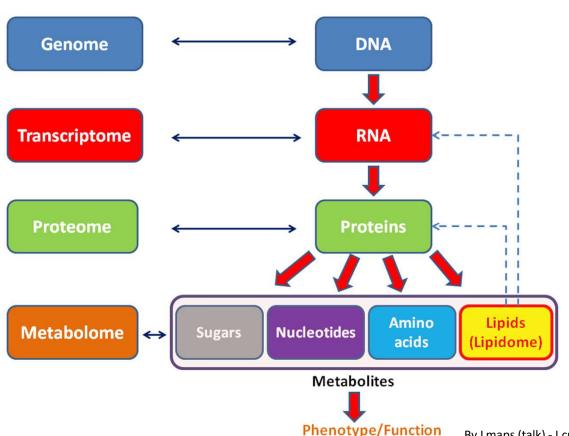
The OMICS World





Definitions





Genomics is focusing on the structure, function, evolution, mapping, and editing of whole genomes. A genome is an organism's complete set of DNA, including all of its genes

The **transcriptome** is the set of all RNA molecules in one cell or a population of cells

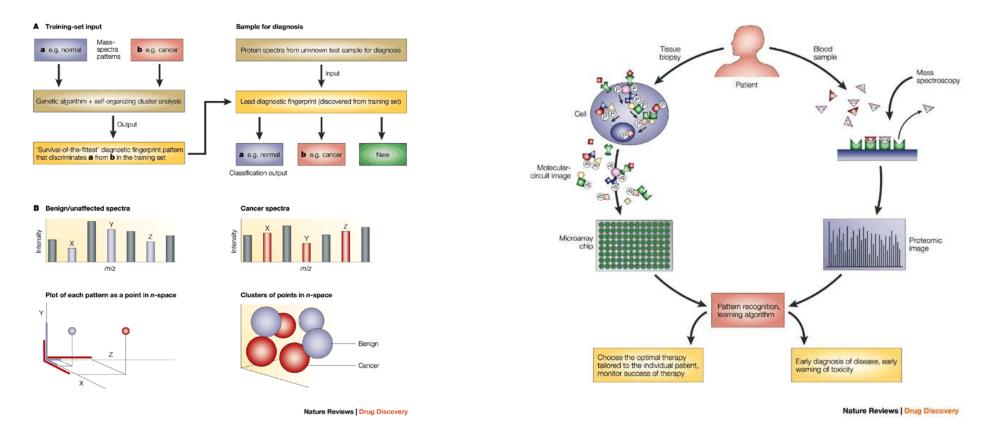
The **proteome** is the entire set of proteins that is produced or modified by an organism or system. This varies with time and distinct requirements, or stresses, that a cell or organism undergoes.

The **metabolome** refers to the complete set of small-molecule chemicals found within a biological sample. The biological sample can be a cell, a cellular organelle, an organ, a tissue, a tissue extract, a biofluid, or an entire organism

By Lmaps (talk) - I created this work entirely by myself., CC BY-SA 3.0, https://en.wikipedia.org/w/index.php?curid=21274382

Proteomics

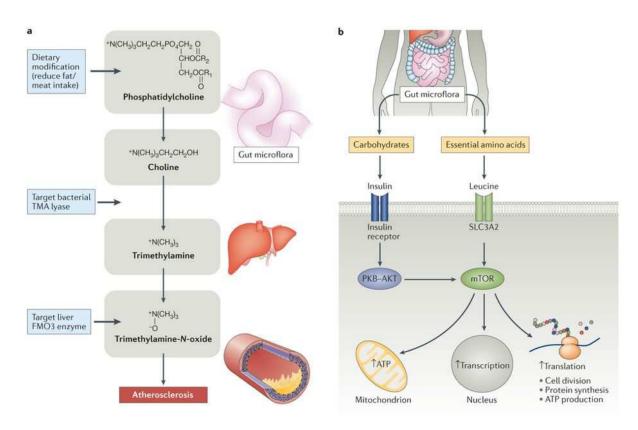




Petricoin, Nature Rev Drug Discov 2002

Metabolomics





Metabolomics is used to

- diagnose cancer
- understand disease mechanisms
- identify novel drug targets
- customize drug treatments
- monitor therapeutic outcomes

Nature Reviews | Drug Discovery

Wishart, Nature Rev Drug Discovery 2016

Personalized Medicine





Norwegian Cancer Genomics Consortium: a platform for research on personalized cancer medicine in a public health system

