

Martin Smieško

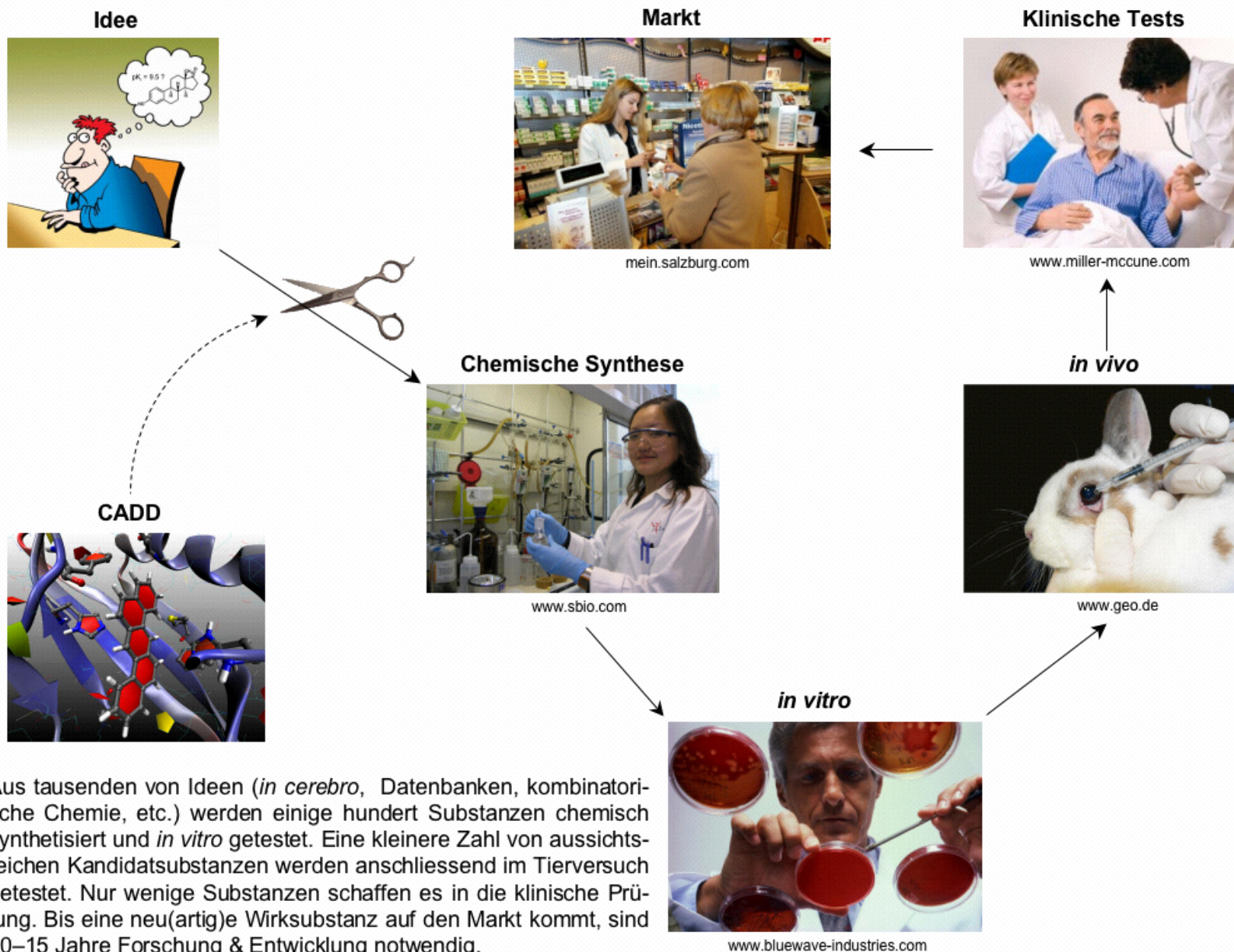
Molecular Modeling : Department of Pharmaceutical Sciences : University of Basel : Switzerland

Computational Toxicology:

Computer-gestützte Voraussage des toxischen Potentials
von Arzneistoffen und Umweltchemikalien



Moderne (computer-gestützte) Entwicklung von Arzneistoffen



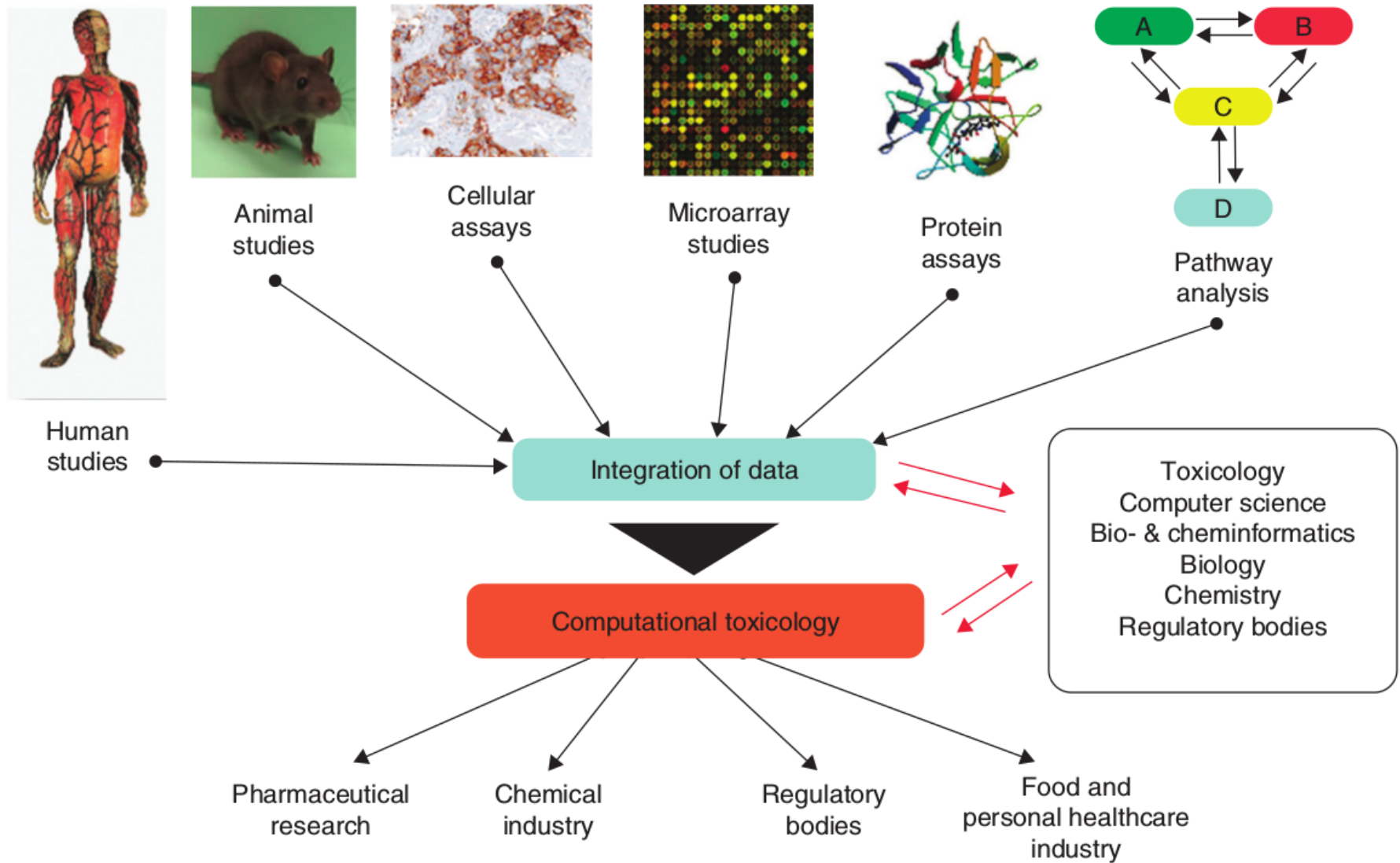
Aus tausenden von Ideen (*in cerebro*, Datenbanken, kombinatorische Chemie, etc.) werden einige hundert Substanzen chemisch synthetisiert und *in vitro* getestet. Eine kleinere Zahl von aussichtsreichen Kandidatsubstanzen werden anschliessend im Tierversuch getestet. Nur wenige Substanzen schaffen es in die klinische Prüfung. Bis eine neu(artig)e Wirksubstanz auf den Markt kommt, sind 10–15 Jahre Forschung & Entwicklung notwendig.



Arzneistoff: Entdeckung / Entwicklung Prozess

Target Discovery	Target Validation	Lead Discovery	Lead Optimization	Pre-clinical ADMET	Clinical Trials
Expression analysis <i>in vitro</i> function Bioinformatics Computational chemical biology	<i>in vivo</i> validation Druggability assesment	High-Throughput Screening CombChem Fragments Structure-based design Virtual Screening <i>de novo</i> design	Traditional Medicinal Chemistry Rational drug design Virtual Screening Focused libraries Drug-likeness	<i>in vitro</i> / <i>in vivo</i> Animal Studies Physiologically-based modeling of bioavailability <i>in silico</i> ADMET Computational systems biology	Phase I (I/II for cancer) Phase II Phase III

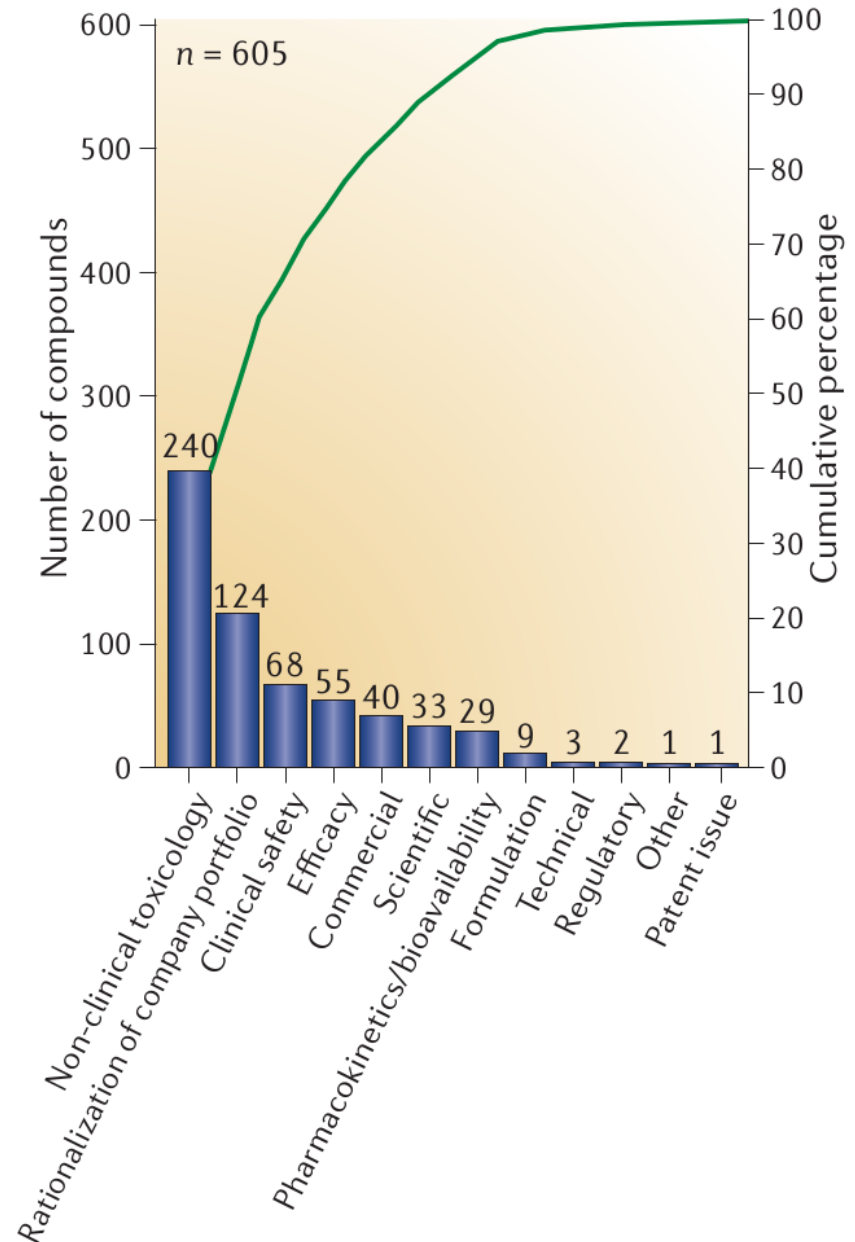




Nigsch F. et al. *Expert Opinion on Drug Metabolism & Toxicology* (2009) , 5, 1-14



- Every single compound entering production must be thoroughly tested and characterized:
 - cosmetics (UV filters, fragrances...)
 - additives (polymer, flame retardants...)
 - agrochemicals
 - drugs
 - colorants & dyes
- 3R (reduction, replacement, refinement)
- Regulatory needs: EC, EPA, BLV... (REACH)
- knowledge gathered can be used to rationally **explain** and **avoid toxic phenomena**
- drug attrition rates



Waring M.J. et al. *Nature Reviews: Drug Discovery* (2015), 14, 475.



Side effect (or adverse effect) of drugs and chemicals

May occur as a result of the unwanted interaction between the compound and bio(macro)molecules involved in:

- Biosynthesis
- Signal transduction
- Transport
- Storage
- Metabolism

the nature of such an interaction can be **specific or unspecific**

biochemical pathway/intermediary metabolism → organelle → cell → organ → organism



Routes of exposure: can the compound get to the possible site of action?

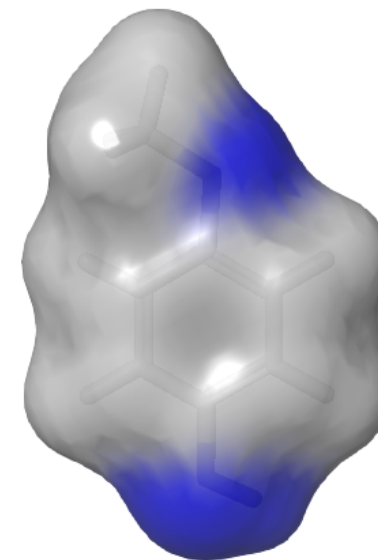
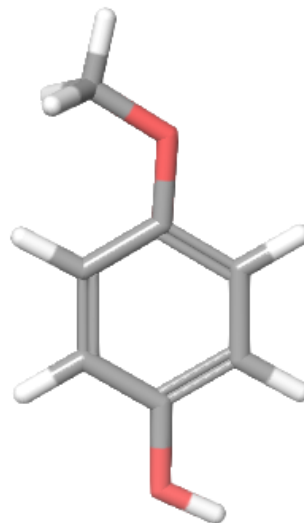
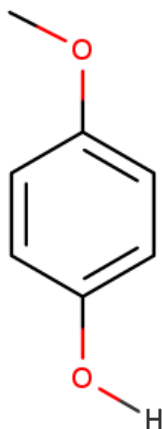
oral : most frequent and best studied because of pharma industry

Lipinski's rule of 5

- MW < 500
- nHB-donor ≤ 5
- nHB-acceptor ≤ 10
- LogP < 5

Veber rules

- PSA < 140 Å²
- nRotBond < 10



MW = 124, nHBdon = 1, nHBacc = 2, LogP = 1.2, PSA = 31 Å², nRotBond = 1

skin : transdermal patches (hormonal or opioid analgetic), cosmetics (shower gel, sunscreens), textile (dyes), plastics (e.g BPA from cash & bills)

inhalation : airborne particles (fumes, fentanyl), volatile chemicals, gases...

special : ocular, bucal...