Ola Myklebost, ola.myklebost@imbv.uio.no

Drug Discovery Today 2015



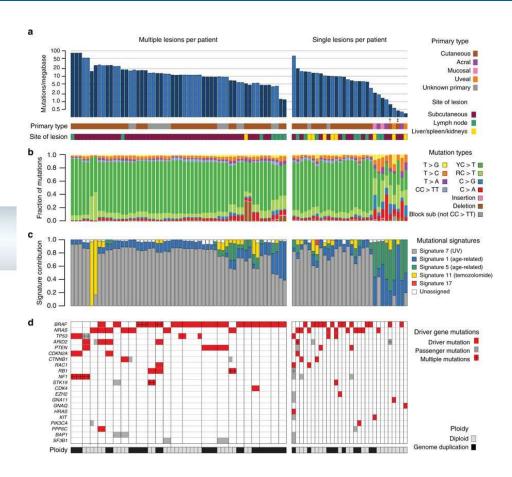
ARTICLE

DOI: 10.1038/s41467-018-05063-1

OPEN

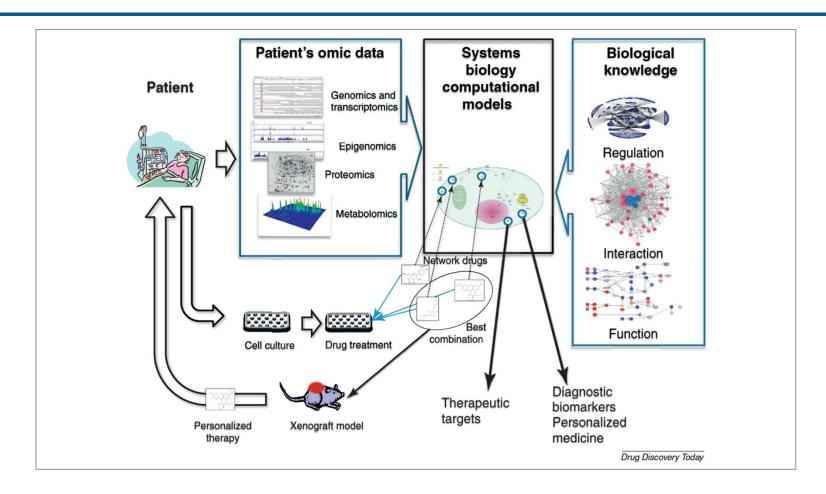
Patterns of genomic evolution in advanced melanoma

E. Birkeland^{1,2}, S. Zhang^{1,2}, D. Poduval^{1,2}, J. Geisler^{3,4}, S. Nakken ^{5,6}, D. Vodak^{5,6}, L.A. Meza-Zepeda^{5,6,7}, E. Hovig ^{5,6,8,9}, O. Myklebost ^{5,6}, S. Knappskog^{1,2} & P.E. Lønning ^{1,2}



Personalized Therapies





Dopazo, DDT 2014

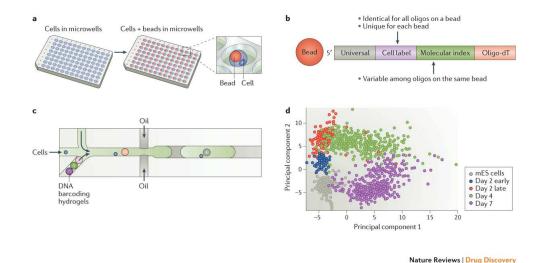
Single Cell Omics



Use classifier to

lineage of tumour

trace cellular



(top of crypt) Biopsy Single-cell Single-cell transcriptomics to analysis with Singleestablish 53 mRNA 53 transcript classifier classifier analysis One progenitorlike tumour cell seeds tumour in model 0.1 Gene families Principal component 2 0 -0.1 -0.2 Immature progenitors: LGR5 progenitor CA2 Shared OLFM4 Enterocyte-like: Enterocyte GUCA2B Other -0.3 Goblet-like: Goblet -0.1Principal component 1

c Colon cancer

a Healthy colon

EpCAM+/CD44+ (stem-like;

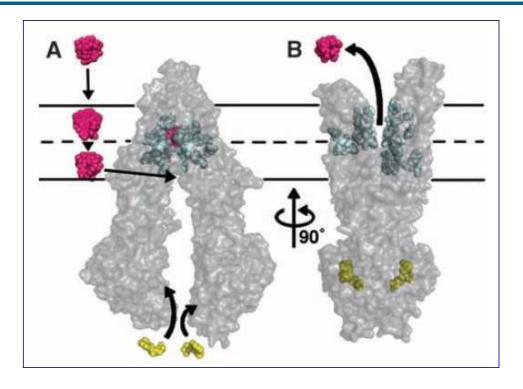
bottom of crypt)
• EpCAM+/CD44+/CD66ahigh

Heath, Nature Rev Drug Discov 2016

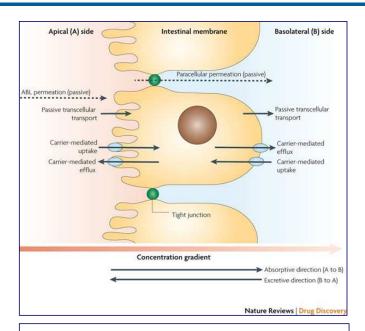
Nature Reviews | Drug Discovery

The Transportome (ABCs)





Aller et al. Science 2009



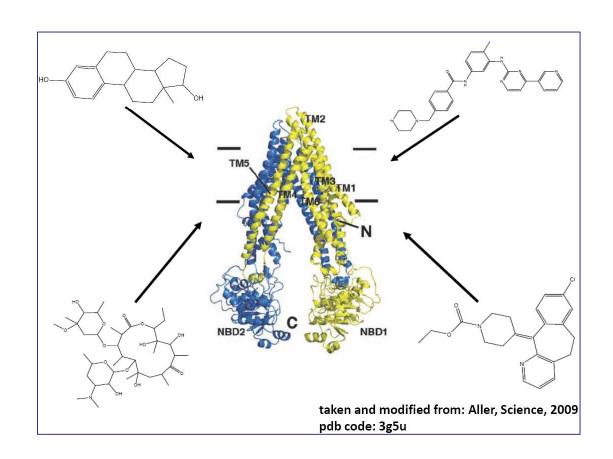
OPINION

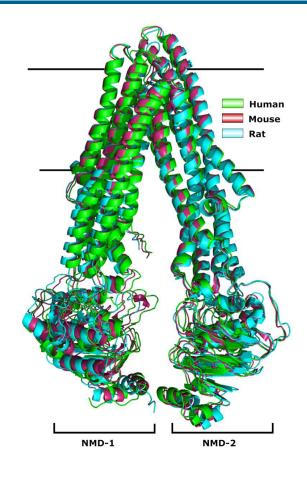
Coexistence of passive and carrier-mediated processes in drug transport

Kiyohiko Sugano, Manfred Kansy, Per Artursson, Alex Avdeef, Stefanie Bendels, Li Di, Gerhard F. Ecker, Bernard Faller, Holger Fischer, Grégori Gerebtzoff, Hans Lennernaes and Frank Senner

P-glycoprotein - Polyspecificity

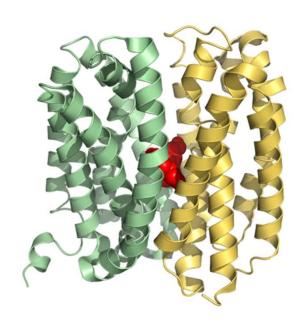


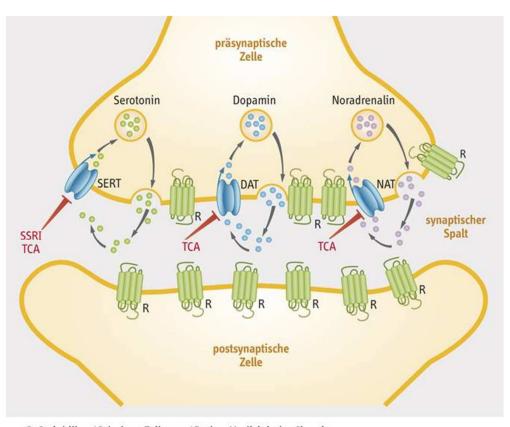




The Transportome (SLCs)







© Steinhilber/Schubert-Zsilavecz/Roth - Medizinische Chemie 2. Auflage, Deutscher Apotheker Verlag, 2010

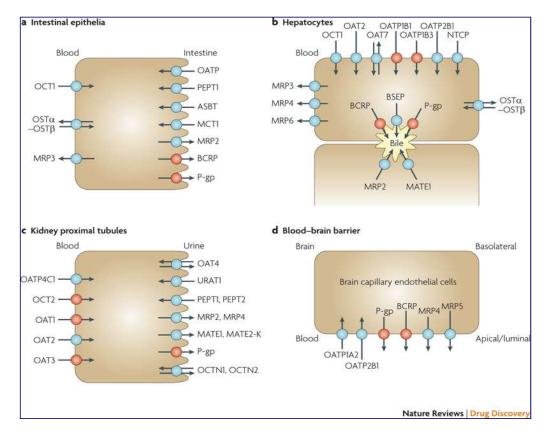
Transporter and ADMET



48 ABC-Transporter 458 SLC-Transporter

FDA asks for testing of the following transporter:

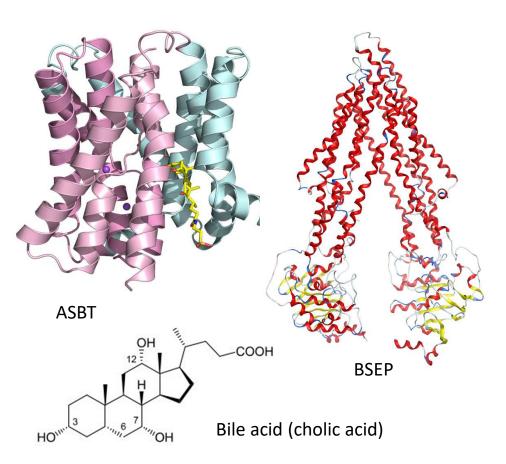
- MDR1 (P-glycoprotein)
- BCRP
- OATP (organic anion transporting polypeptide)
- OCT2 (organic cation transporter)
- OAT1/3 (Organic anion transporter)

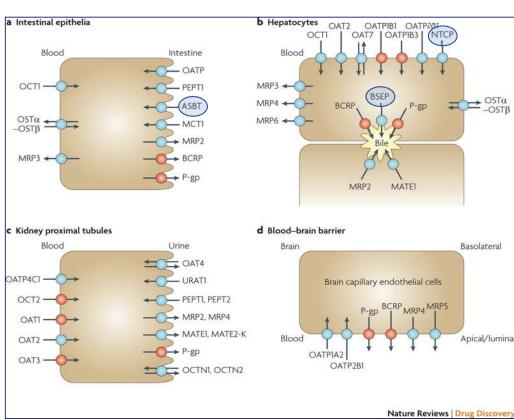


Nature Reviews Drug Discovery 9, 215-236 (March 2010)

Enterohepatic Bile Acid Circuit







Nature Reviews Drug Discovery 9, 215-236 (March 2010)

Prediction of Hepatotoxicity





Does hepatic transporters' information help to predict hepatotoxicity?

DILI	Hyperbilirubinemia	Cholestasis
Not really:	Partially:	Substantially:
> Complex system	➤Transporters ↑ ranked dscrs	➤Increase model's performance
> use of toxicity reports	➤MRP2 & UGT1A1 also involved	➤ Synergistic effect- No predominant transporter identified
		➤ More transporters most probably contribute

Kotsampasakou, Eur J Pharm Sci 2017; JCIM 2017; Toxicology 2017

Transporter mediated DDI

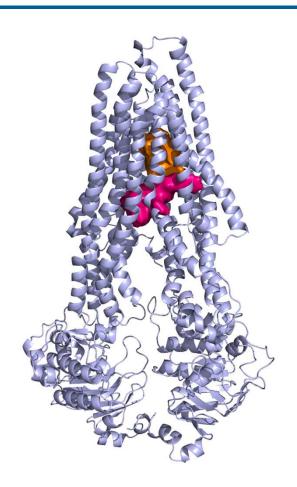


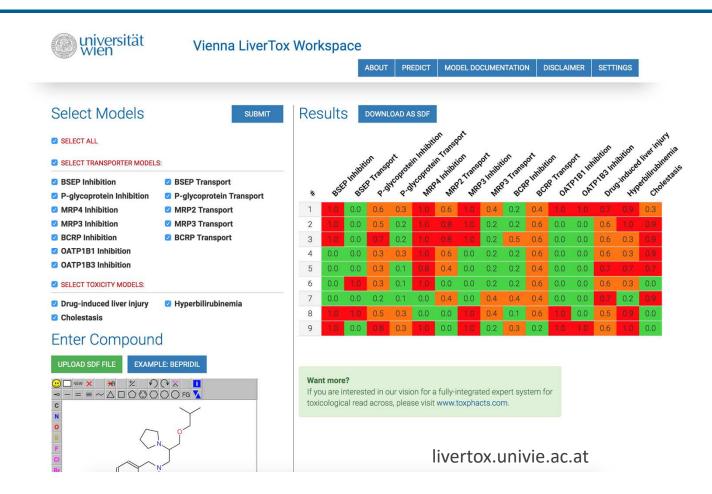
Interacting Drug	Affected Drug	Consequence	Fold Changes in Substrate Plasma AUC
Quinidine	Digoxin	Digoxin Exposure 1.7-fold ↑	P-glycoprotein (P-gp, MDR1) Inhibition
Rifampin	Digoxin	Digoxin Exposure 30% ↓	P-gp Induction
Dronedarone	Digoxin	Digoxin Exposure 2.6-fold ↑	P-gp Inhibition
Probenecid	Cephradine	Cephradine Exposure 3.6-fold ↑	Organic Anion Transporter (OAT) Inhibition
Cimetidine	Metformin	Metformin Exposure 1.4-fold ↑	Organic Cation Transporter (OCT) Inhibition
Cyclosporine	Rosuvastatin	Rosuvastatin Exposure 7-fold ↑	Organic Anion Transporting Polypeptide (OATP) Inhibition & Breast Cancer Resistance Protein (BCRP) Inhibition
Lopinavir/ Ritonavir	Rosuvastatin	Rosuvastatin Exposure 2-fold ↑	OATP Inhibition 4