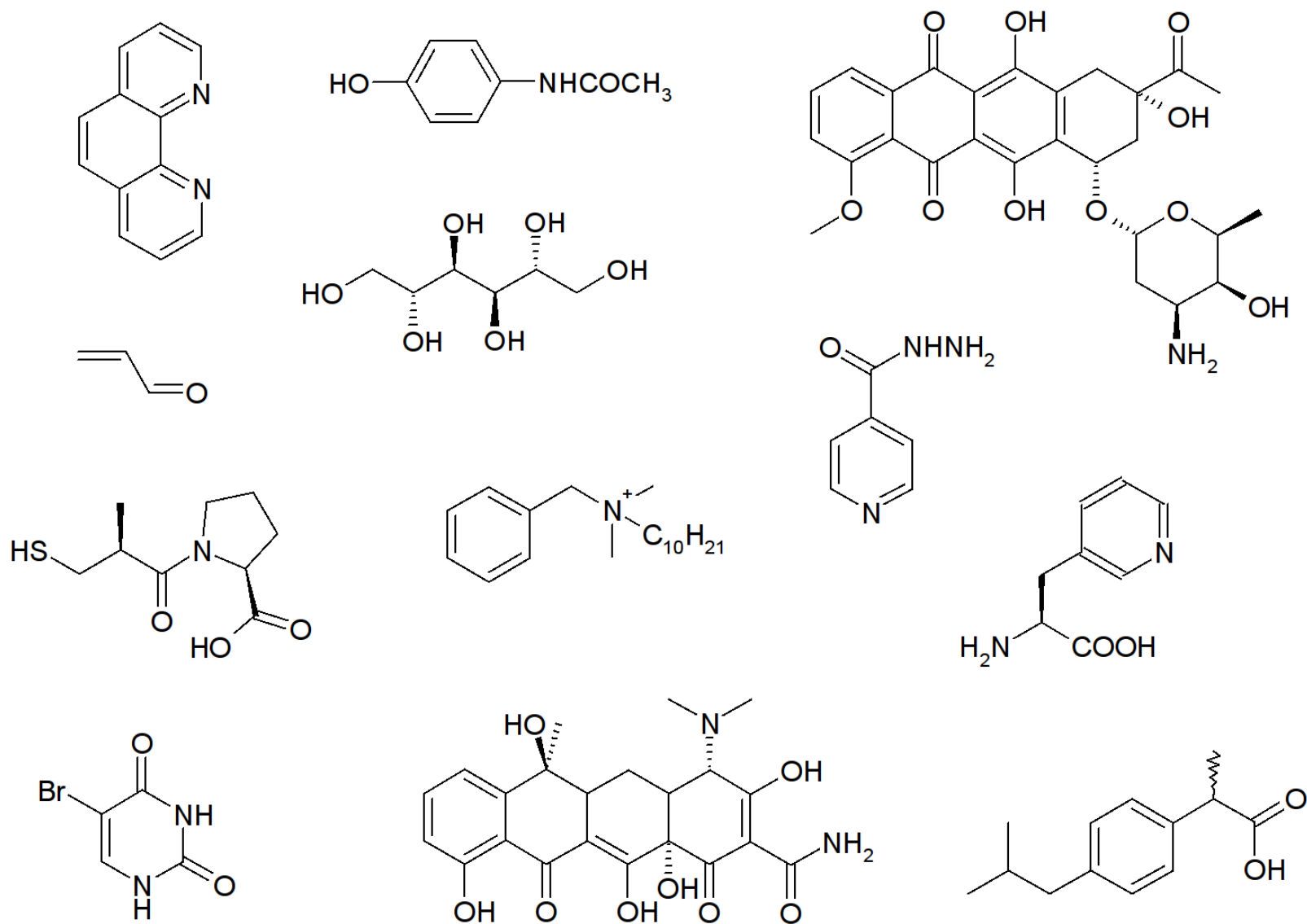
The causal relationship has to be clear – a model has to be able to explain the the side effect and detect/predict similar behavior for new entities:

- **reactive functional groups** – interaction with biomacromolecules forming covalent bonds (electrophilicity, HOMO/LUMO)
- **metabolically unstable groups, fragments, arrangements**
- **chelating groups** – interaction with trace elements (Ca, Fe)
- **metabolites** - interaction with biomacromolecules, off-target binding
- **pharmacokinetics** – compartments, accumulation, blood-brain barrier, placental barrier
- **surface activity** – cell lysis (saponins)
- **isomery R/S, cist/trans** – active/inactive ingredient
- **off-target binding** – anti-target Nr.1 hERG K⁺ (human ether-à-go-go related gene postassium) channel, cytochromes (inhibition/transformation), endocrine system

Many aspects can be detected by simple looking & thinking!



Comparative (Recognition) approach: shape, polarity, chelating capabilities, solubility, similarity to primary metabolites, Lipinski and Veber rules...





Database searching (1):

The Binding Database: compounds with activities, <http://www.bindingdb.org/bind/index.jsp>

ChEMBL Database: > 620k compounds, > 2.4M activities, <http://www.ebi.ac.uk/chembl/db/>

TOXNET: general toxicity database, many sub databases, <http://toxnet.nlm.nih.gov/index.html>
sub-databanks:

ChemIDplus Chemical Identification/Dictionary

HSDB Hazardous Substances Data Bank

CCRIS Chemical Carcinogenesis Information

CPDB Carcinogenic Potency Database

GENETOX Genetic Toxicology Data

IRIS Integrated Risk Information, quantitative human carcinogenic/hazard data

ITER International Toxicity Estimates for Risk

LactMed Drugs and Lactation Database

TRI Toxics Release Inventory

TOXMAP Environmental Health e-Maps

Haz-Map Occupational Exposure/Toxicology

Household Products Health & Safety Information on Household Products



Database searching (2):

ToxCast Program - <http://epa.gov/ncct/toxcast/>

DSSTox - http://www.epa.gov/dsstox_structurebrowser/

Acute Toxicity Database - for Aquatic Species <http://www.cerc.usgs.gov/data/acute/acute.html>

ECOTOX - toxicity data derived predominantly from peer-reviewed literature for aquatic organisms, terrestrial plants and wildlife species, <http://cfpub.epa.gov/ecotox/>

SKIN DEEP - <http://www.cosmeticsdatabase.com/index.php>

Drug-Induced Toxicity Related Proteins Database

<http://bioinf.xmu.edu.cn/databases/DITOP/index.html>

PAN Pesticide Database - <http://www.pesticideinfo.org/>

ACuteTox - Predicting Human Acute Toxicity, <http://www.acutetox.eu/>

ZINC - free database of commercially-available compounds for virtual screening
<http://zinc.docking.org/choose.shtml>

Chemical Structure Lookup Service - 46 million unique structures

<http://cactus.nci.nih.gov/cgi-bin/lookup/search>

EC inventory – a database of the existing chemical substances

http://ecb.jrc.ec.europa.eu/qsar/information-sources/ec_inventory/



Das Modell!

„It can scarcely be denied that the supreme goal of all theory is to make the irreducible basic elements as simple and as few as possible without having to surrender the adequate representation of a single datum of experience.“

Albert Einstein 1933

z.B.:

Separates Kleinmolekül:

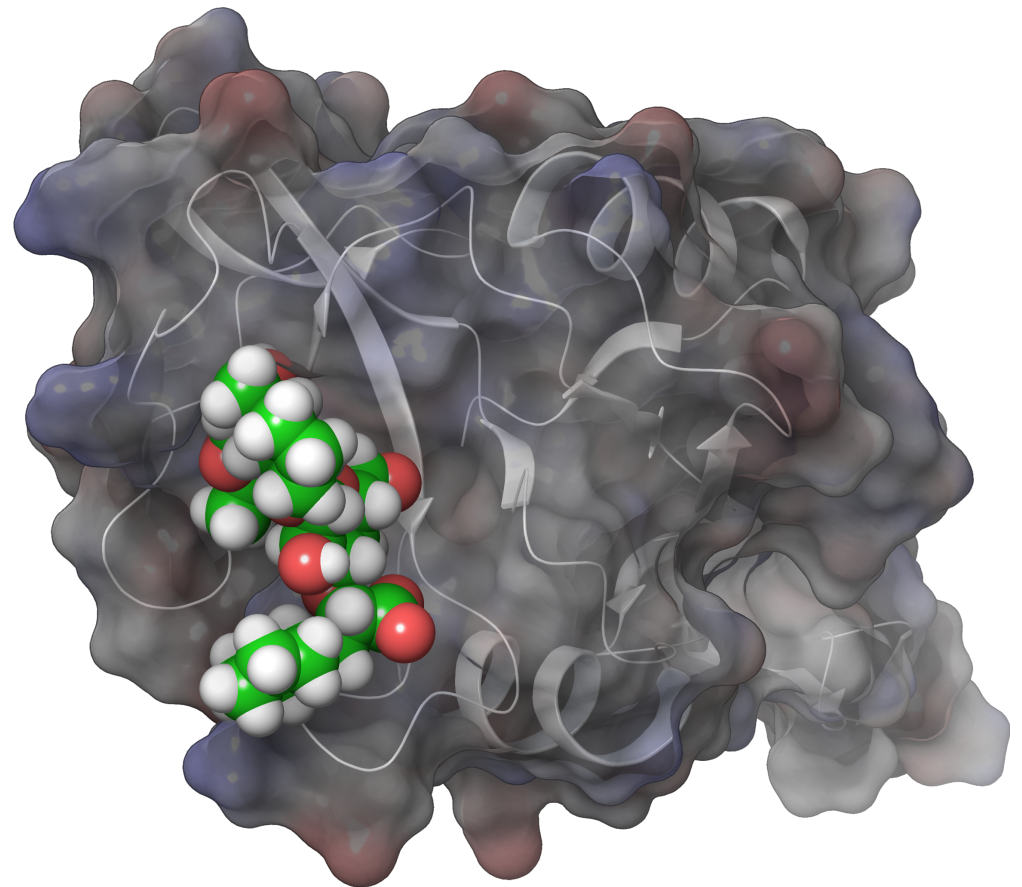
- Physikochemische Eigenschaften
- Deskriptoren
- Bioverfügbarkeit

Protein-Ligand Komplex:

- Wechselwirkungsenergie
- Interne Spannung

Protein-Ligand Komplex im Wasser:

- Bindungsaffinität
- Halbwertszeit (Residenzzeit)





Nur ein Modell!



"This is not a pipe" By René Magritte, 1898-1967

**Nie vergessen: dass was wir sehen ist nur ein Modell,
nicht die Realität!**



Modeling = Creating a (computer) model for observed phenomena at various levels

- qualitative models: simple rule based, decision trees (e.g. *if soluble and contains a C=N-OH functional group...*), expert systems, artificial intelligence
- quantitative models (QSARs):

$$f(\mathbf{x}) = (\text{side}) \text{ effect} \xrightarrow{\text{?}} \text{toxicity}$$

- Where \mathbf{x} can be:
 - 1-dimensional information, e.g. LogP, molecular weight
 - 2-dimensional information, e.g. connectivity, branched vs. linear
 - 3-dimensional information, e.g. conformation of a ligand
 - multi-dimensional information (multiple conformers, protonation states)
- Setubal principles:
 - defined endpoint, unambiguous algorithm, defined domain of applicability, appropriate measures of goodness-of-fit, robustness and predictivity, mechanistic interpretation



Free modeling resources (1):

OpenTox (interoperable predictive toxicology framework) - <http://www.opentox.org/>

LAZAR - <http://lazar.in-silico.de/>

Molinspiration - gives Nuclear Receptor Ligand likeness (also Kinase, GPCR and Ion Channel Ligand likeness), <http://www.molinspiration.com/cgi-bin/properties>

QSPR/OCHEM - build online QSARs, <http://qspr.eu/>

European Joint Research Center (Ispra, Italy) :

DART - designed for the ranking of chemicals according to their environmental and toxicological concern

Toxtree - places chemicals into categories and predicts various kinds of toxic effect by applying decision tree approaches

Toxmatch - encodes several chemical similarity indices to facilitate the grouping of chemicals into categories and read-across,

Virtual Computational Chemistry Laboratory - property calculations
<http://www.vcclab.org/>



Free modeling resources (2):

EPI Suite - suite of physical/chemical property and environmental fate estimation, US EPA,
<http://www.epa.gov/opptintr/exposure/pubs/episuite.htm>

OncoLogic® - A Computer System to Evaluate the Carcinogenic Potential of Chemicals,
<http://www.epa.gov/oppt/sf/pubs/oncologic.htm>

T.E.S.T. - estimate acute toxicity using the QSAR methodologies
<http://www.epa.gov/nrmrl/std/cppb/qsar/#TEST>

OECD QSAR Toolbox - tool for profiling mechanisms, chemical grouping and readacross,
<http://www.oecd.org/env/ehs/risk-assessment/theoecdqsartoolbox.htm>

CAESAR – Computer Assisted Evaluation of Industrial chemical substances
<http://www.caesar-project.eu/>



Commercial modeling resources:

ADMET predictor - <http://www.simulations-plus.com>

TOPKAT from Accelrys - <http://www.accelrys.com>

Pallas - <http://www.compudrug.com>

Derek - <http://www.lhasalimited.org>

MultiCASE - <http://www.multicase.com>

MDL QSAR - <http://www.symyx.com>

BioEpisteme - <http://www.prousresearch.com>

ACD ToxSuite - <http://www.acdlabs.com>

OASIS TIMES - <http://www.oasis-lmc.org>

Molcode Toolbox - <http://molcode.com>

...



Statische Modellierung – ToxMatch

Toxmatch
File Training set Test set Help

File Descriptors Groups View Similarity

C:\Documents and Settings\Administrator\Desktop\LLNA_mech.sdf

Structure

Properties	
#	1
CasRN	1106-51-4106-51-4
DWR_short	MA
EC3	0.0099
Potency_class	extreme
SMILES	O=C1C=CC(=O)C=C1
Title	p-Benzoquinone

Properties	
#	2
CasRN	123-31-9123-31-9
DWR_short	MA
EC3	0.11
Potency_class	strong
SMILES	Oc1ccc(cc1)O
Title	Hydroquinone

Chart Similarity histogram Similarity matrix

Rows: Training set Columns:

Toxmatch
File Training set Test set Help

File Descriptors Groups View Similarity

D:\src\installers\Toxmatch\1.1\stream\bin\data\EPAFHM_v3b...

Structure

Properties	
#	1
CasRN	61096-84-2
ChemName...	4-(hexyloxy)...
LC50_mg	2,67
LogP	3,768
MOA	REACTIVE
eHOMO	-9,6333
eLUMO	-0,9057

Chart Similarity histogram Similarity matrix

Training set

- file data\EPAFHM_v3b_617_10Apr2006_3D...
- Inert chemicals (Narcotics)
- Less inert chemicals (Polar Narcotics)
- Reactive chemicals
- Specifically acting chemicals
- Unknown mode of action

Test set

Chart Similarity histogram Similarity matrix

Y-axis: Test set.Euclidean distance (descriptors,kNN).Specifically acting chemicals

X-axis: Training set.Euclidean distance (descriptors,kNN).Inert chemicals (Narcotics)

Legend:

- Inert chemicals (Narcotics)
- Less inert chemicals (Polar Narcotics)
- Reactive chemicals
- Specifically acting chemicals
- Unknown mode of action

X: Training set.Euclidean distance (descriptors,kNN).Inert chemicals (Narcotics)

Y: Training set.Euclidean distance (descriptors,kNN).Specifically acting chemicals

Training/Test similarity Descriptors Similarity vs. Activity Descriptors vs. Activity

Color Labels Show

http://ihcp.jrc.ec.europa.eu/our_labs/computational_toxicology/qsar_tools/toxmatch



Expertensysteme – ToxTree

Toxtree (Estimation of Toxic Hazard – A Decision Tree Approach) v2.1.0

File Edit Chemical Compounds Toxic Hazard Method Help

Enter SMILES: Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1 Go!

Available structure attributes

SMILES	Oc1ccc(cc1)/C(CC)=C...
cdk:Comment	Created from SMILES
toxTree.tree.cramer....	High (Class III)
toxTree.tree.cramer....	1N,2N,3N,5N,6N,7N,...

Structure diagram

Toxic Hazard by Cramer rules

Estimate

Low (Class I)

Intermediate (Class II)

High (Class III)

Verbose explanation

Cramer rules

- Q1. Normal constituent of the body **No** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q2. Contains functional groups associated with enhanced toxicity **No** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q3. Contains elements other than C,H,O,N,divalent S **No** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q5. Simply branched aliphatic hydrocarbon or a common carbohydrate **No** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q6. Benzene derivative with certain substituents **No** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q7. Heterocyclic **No** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q16. Common terpene **No** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q17. Readily hydrolysed to a common terpene **No** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q19. Open chain **No** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q23. **Aromatic Yes** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q27. **Rings with substituents Yes** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q28. **More than one aromatic ring Yes** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q29. Readily hydrolysed **No** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1
- Q33. Has sufficient number of sulphonate or sulphamate groups **No** Class **High (Class III)** Oc1ccc(cc1)/C(CC)=C(CC)\c1ccc(O)cc1

First Prev 1 / 1 Next

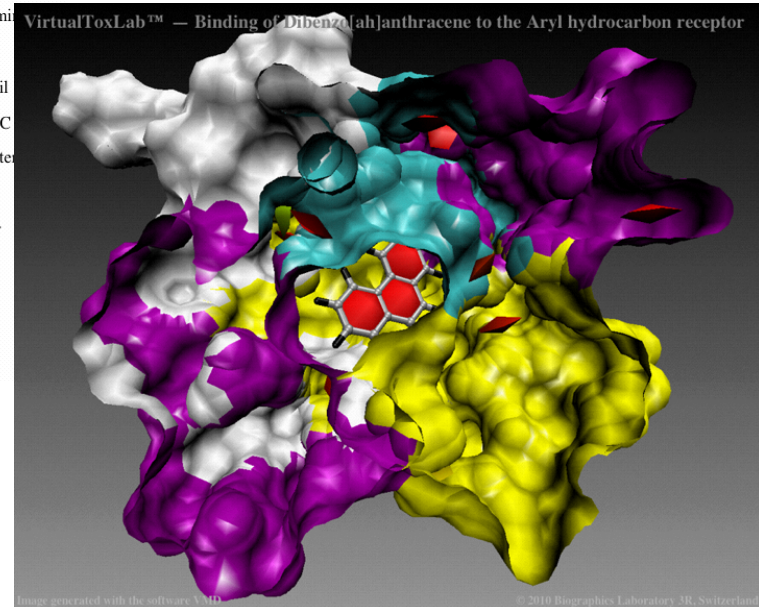
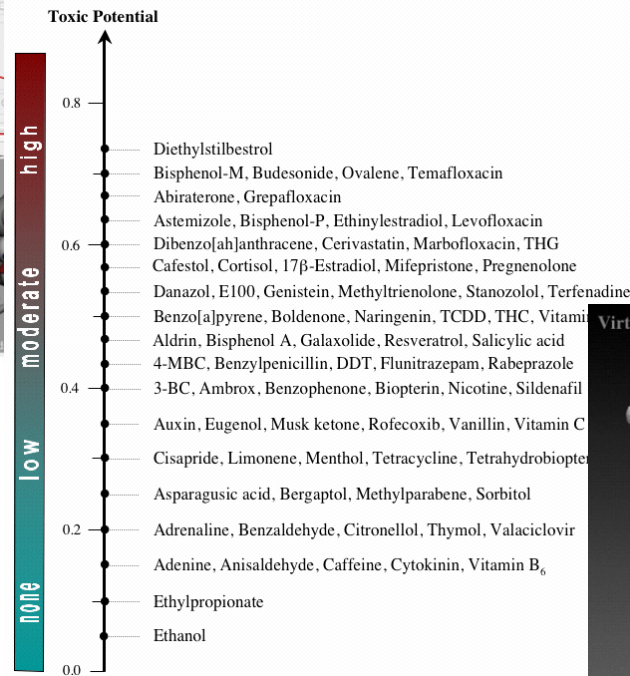
http://ihcp.jrc.ec.europa.eu/our_labs/computational_toxicology/qsar_tools/toxtree



"Ab initio" 3D-Modellierung – VirtualToxLab

Das **toxische Potential** einer Substanz wird nicht durch Vergleich mit anderen Verbindungen (deren Toxizität bekannt ist) abgeleitet, sondern durch die **Simulation** und **Quantifizierung** von **Protein-Ligand-Wechselwirkungen** auf atomarer Ebenen abgeschätzt. Proteine, welche unerwünschte Effekte vermitteln, werden als "off-targets" bezeichnet.