Taken from Zhang, fda.gov

Transporter and Toxicity







Folding Deficiencies & Diseases



ABCA1 Tangier disease

ABCA3 Fatal surfactant deficiency

ABCA4 Stargardt disease

ABCB1

ABCB4 Progressive Familial Intrahepatic Cholestasis type 3, PFIC3

ABCB11 Progressive Familial Intrahepatic Cholestasis type 2, PFIC2

Benign Recurrent Intrahepatic Cholestasis type 2, BRIC2

ABCC2 Dubin-Johnson

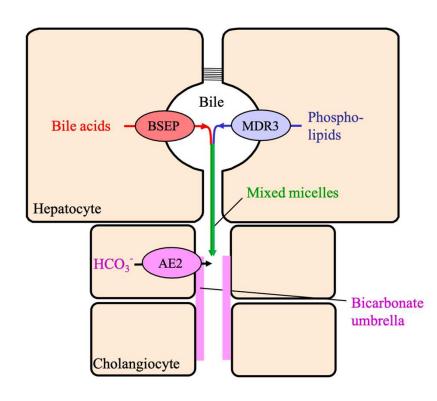
ABCC4

ABCC7 Cystic Fibrosis

ABCC8

ABCC11

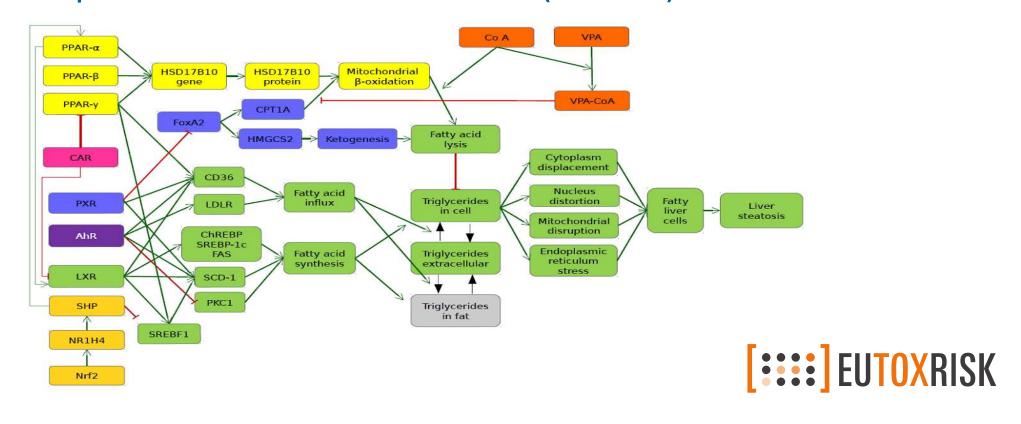
ABCG2 gout



Toxicogenomics



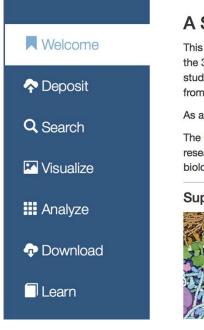
Hepatic Steatosis AOP Network (6 AOPs)



Structural Genomics







A Structural View of Biology

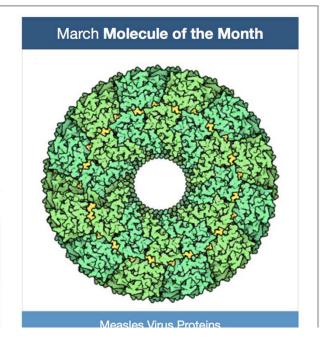
This resource is powered by the Protein Data Bank archive-information about the 3D shapes of proteins, nucleic acids, and complex assemblies that helps students and researchers understand all aspects of biomedicine and agriculture, from protein synthesis to health and disease.

As a member of the wwPDB, the RCSB PDB curates and annotates PDB data.

The RCSB PDB builds upon the data by creating tools and resources for research and education in molecular biology, structural biology, computational biology, and beyond.

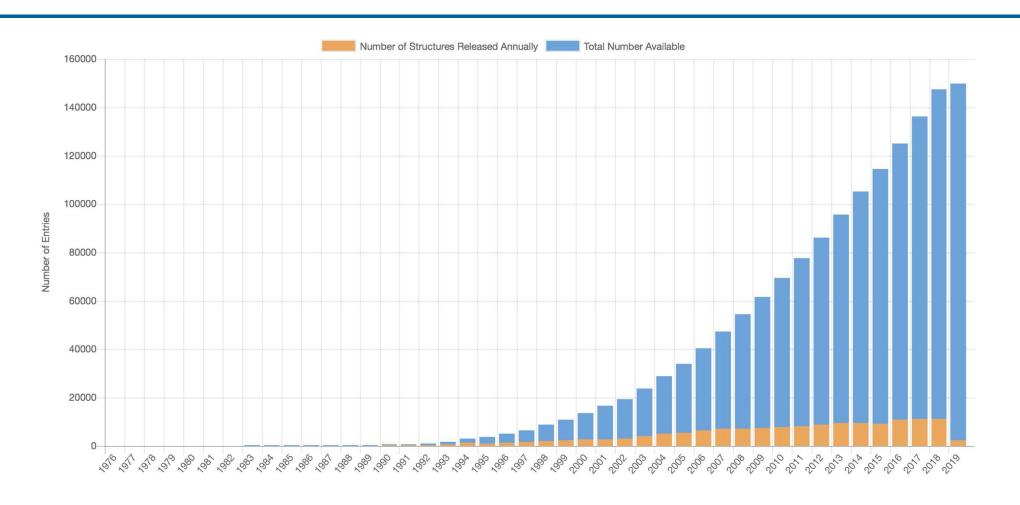
Superbugs! How Bacteria Evolve Resistance to Antibiotics





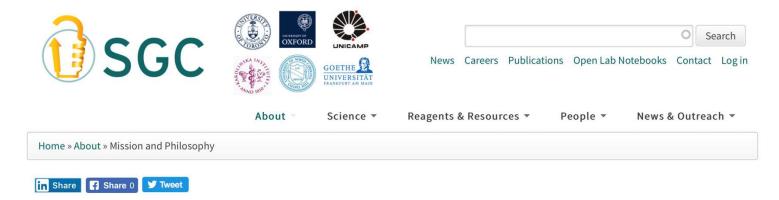
Structural Genomics



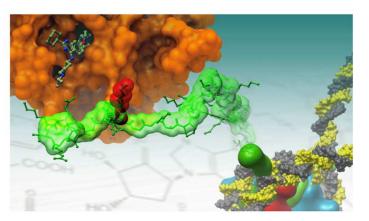


Structural Genomics Consortium





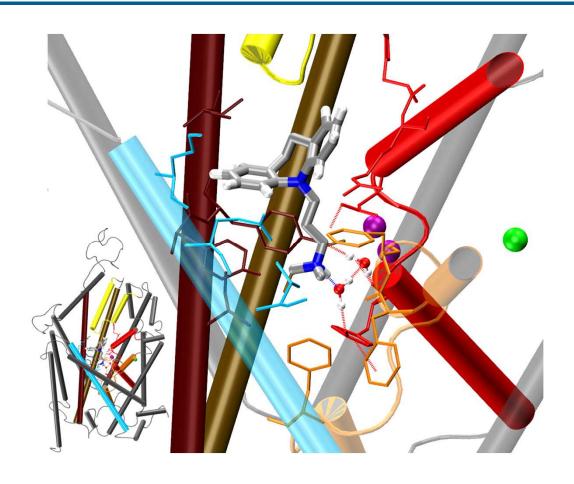
Pioneering Science to Inspire Pioneering Medicines

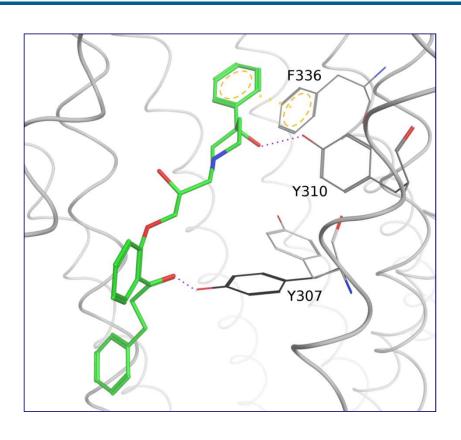


The SGC catalyses research in new areas of human biology and drug discovery by focusing explicitly on less well-studied areas of the human genome .

Structural Genomics







Klepsch, JCIM 2012

Data, data, data













Data Submit Download Help

Q Search All

Enter a study id, dbSNP id, MeSH/HPO phenotype term, keywords, author names, HGNC gene symbols, chromosomal regions or PUBMED identifier (e.g. HGVST307, rs2317951, Pancreatic cancer, Todd JA, ADAM19, chr12:13234..4534534, 17554300)



GWAS Central provides a centralized compilation of summary level findings from genetic association studies, both large and small. We actively gather datasets from public domain projects, and encourage direct data submission from the community. See more..