<http://www.virtualtoxlab.org>





Emil Fischer – „Vater“ des Molecular Modeling



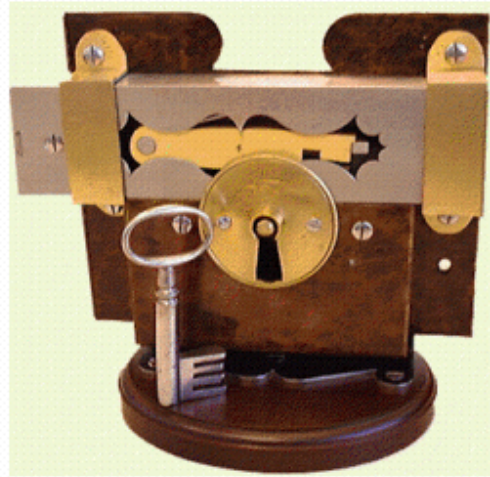
nobelprize.org

Schloss-Schlüssel-Prinzip (1894)

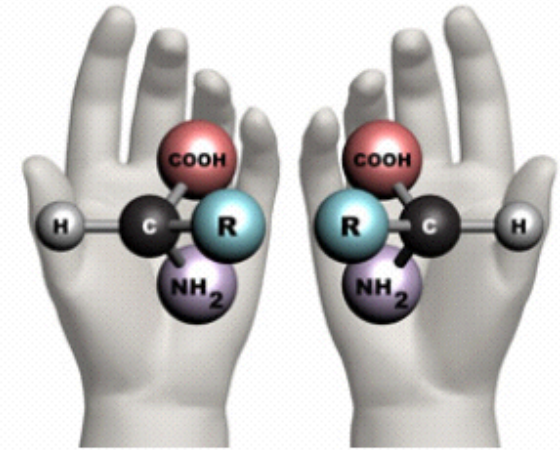
Emil Fischer (1852–1919)
1902: Nobelpreis für Chemie



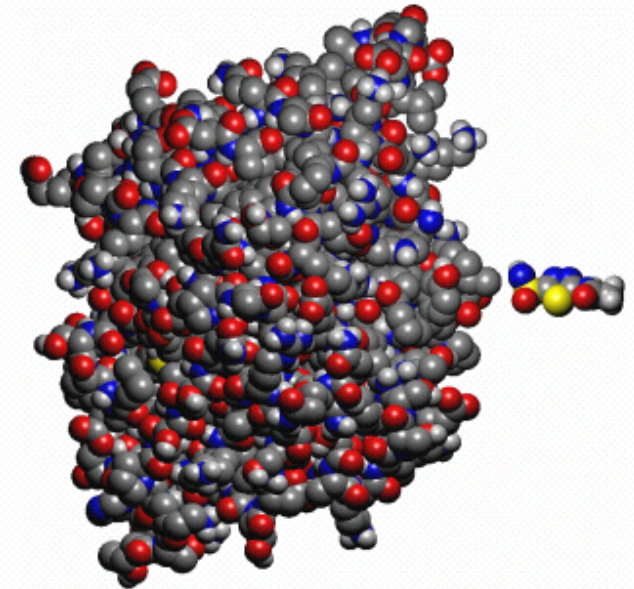
muarchives.missouri.edu



oldlockandkeyco.co.uk



enantiomorphic.blogspot.com



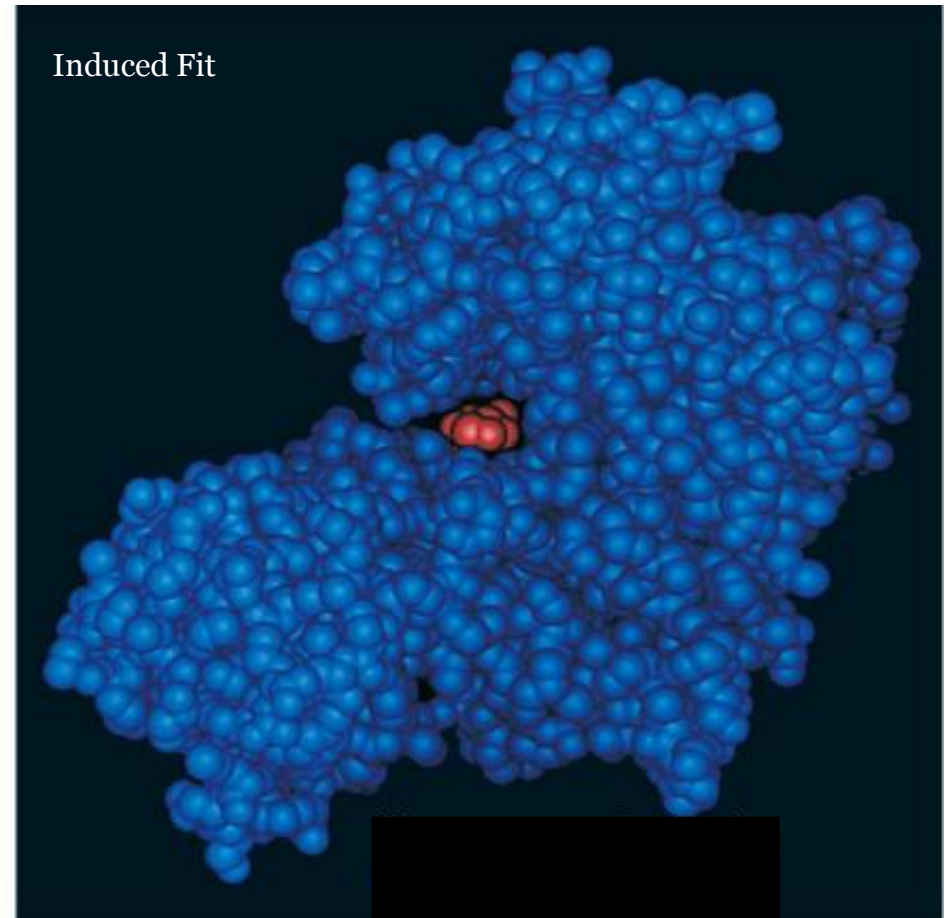
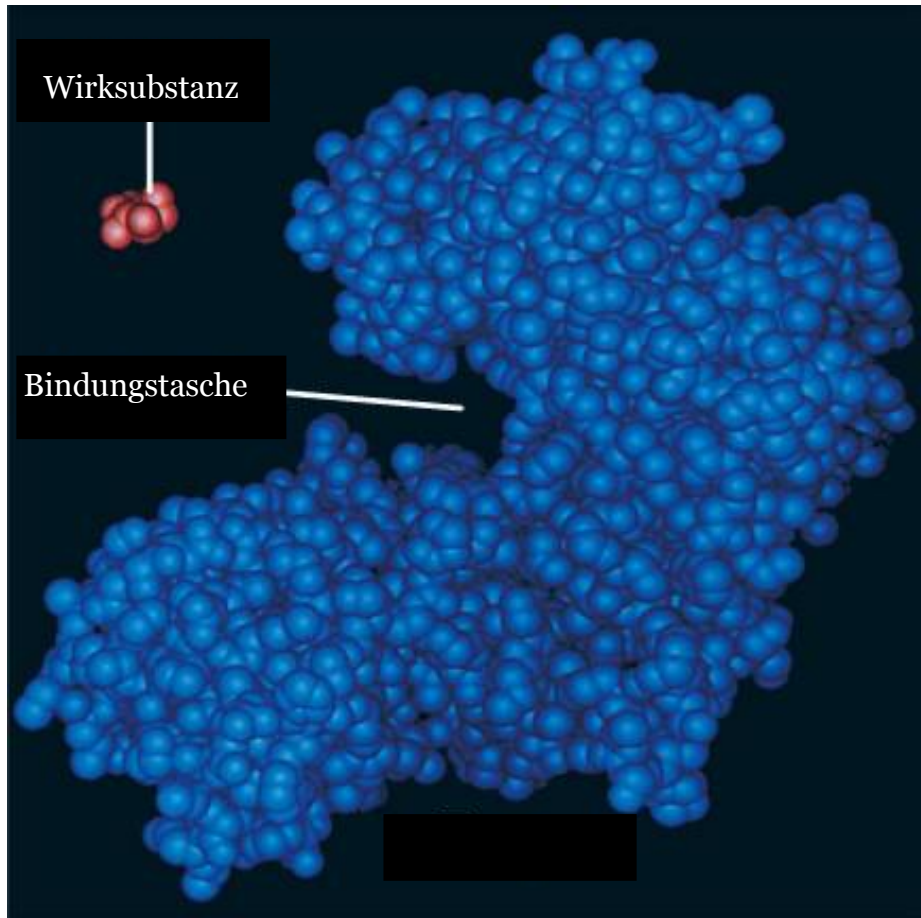
Carboanhydrase (Schloss) + Acetazolamid (Schlüssel)

“Um ein Bild zu gebrauchen, will ich sagen, dass Enzym und Glykosid zueinander passen müssen, wie Schloss und Schlüssel, um eine chemische Wirkung aufeinander ausüben zu können.”

Emil Fischer (1894)



Induced Fit: Biologisches Schloss+Schlüssel sind flexibel

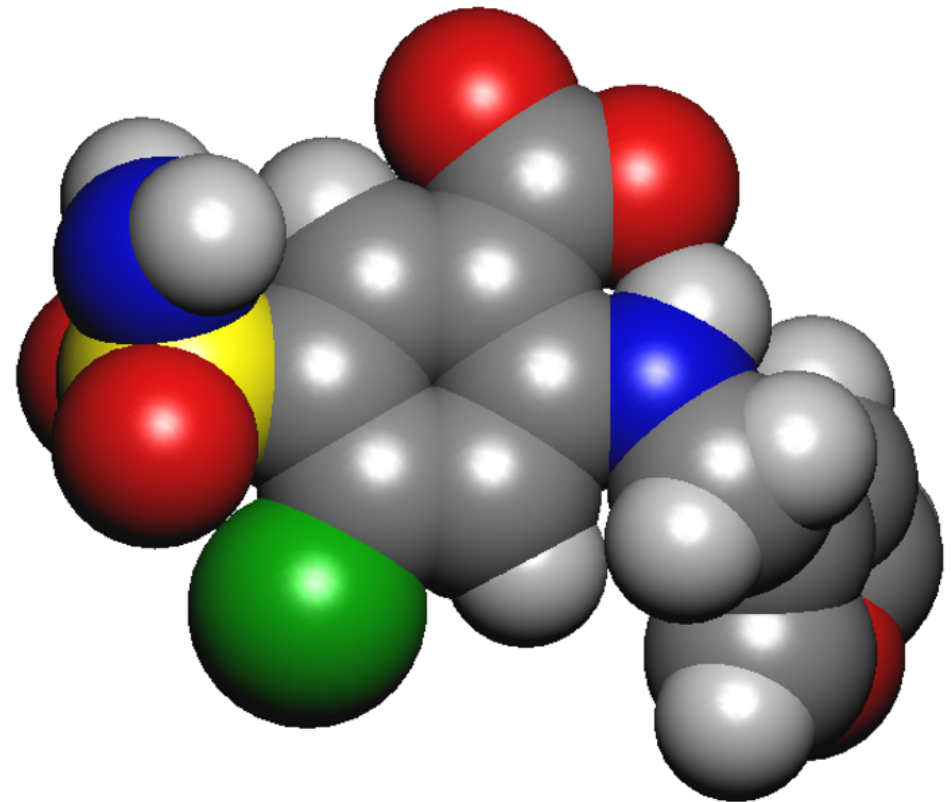
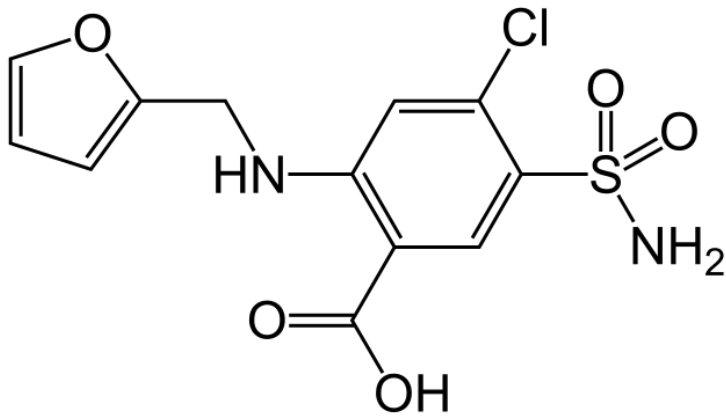


bio1151.nicerweb.com

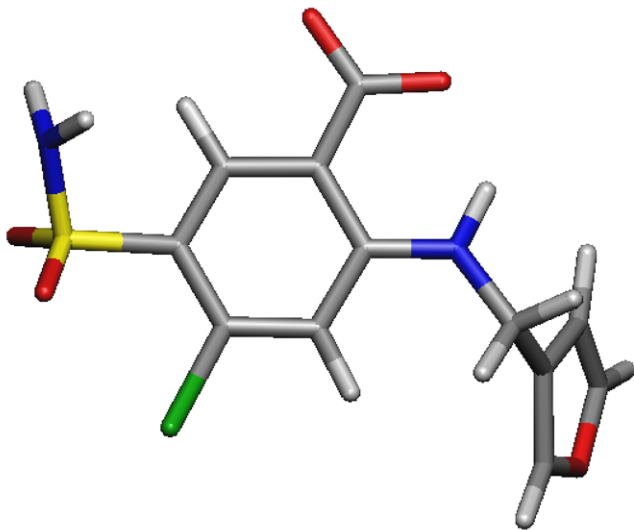
Diese gegenseitige Anpassung ist eine Ursache von Arzneistoffnebenwirkungen



Biologische Schlüssel – interaktives 3D-Modellbuilding

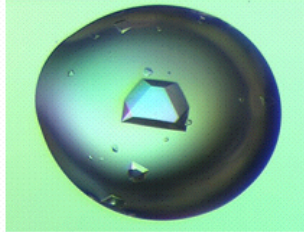


Furosemid – ein Diuretikum





> 135 000 Biologische Schlösser – Protein Data Bank (PDB)



Proteinkristall
ttplabtech.com

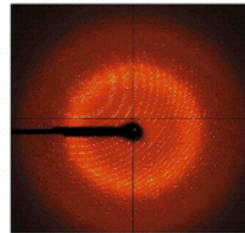
$$\rho(x,y,z) = 1/V \cdot \sum_{hkl} F_{hkl} \cdot e^{-2\pi i(hx+ky+lz)}$$



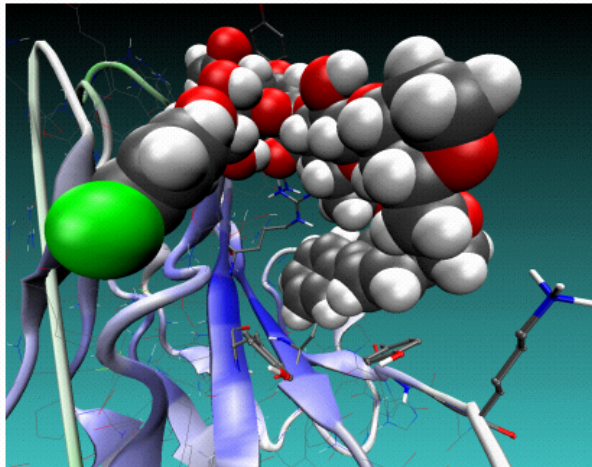
Diffraktometer
lks.physik.uni-erlangen.de



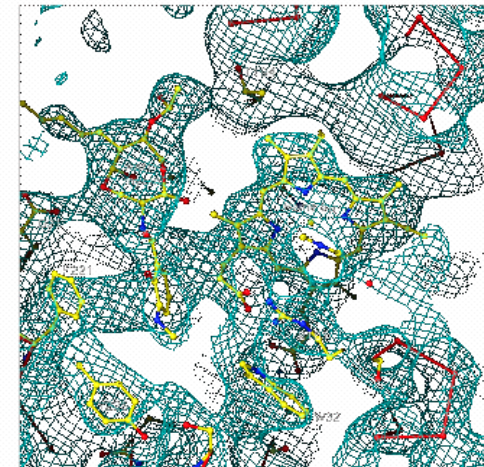
Max Perutz und John Kendrew: Nobelpreis 1964
nobelprize.org



Beugungsmuster
lbl.gov



Atomistisches Modell



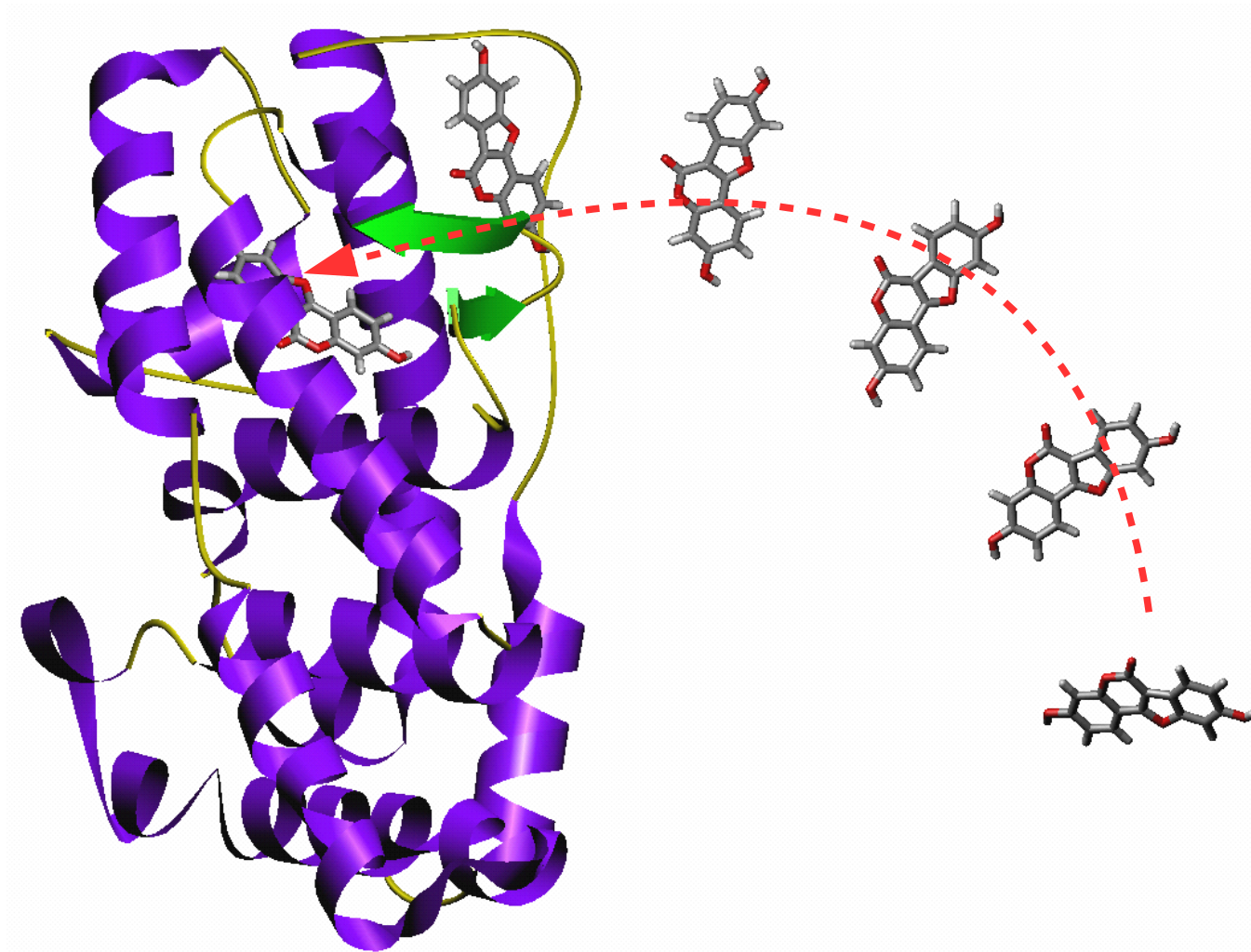
Elektronendichtekarte
lbl.gov

X-ray + NMR + Cryo-EM + ...



Molecular Docking in Computational Toxicology

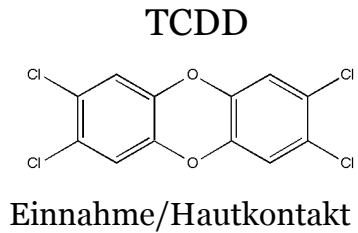
Methoden des struktur-basierten Designs im Einsatz



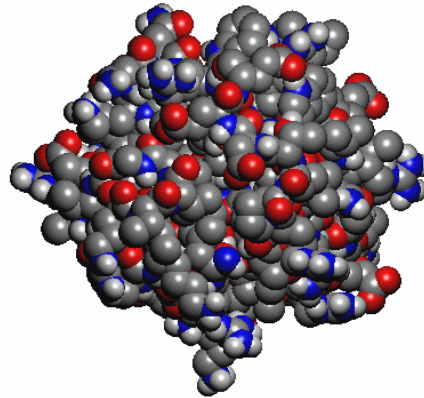
Andocken einer Substanz in die Bindungstasche (3D-Struktur) eines Proteins



Simulation von Rezeptor-vermittelten Nebenwirkungen



Bindung

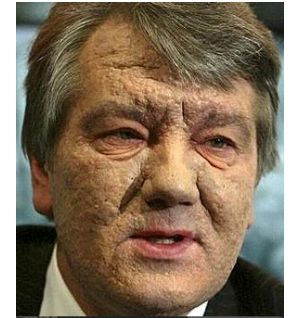


Signalweiterleitung

Manifestation der Toxizität



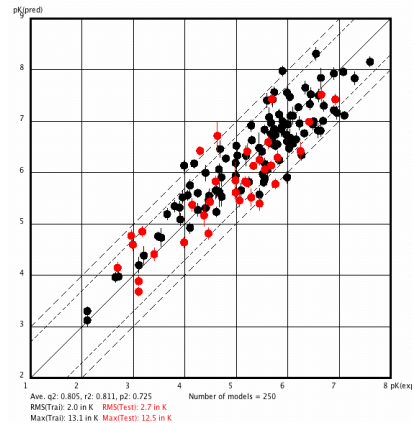
Seveso-Opfer 1976
www.brooklyn.cuny.edu



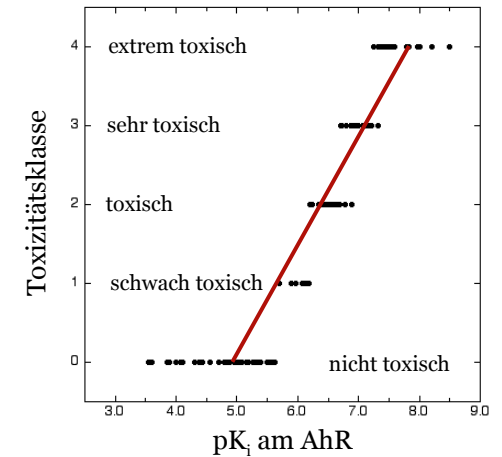
V. Juschtschenko 2004
www.blick.ch

Simulation der Bindung ans Zielprotein (AhR)

Konsequenz: Aus der Quantifizierung der Bindungsaffinität zu einem Protein, das unerwünschte Wirkungen vermittelt lässt sich das "toxische Potential" der Verbindung, nicht aber deren Toxizität abschätzen.

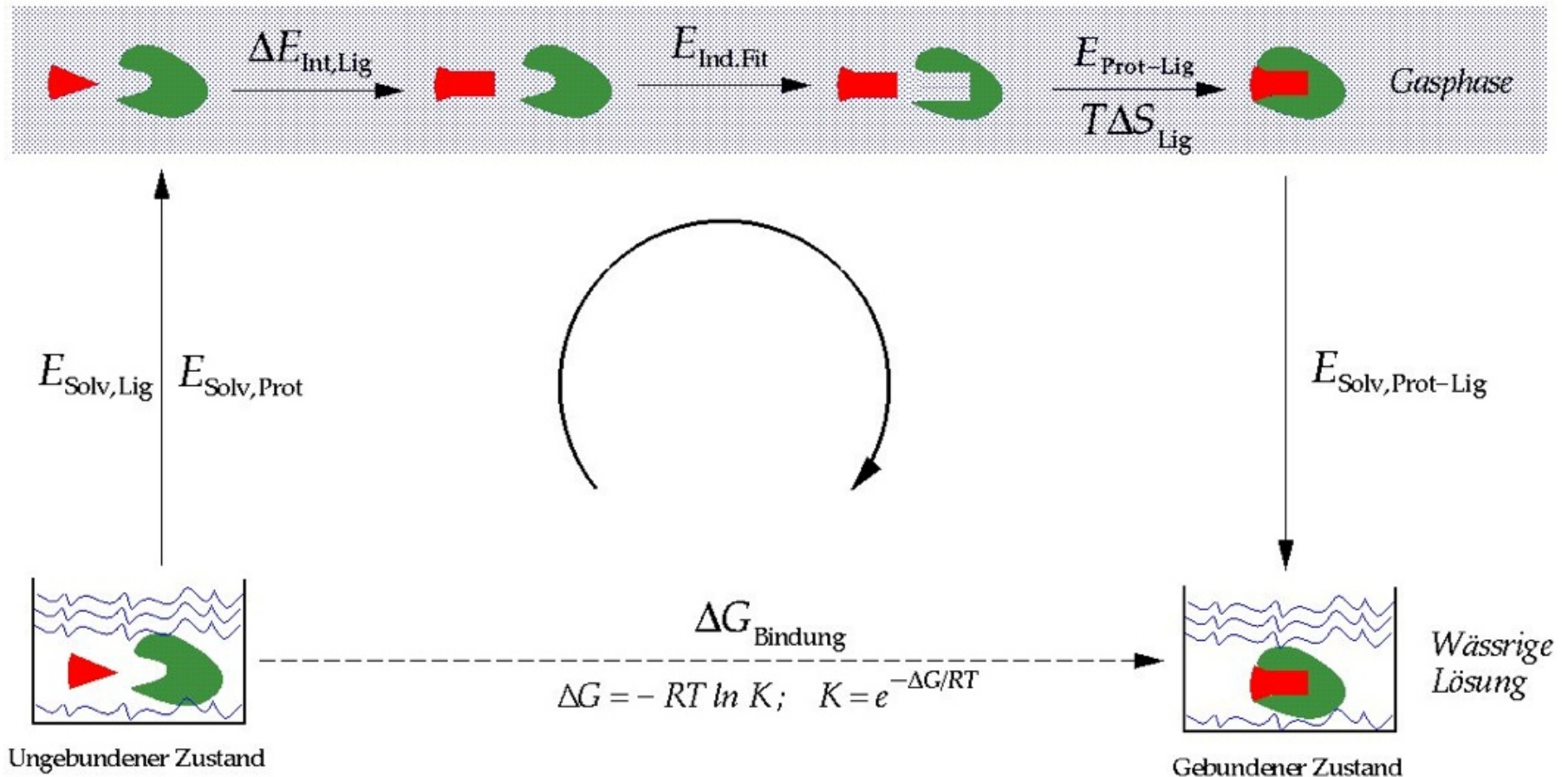


QSAR





Berechnung der Bindungsaffinität (ΔG) der Wirksubstanz

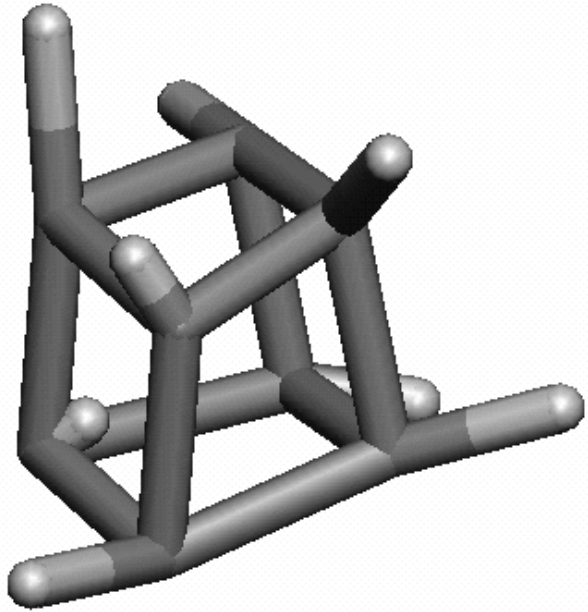


ΔG ist eine Zustandsgrösse, d.h. sie hängt nicht vom eingeschlagenen Weg ab.

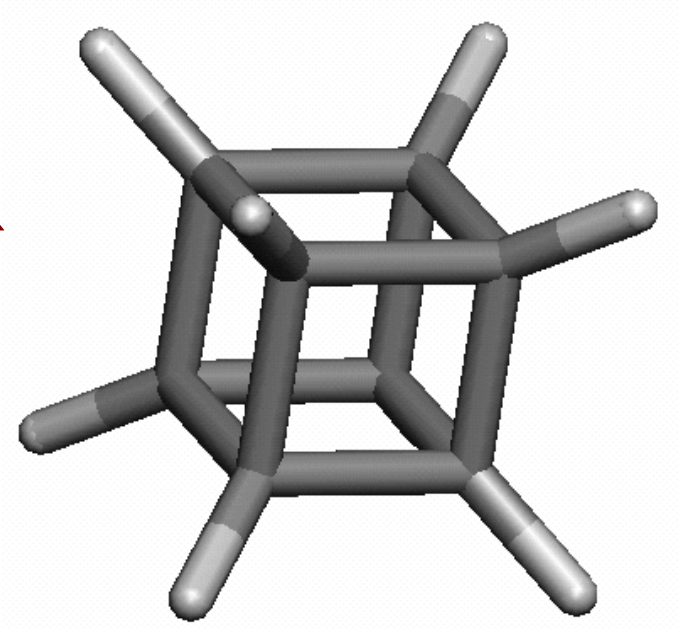


Zentrale Philosophie:

Struktur und Energie eines Moleküls sind in engem Zusammenhang



Energieminimierung
Strukturoptimierung



Definition: Hohe Energie = Instabiles System

Die Energie von Molekülen lässt sich mit Molekülmechanikrechnungen (Kraftfeldrechnungen) minimieren. Dabei wird deren Struktur optimiert.

Tiefe Energie = Stabiles System



Das Kraftfeld – das Gehirn von Moleküloptimierungen

$$E_{total} = \sum_{bonds} K_r (r - r_{eq})^2 + \sum_{angles} K_\theta (\theta - \theta_{eq})^2 + \sum_{torsions} \frac{V_n}{2} [1 + \cos(n\phi - \gamma)] +$$

$$\sum_{nb\ pairs} \frac{q_i \cdot q_j}{4\pi\epsilon_0 D(r) r_{ij}} + \sum_{nb\ pairs} \left(\frac{A}{r_{ij}^{12}} - \frac{B}{r_{ij}^6} \right) +$$

$$\sum_{H\ bonds} \left(\frac{C}{r_{ij}^{12}} - \frac{D}{r_{ij}^{10}} \right) \cdot \cos^2(\theta_{Don-H\cdots Acc}) \cdot \cos^n(\omega_{H\cdots Acc-LP}) +$$

$$\sum_{metal\ pairs} \frac{q_i^{CT} \cdot q_j^{CT}}{4\pi\epsilon_0 D(r) r_{ij}} + \sum_{metal\ pairs} \left(\frac{E}{r_{ij}^{12}} - \frac{F}{r_{ij}^{10}} \right) +$$