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28/09/2018 Update to GWAS Central meta-data used in data citation research Read more...

13/09/2018 GWAS Central data release September 2018 Read more...

14/11/2017 GWAS Central data release November 2017 Read more.

See all news ..



Use GWAS Central as a data source

GWAS Central contains 69,986,326 associations between 2,974,967 unique SNPs and 829 unique MeSH disease/phenotype

GWAS Central data content is available in its entirety to researchers as part of a collaboration. To discuss your requirements, send an email to help@gwascentral.org.



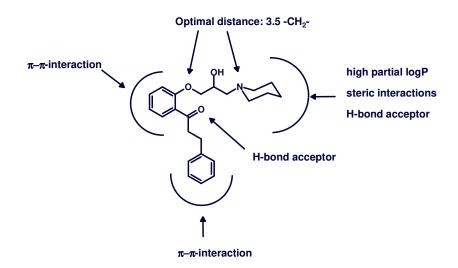
Frequently asked questions

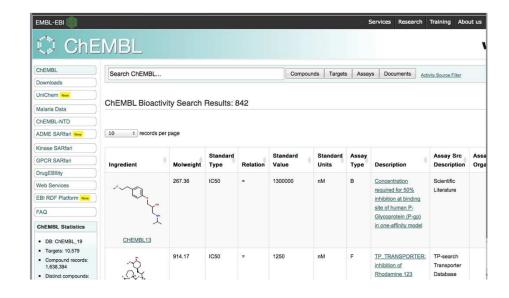
- How do I find phenotypes of interest?
- How do I find genes/regions of interest?
- How do I find markers of interest?
- How do I use the Browser to identify regions of interest?
- How do I submit my own data to GWAS Central?

gwascentral.org

Data, data, data















"What is the selectivity profile of known p38 inhibitors?"



"Let me compare MW, logP and PSA for known oxidoreductase inhibitors"



"Find me compounds that inhibit targets in NFkB pathway assayed in only functional assays with a potency <1 µM"