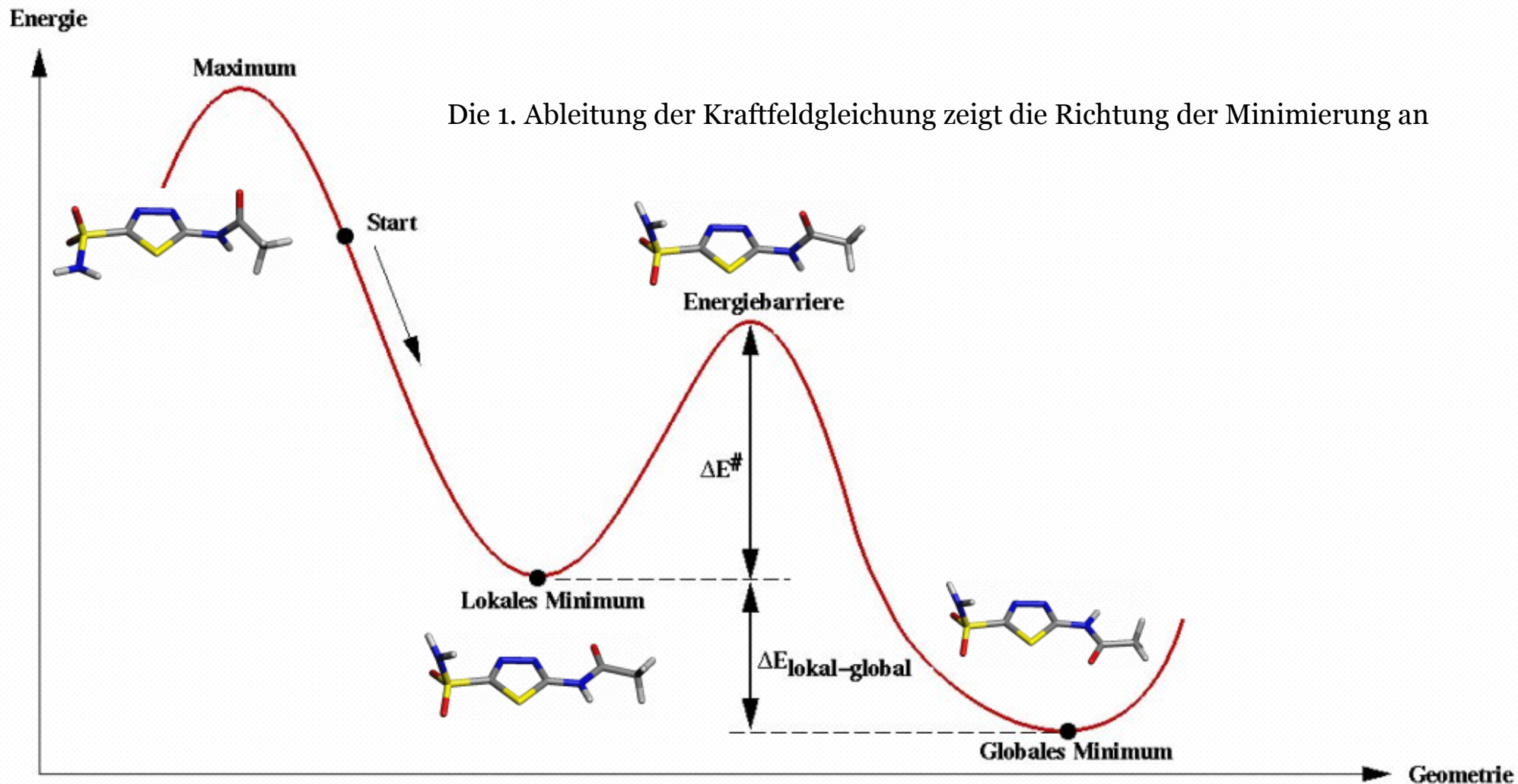
$$\sum_{atoms} -\frac{1}{2} \alpha_i [\vec{E}_i^\circ \cdot \vec{E}_i]$$

J. Am. Chem. Soc. 1990, 112, 4759–4767
ChemMedChem 2010, 5, 2088–2101

Die Kraftfeldgleichung erstellt die Beziehung zwischen Struktur und Energie



Der „Minimizer“ – der Motor von Moleküloptimierungen

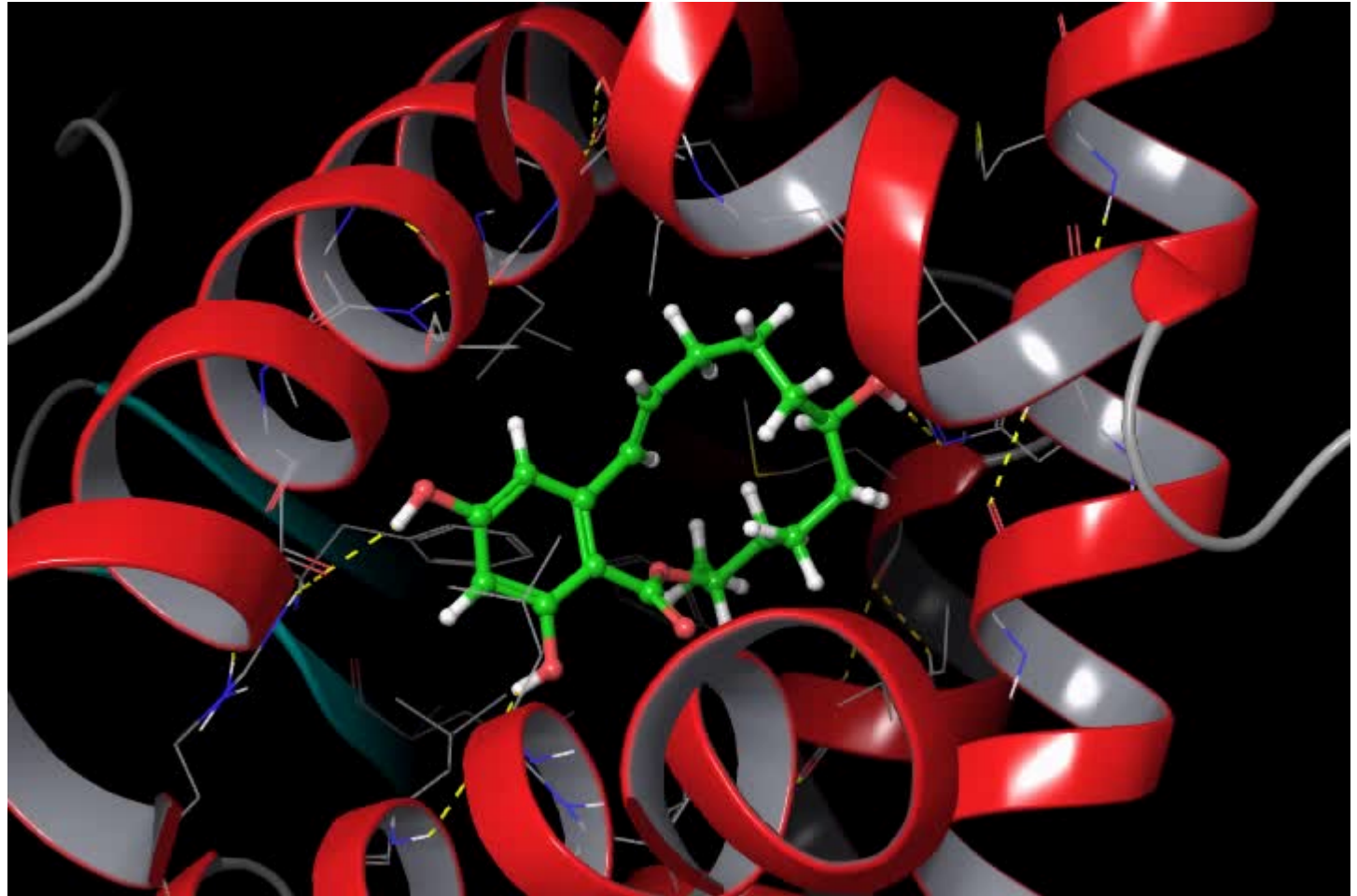
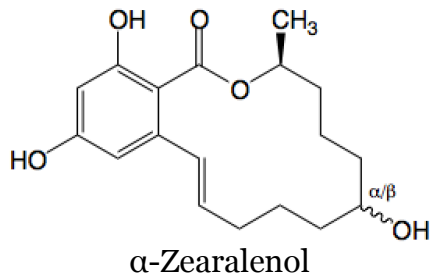


Molekülmechanik-Optimierungen enden immer im nächsten lokalen Minimum



Moleküldynamik-Simulationen

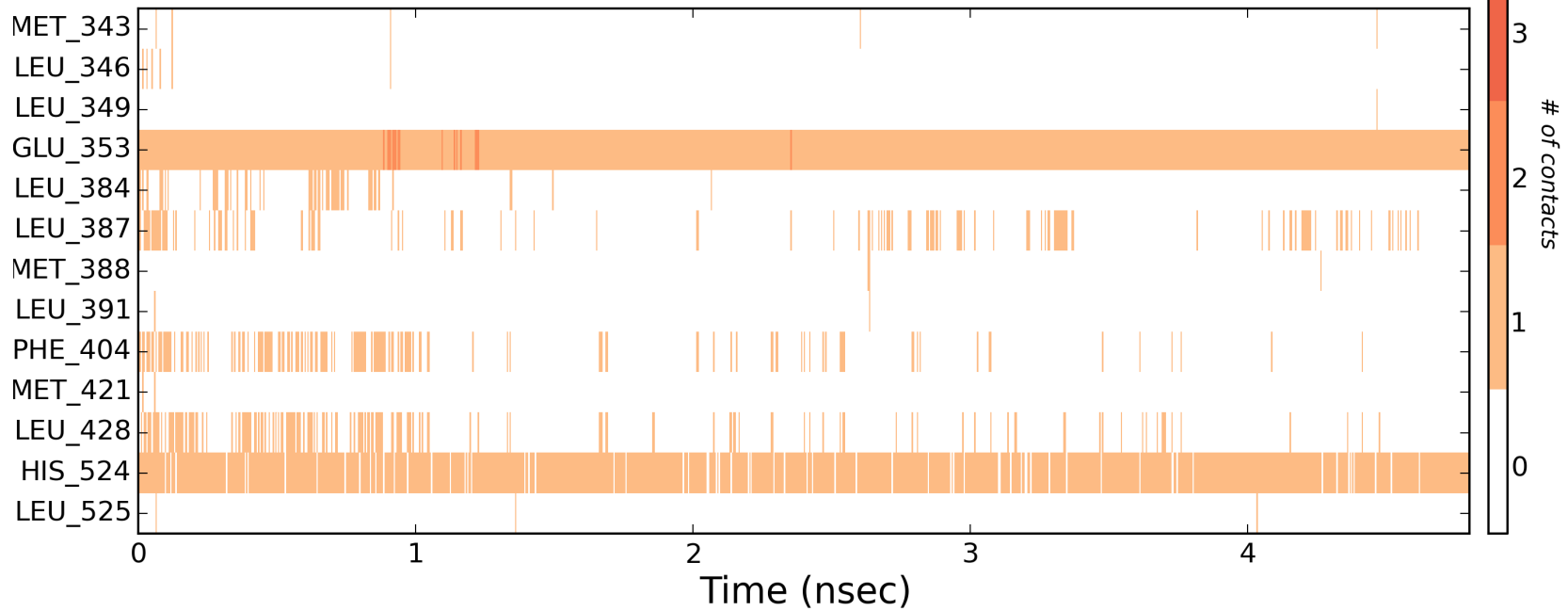
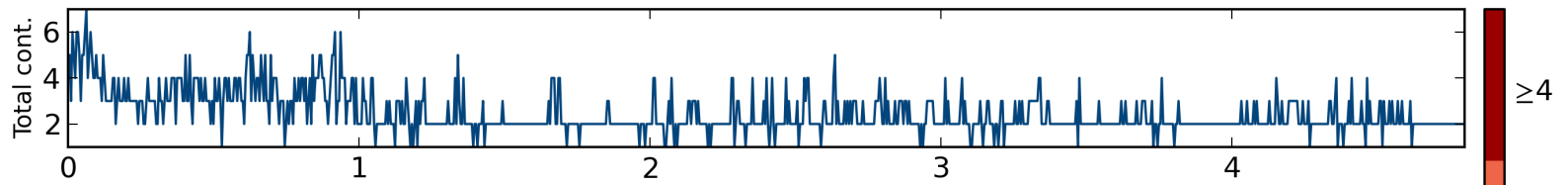
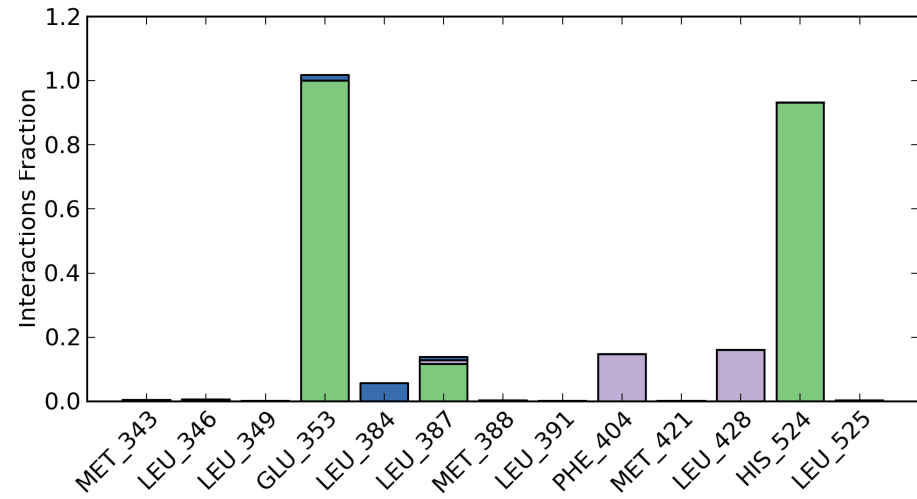
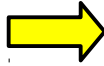
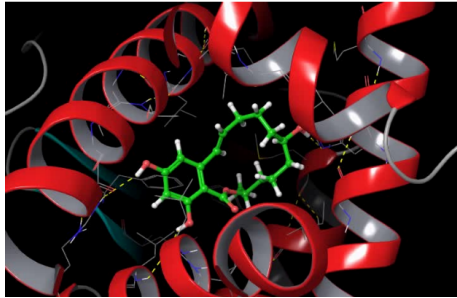
Newton'sche Bewegungsgleichung (1687): $r(t+\Delta t) = r(t) + \partial r/\partial t \cdot \Delta t + 0.5 \cdot \partial^2 r/\partial t^2 \cdot \Delta t^2$



4.8 ns MD simulation of docked α -zearalenol at the Estrogen receptor α
(Software *Desmond*, *D.E.Shaw*, *New York*)



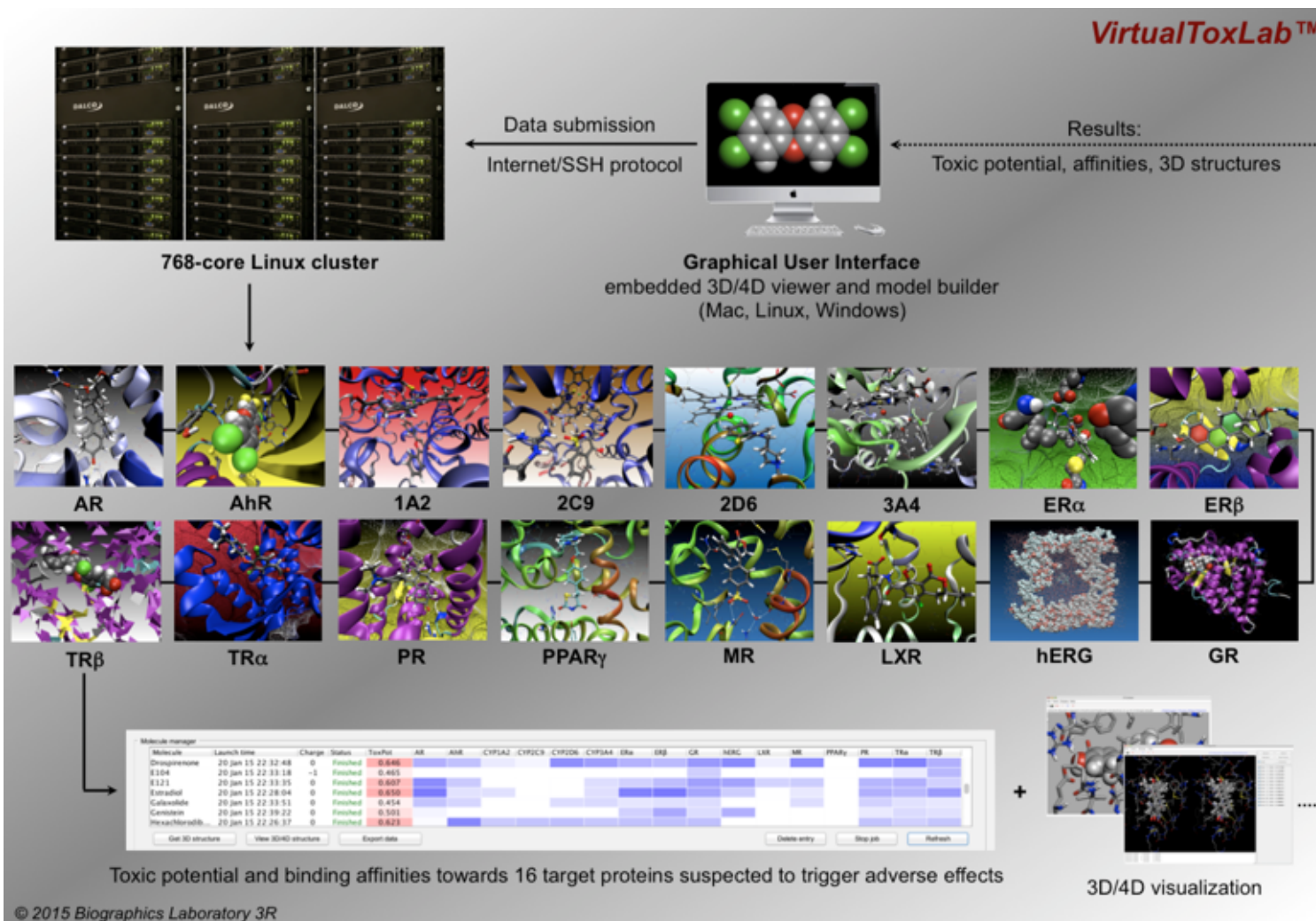
MD Simulation





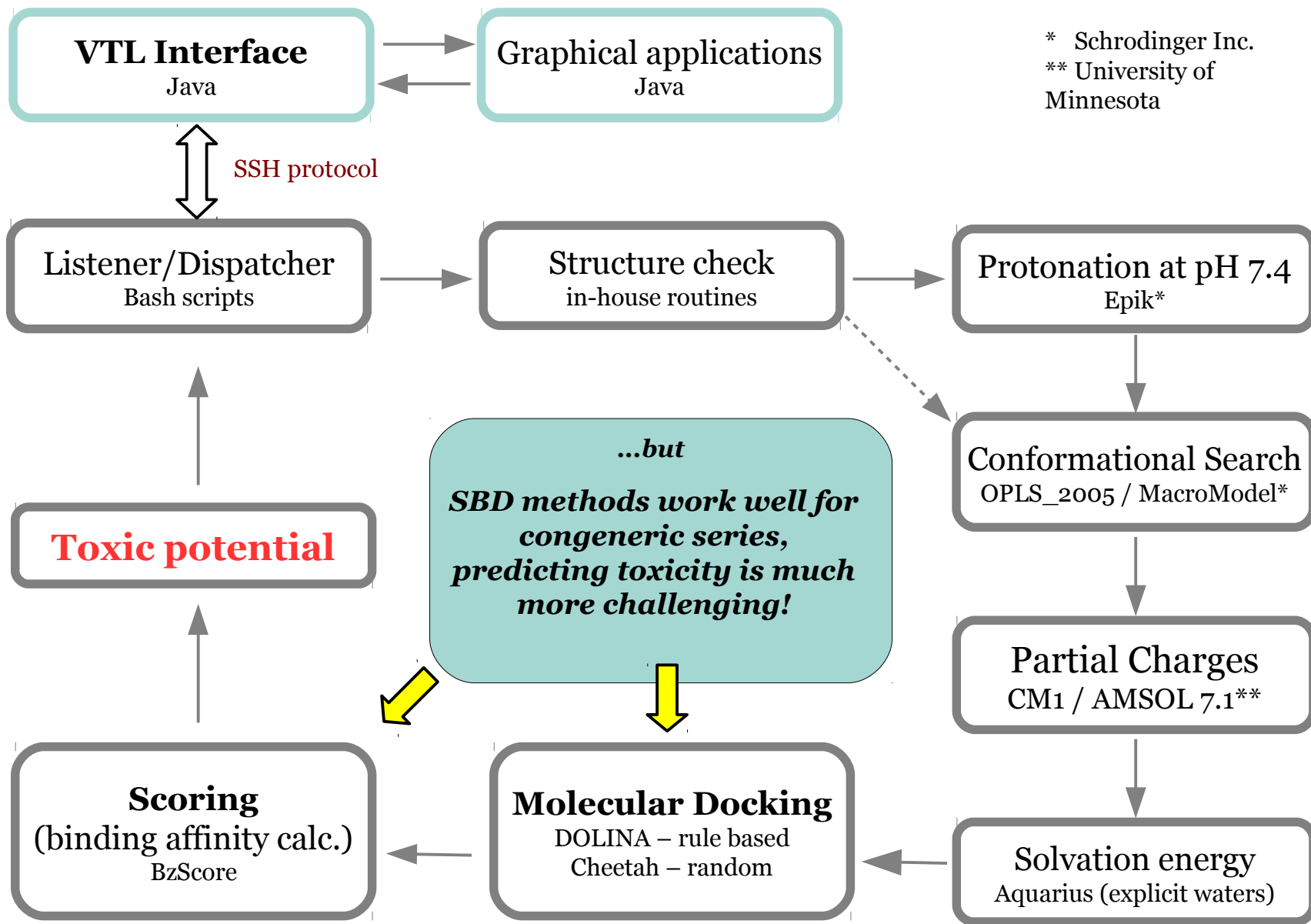
VirtualToxLab

Automatisierte Voraussage des toxischen Potentials von Arzneistoffen, (Umwelt-) Chemikalien und Naturstoffen





VirtualToxLab – Technisches Flussdiagramm

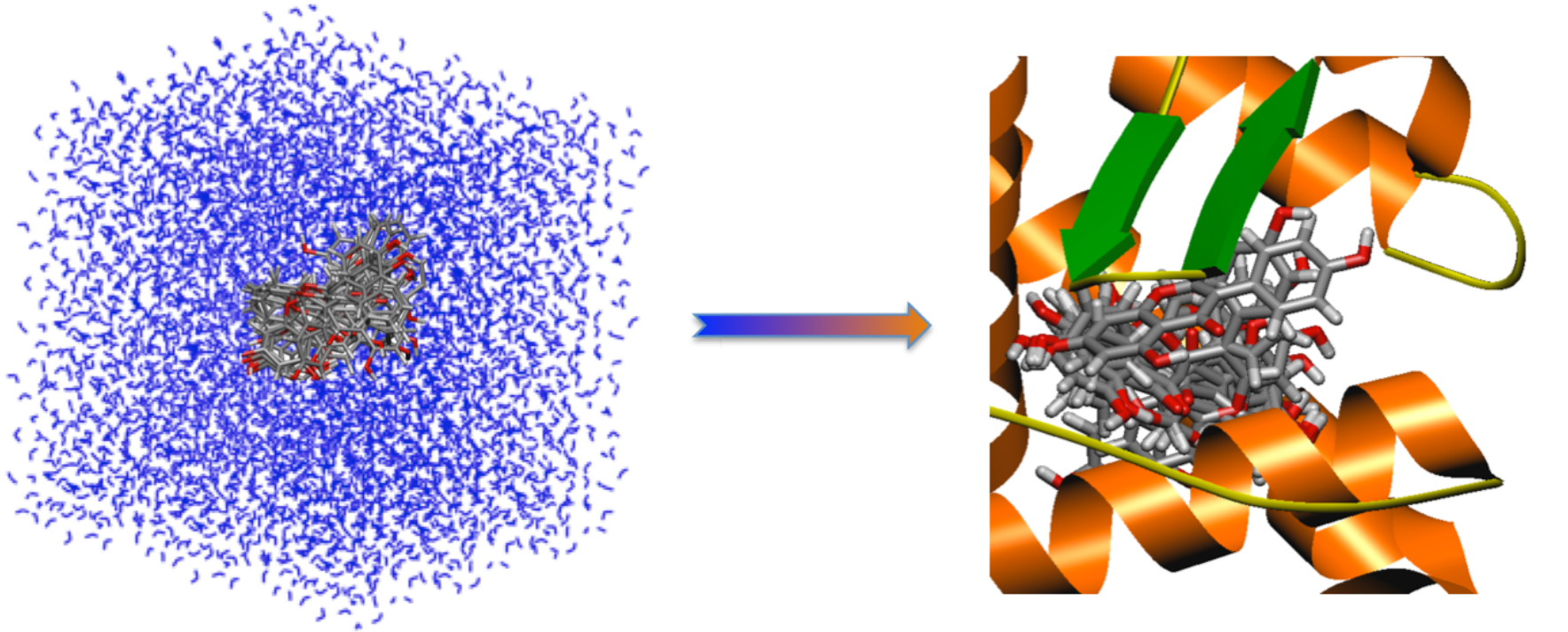




VirtualToxLab – Boltzmann Bewertung (4D)

Direkte Bewertung des Wasser-Protein-Übergangs einer Wirksubstanz (4D Boltzmann-Ensemble)

Beispiel: Genistein → Estrogen receptor β



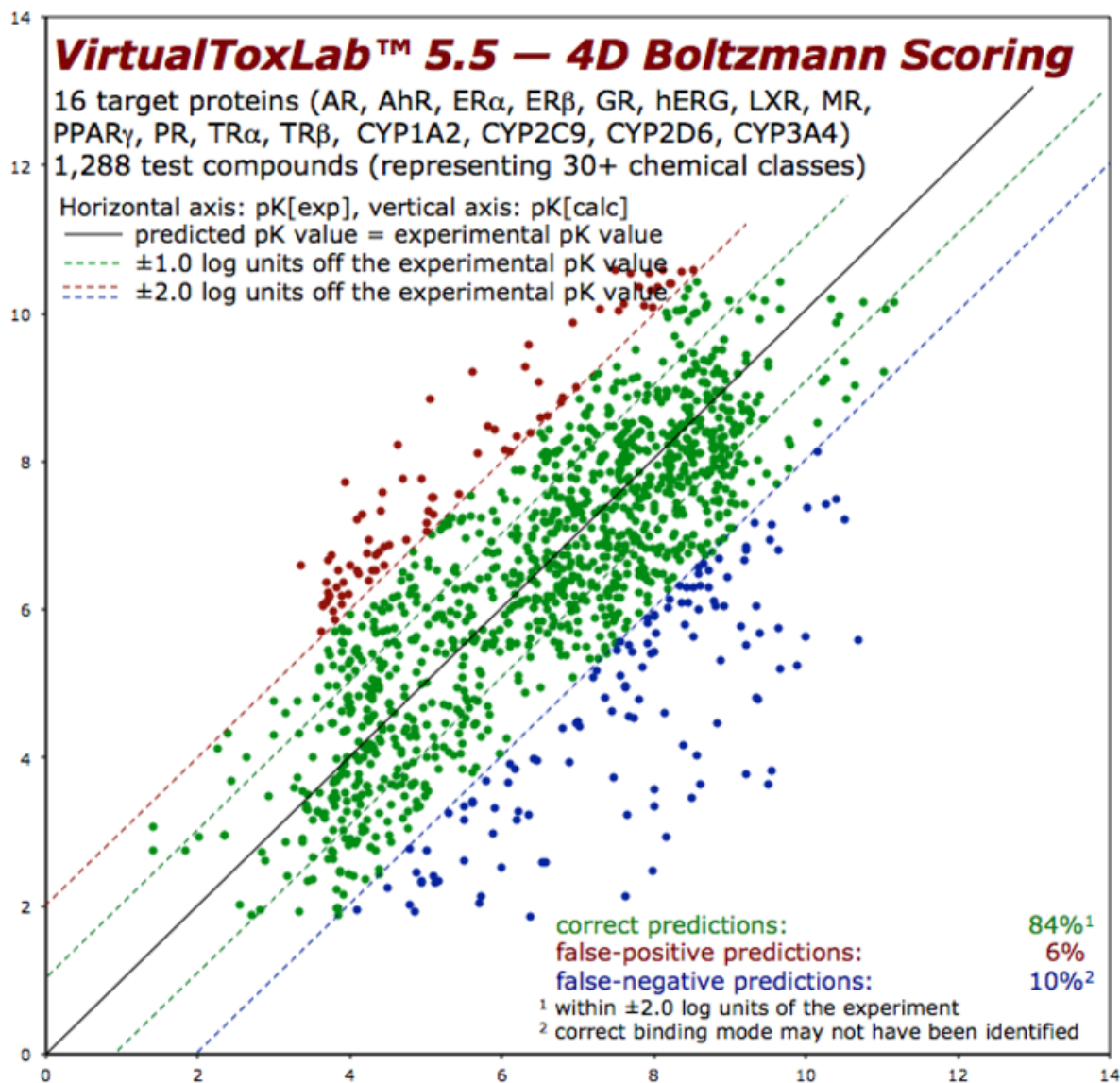
Water-bound ligand: $E_{BZW} = -36.262$ kcal/mol

Protein-bound ligand: $E_{BZW} = -47.006$ kcal/mol

$\Delta E_{BZW} = -10.774$ kcal/mol \rightarrow converting ΔE into K using: $K = e^{-\Delta E/RT} \rightarrow K_{\text{calc}} = 9.66 \times 10^{-9}$ M ($K_{\text{exp}} = 1.2 \times 10^{-8}$ M)



VirtualToxLab – Validierung anhand von 1,288 Substanzen





VirtualToxLab – Grafische Schnittstelle (Interface)

VirtualToxLab Interface

Login VirtualToxLab Manager Settings

Molecule manager

Molecule	Launch time	Charge	Status	ToxPot	AR	AhR	CYP1A2	CYP2C9	CYP2D6	CYP3A4	ER α	ER β	GR	hERG	LXR	MR	PPAR γ	PR	TR α	TR β	
Danazol	8 May 15 09:40:05	0	Finished	0.612																	
DDT	8 May 15 09:40:15	0	Finished	0.462																	
Dexamethasone	8 May 15 09:40:40	0	Finished	0.693																	
Diethylstilbestrol	8 May 15 09:40:51	0	Finished	0.522																	
Drospirenone	8 May 15 09:41:01	0	Finished	0.601																	
Ethinylestradiol	8 May 15 09:41:11	0	Finished	0.598																	
Estradiol	8 May 15 09:36:38	0	Finished	0.606																	
Flecainide	8 May 15 09:41:22	+1	Finished	0.576																	
Fluticasone	8 May 15 09:41:35	0	Finished	0.669																	
Gestodene	8 May 15 09:41:46	0	Finished	0.603																	
Glaucine	8 May 15 09:41:56	+1	Finished	0.514																	
Limonene	8 May 15 09:42:11	0	Finished	0.063																	
Liothyronine	8 May 15 09:42:21	0	Finished	0.539																	
Methylparabene	8 May 15 09:42:35	0	Finished	0.214																	
Methyltrienolone	8 May 15 09:42:47	0	Finished	0.541																	
Mibolerone	8 May 15 09:42:57	0	Finished	0.572																	
Mifepristone	8 May 15 09:43:27	0	Finished	0.675																	
Musk xylene	8 May 15 09:43:38	0	Finished	0.394																	
Neutral red	8 May 15 09:43:42	0	Finished	0.357																	
Nifekalant	8 May 15 09:44:08	+1	Finished	0.686																	

*Fingerprinting:
Color depth indicates affinity.
Upon hovering (mouse over),
the numeric affinity is displayed.*

Fluticasone (GR) = 1.46 nM **

Get 3D structure View 3D/4D structure Export data Export binding data (csv) Delete entry Stop job Refresh

Select target protein(s)

- Androgen
- Aryl Hydrocarbon
- CYP450-1A2
- CYP450-2C9
- CYP450-2D6
- CYP450-3A4
- Estrogen alpha
- Estrogen beta
- Glucocorticoid
- hERG K+ channel
- Liver X
- Mineralocorticoid
- PPAR gamma
- Progesterone
- Thyroid alpha
- Thyroid beta

Download 3D structure of ligand-protein complex (PDB)

Select target protein(s)

Toxic potential (ranging from 0.0 to 1.0)

Tokens left: 8201

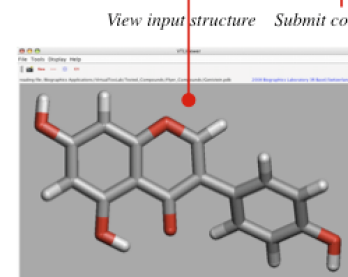
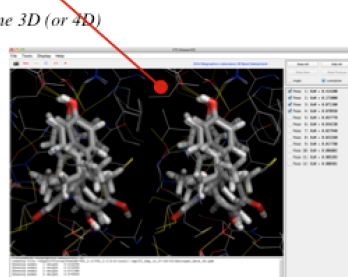
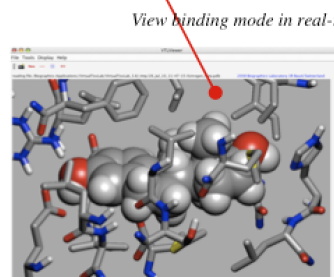
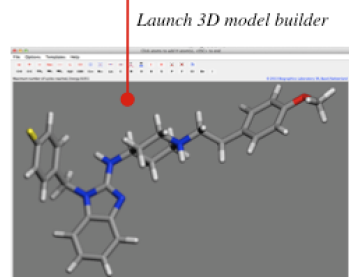
Protonation state: automatic (pH 7.4)

Conformation sampling: standard

Submit molecule

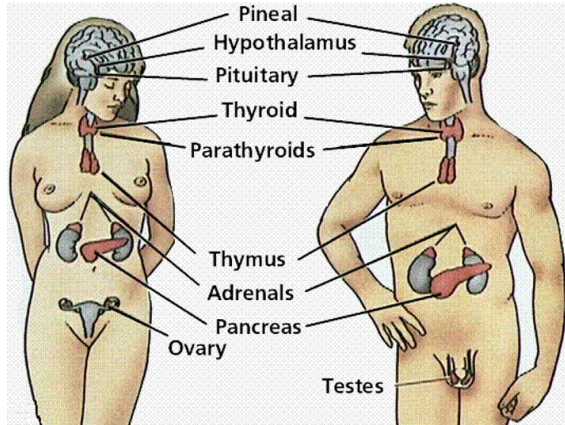
VTL Builder Structure file: /Users/Biograft/VirtualToxLab/Genistein.pdb Browse View input Submit