ChEMBL

DrugBank

Gene Ontology

Wikipathways

GeneGo

ChEBI

Uniprot

UMLS

GVKBio

ConceptWiki

ChemSpider

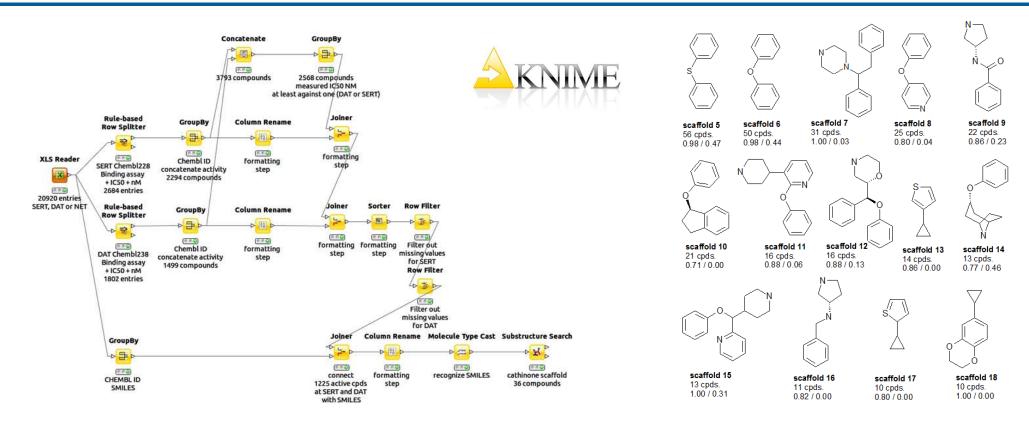
TrialTrove

TR Integrity

Approaching complex research questions needs integration of data sources

The Power of Workflows

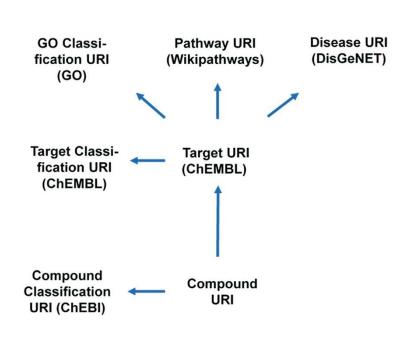




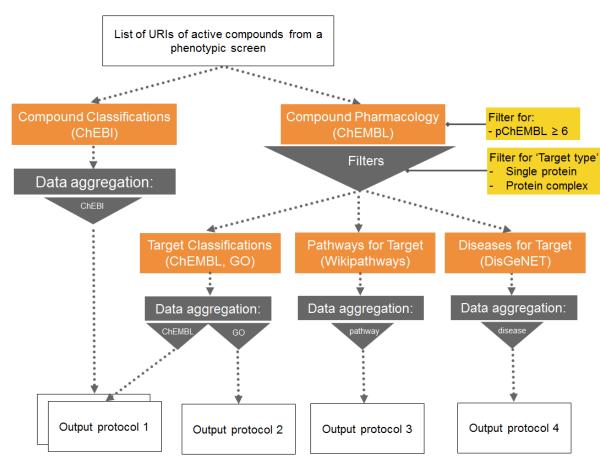
Zdrazil, MedChemComm 2016

Phenotypic Screening



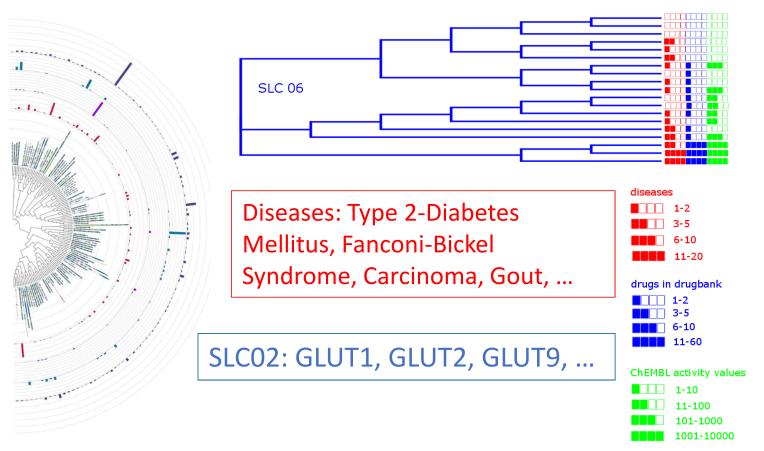


Digles, Med Chem Commun 2016



SLC data analysis





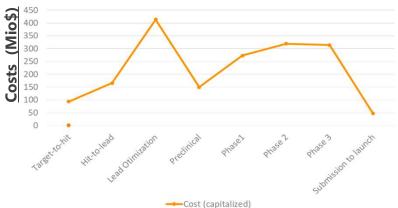
- Priorisation of SLCs
- Chemical space analysis of ligands
- Proposal for assay type
- Automatic generation of SCL dossiers in ppt format
- Domain analysis across families

RESOLUTE

Toxicological Read Across



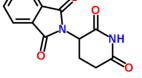












Thalidomide



Similarity Search

Al-driven read across using various similarity algorithms and bioisostery



Data Extraction

Simultaneously search across various data sources including in-house data bases

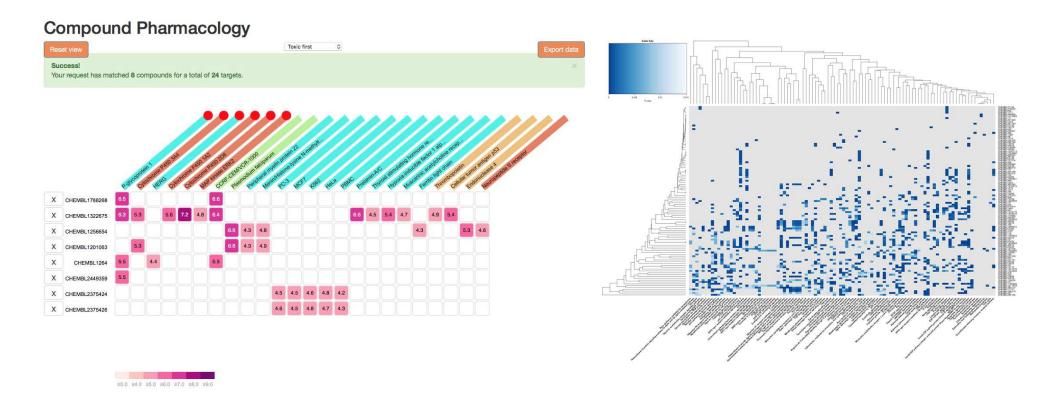


Data Analysis

Results in a standardised and aggregated form and state of the art data visualisation

Toxicological Read Across





Toxphacts.com

Withdrawn compounds from ChEMBL

Take Home Messages



OMICS technologies open the way to personalized diagnosis and treatment

Data integration and big data analytics is key to fully exploit the potential of OMICS – use workflows

Watch out for microbiomics

Pharmacoinformatics Research Group Department of Pharmaceutical Chemistry