Messages: None. Load: 44 %

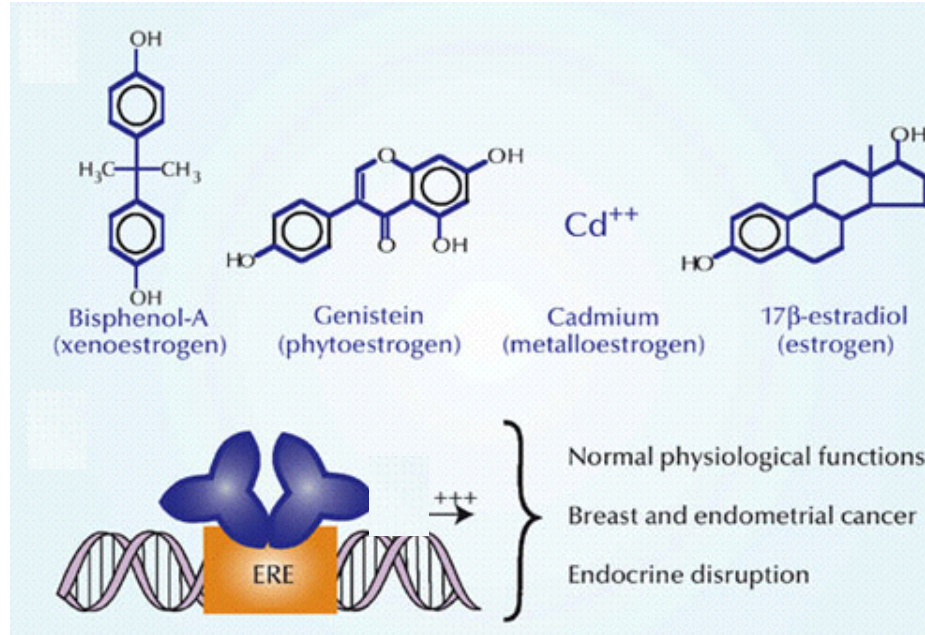




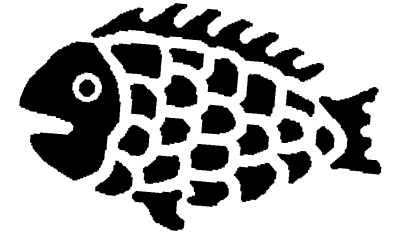
Nebenwirkungen/Toxizität: Endokrine Störungen



www.eco-thinker.com

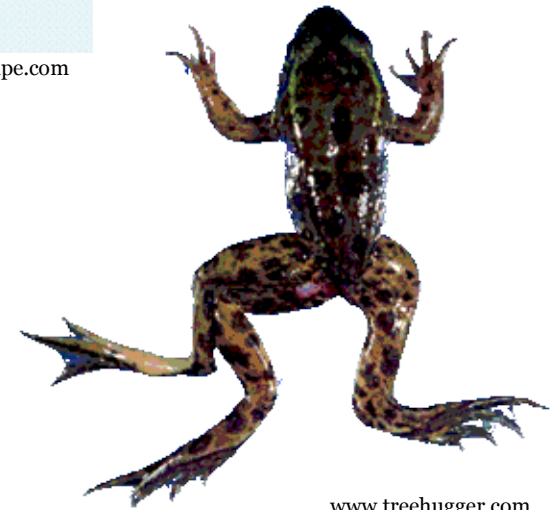


www.medscape.com



www.nutri-notes.com

Endokrine Disruptoren (hormonell aktive Substanzen) – auch “Tarnkappenchemikalien” genannt – sind körperfremde Substanzen, die wie Hormone ins Endokrine System ein-greifen können und dort zerstörerische Wirkungen entfalten können. Solche Substanzen wurden mit toxischen Effekten in Tieren in Verbindung gebracht und lassen vermuten, dass kleinste Mengen beim Menschen vergleichbare Effekte hervorrufen können.

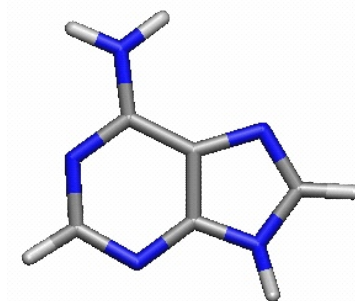
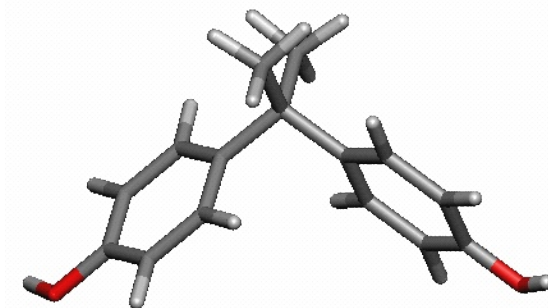
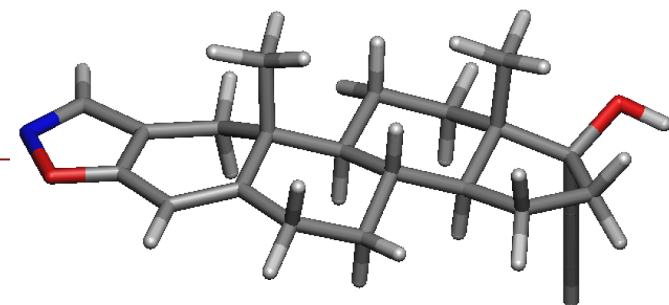
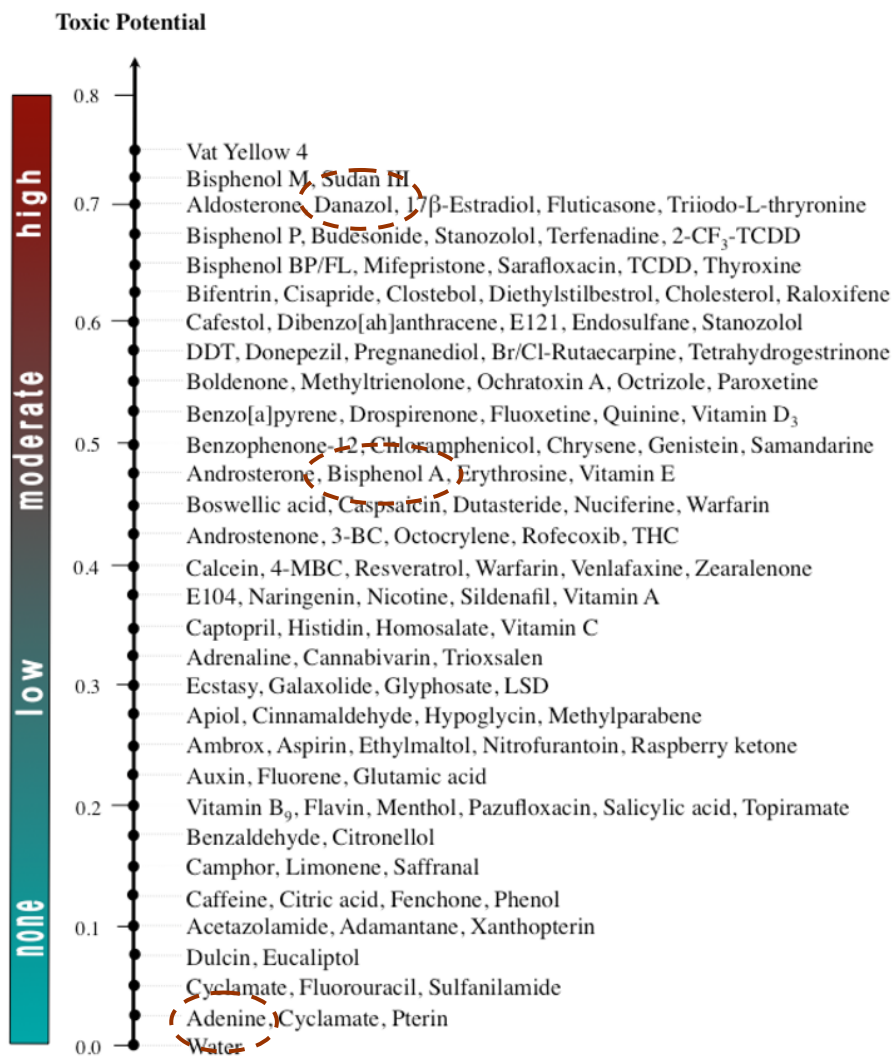


www.treehugger.com

☞ Diethylstilbestrol, Thalidomid: vom Markt genommen

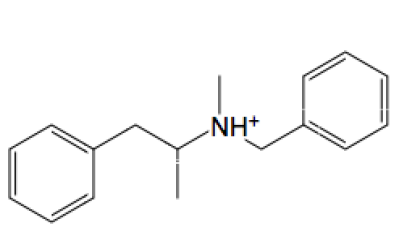


VirtualToxLab – "Toxicity Alerts"

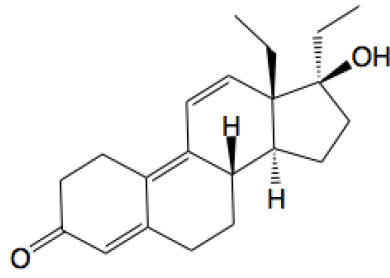




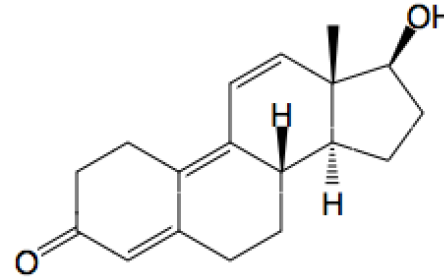
VirtualToxLab – Analyse von verbotenen Dopingsubstanzen



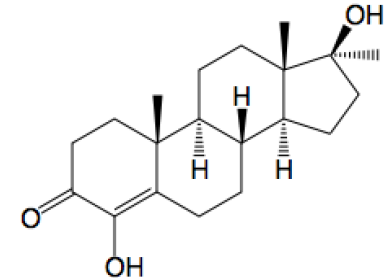
Benzphetamin



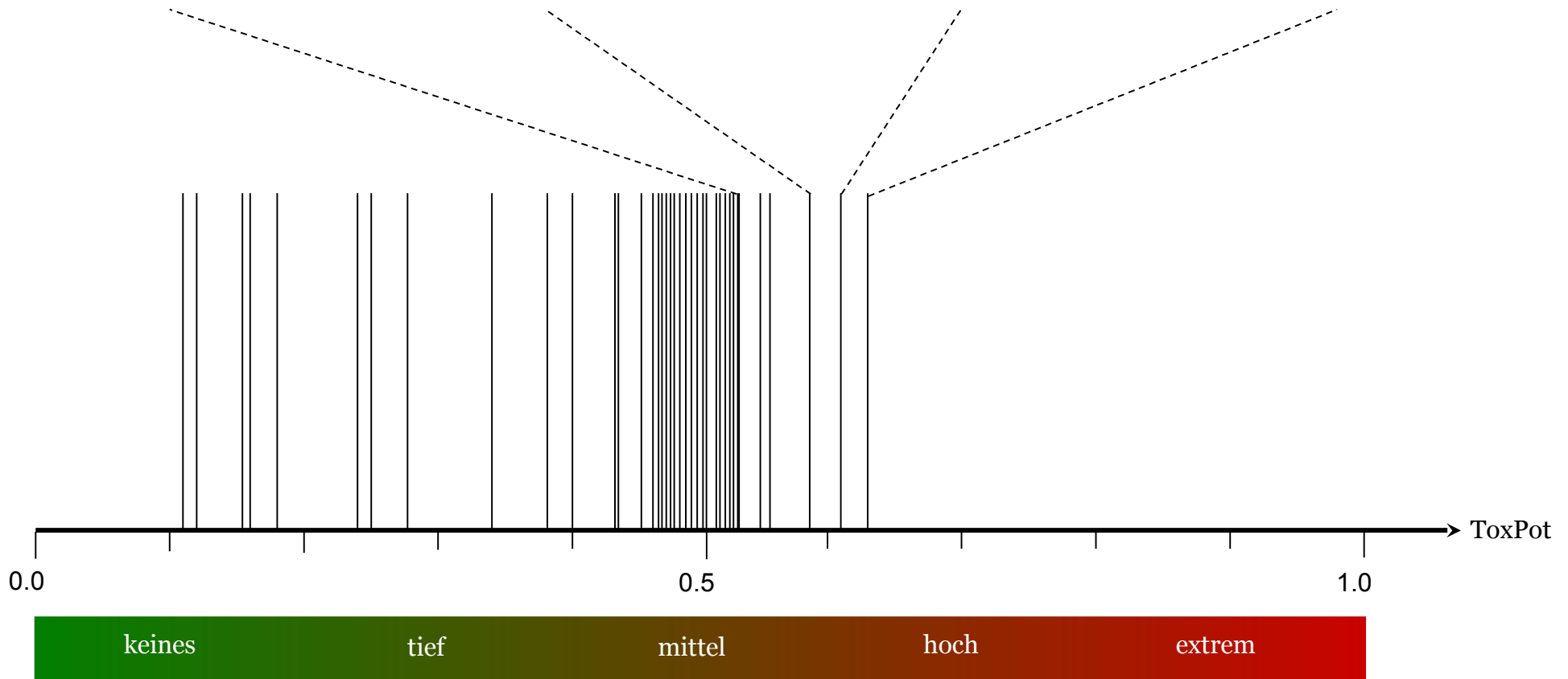
Tetrahydrogestrinon



Trenbolon

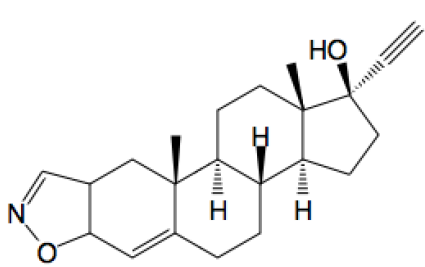


Oxymesteron

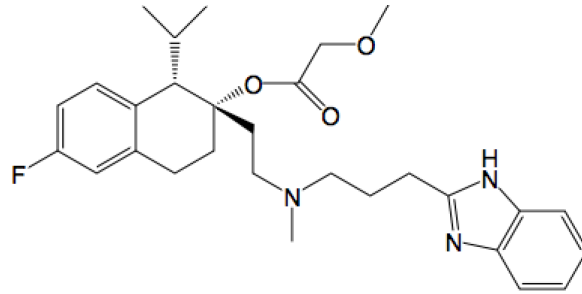




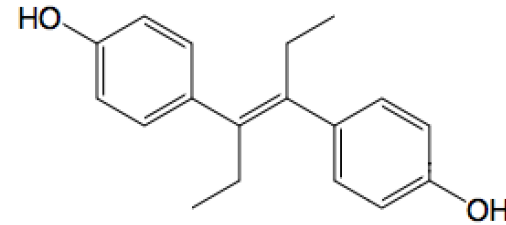
VirtualToxLab – Vom Markt zurückgezogene Substanzen



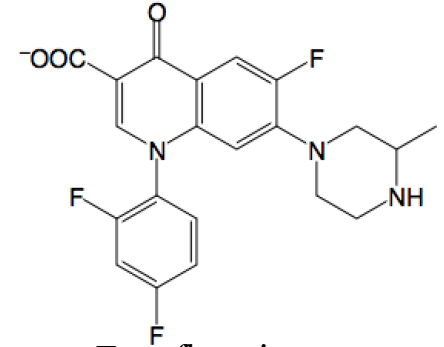
Danazol



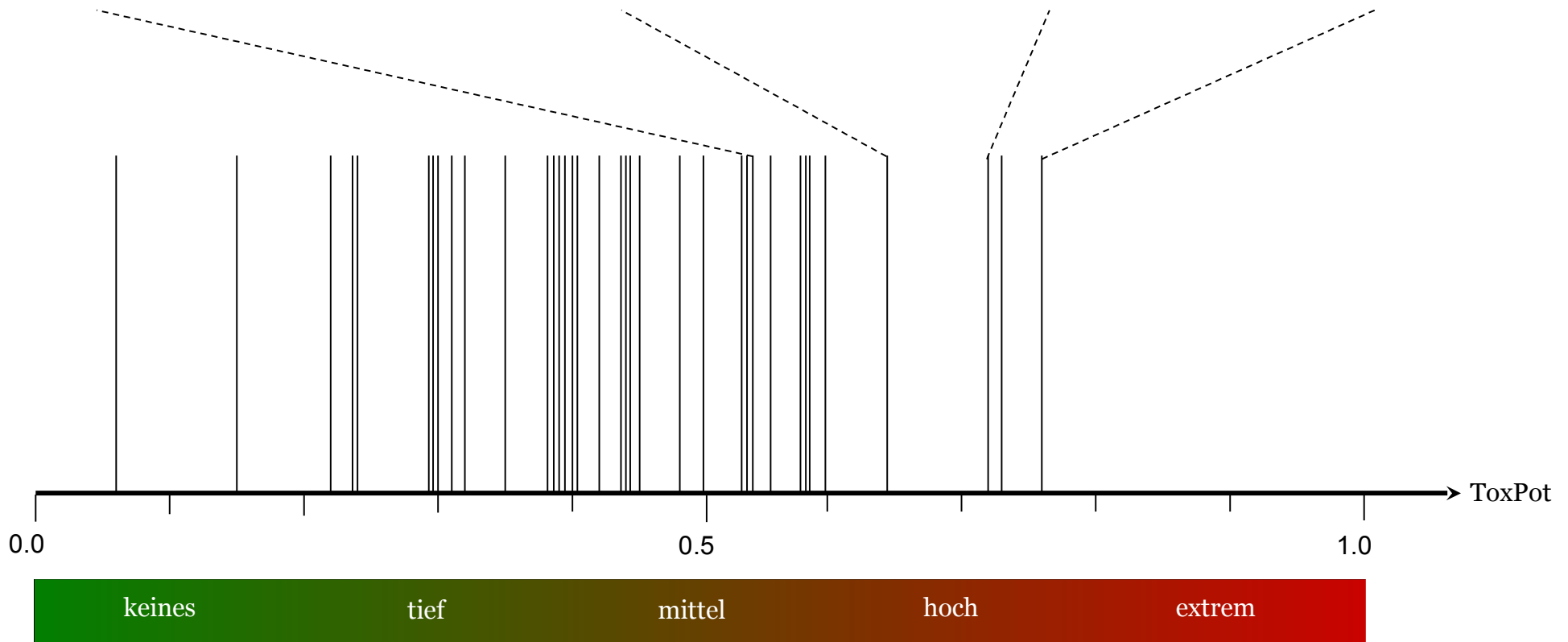
Mibefradil



Diethylstilbestrol

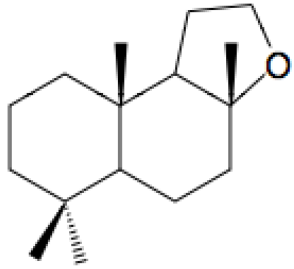


Temafloxacin

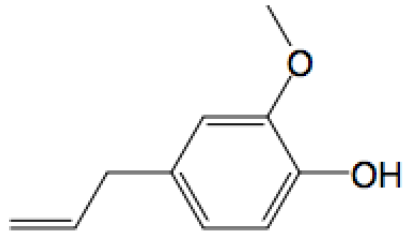




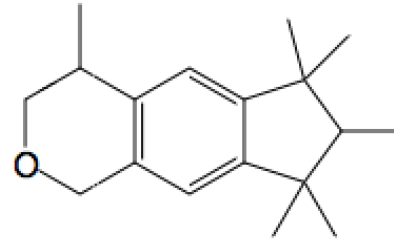
VirtualToxLab – Duftstoffe in Parfüms



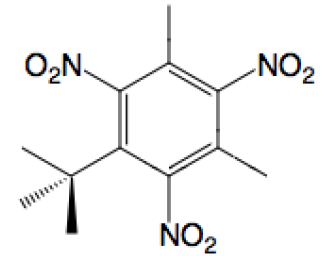
Ambrox



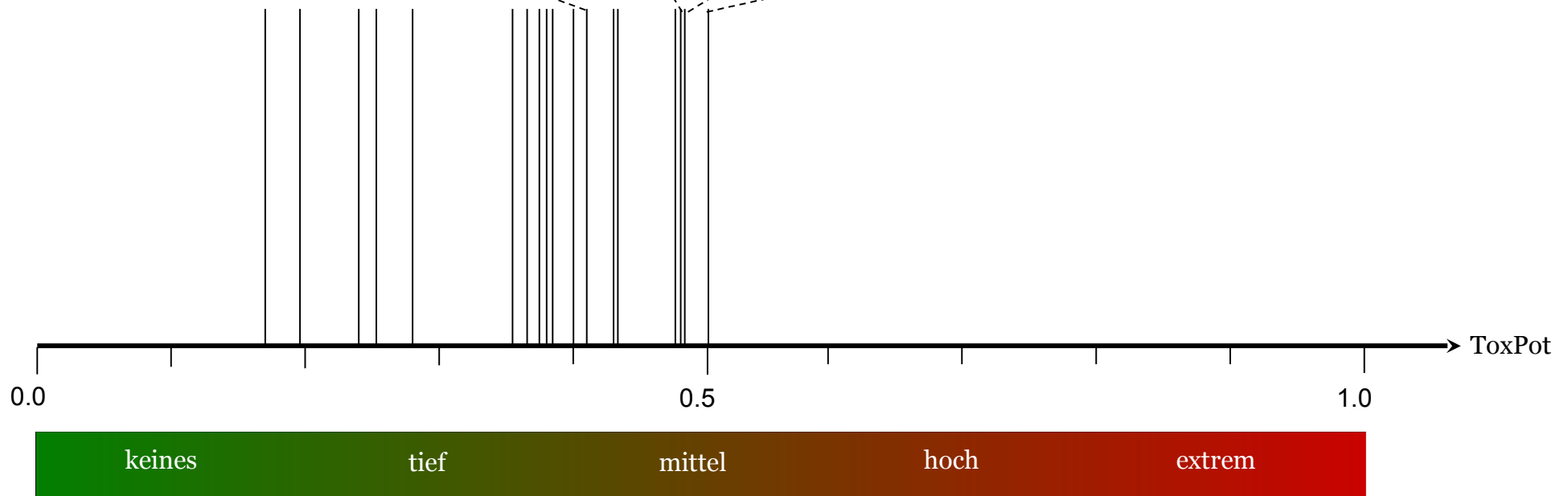
Eugenol



Galaxolid

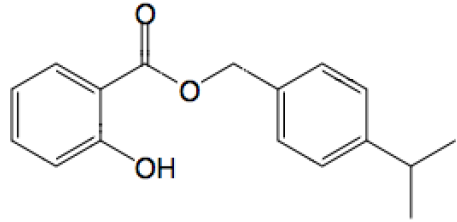


Musk xylen

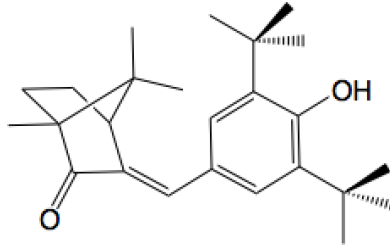




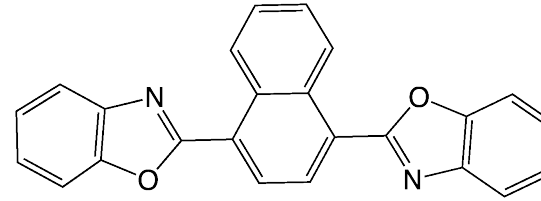
VirtualToxLab – UV-Filter und einige ihrer Metaboliten



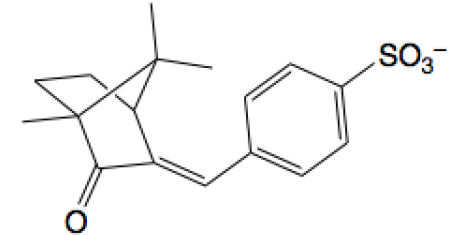
4-Isopropylbenzylsalicylate



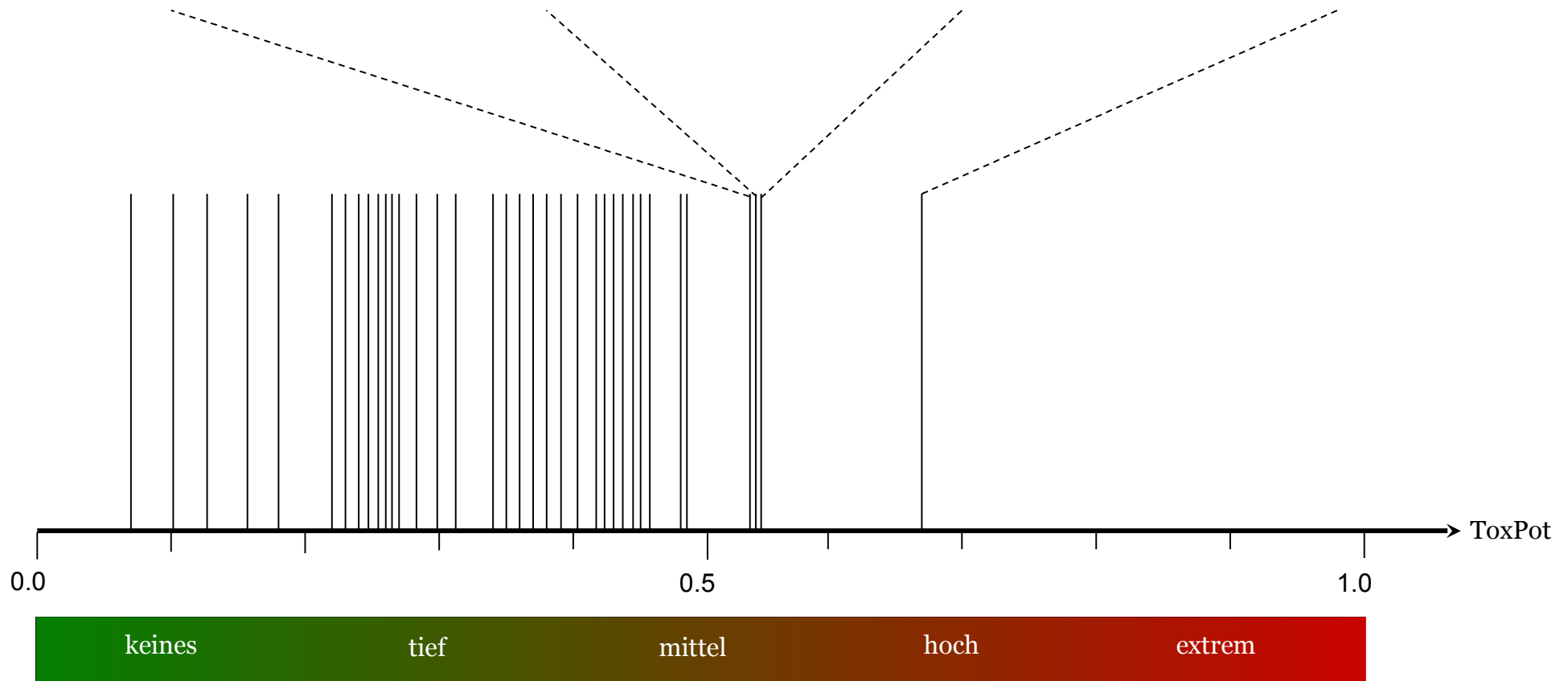
Di-tert.-butylhydroxybenzylidenecamphor



Dibenzoxazinylnaphtalene



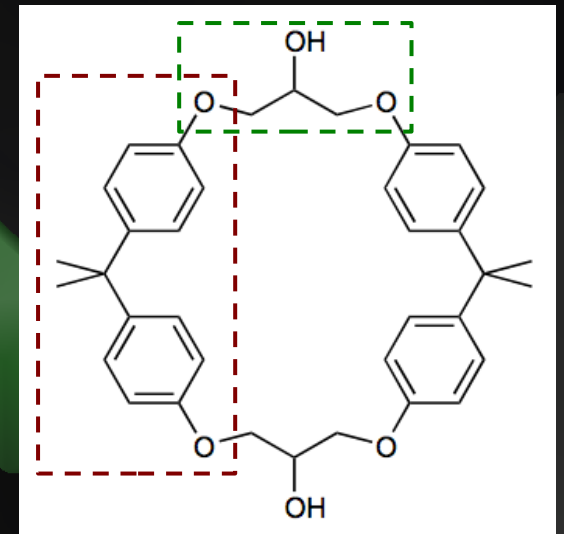
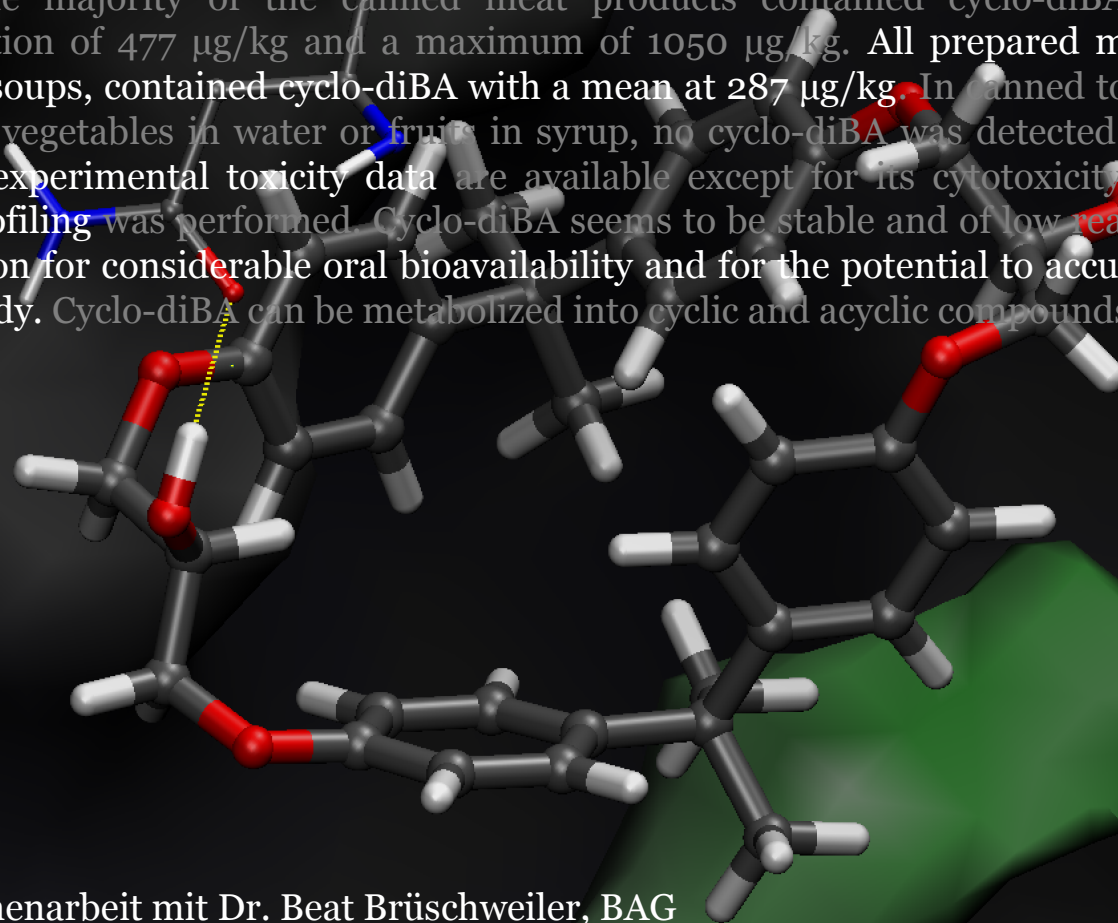
4-Methylbenzylidenecamphor sulfonic acid





Cyclo-diBA — Toxisches Nebenprodukt in Konservendosen

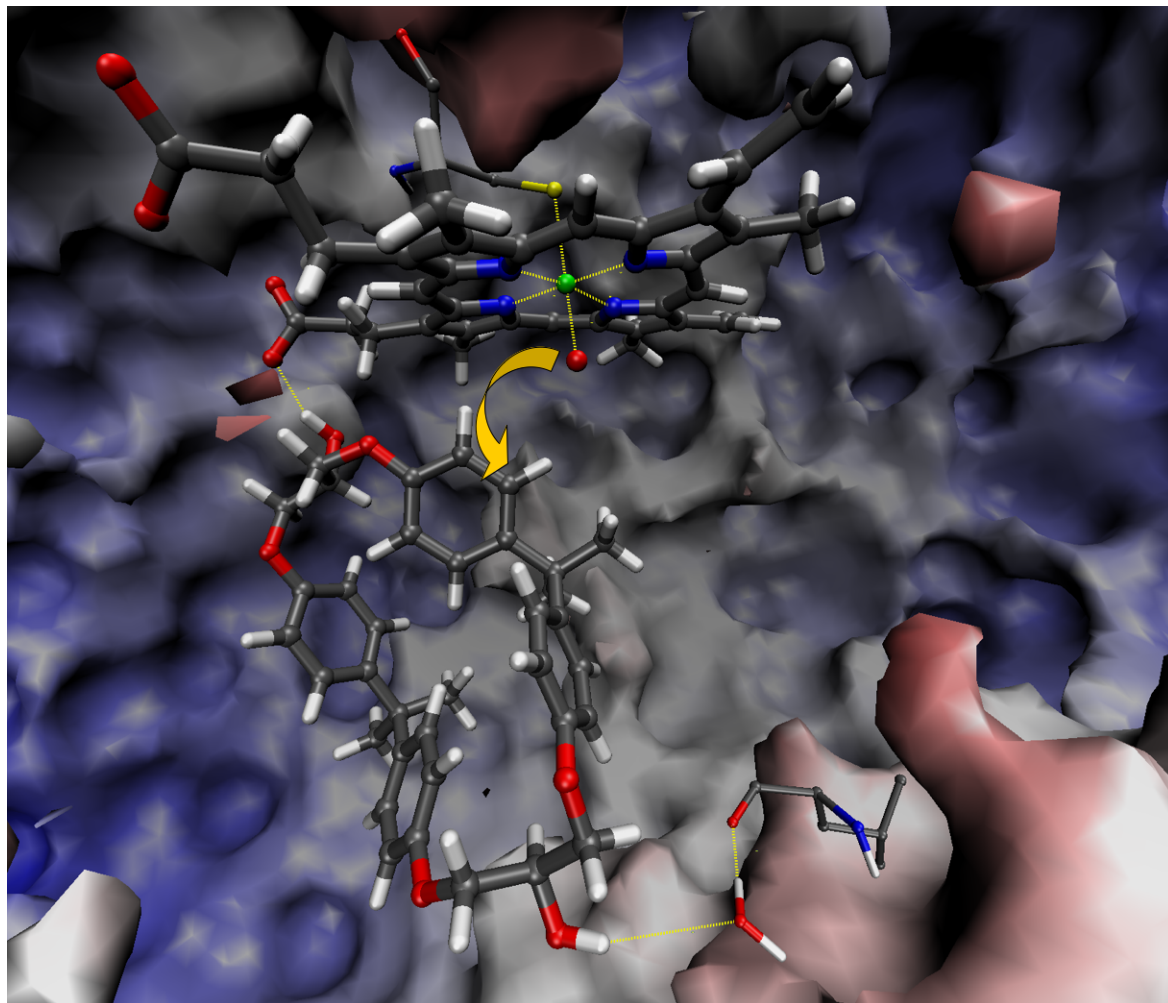
Cyclo-diBA, the cyclic product formed from bisphenol A and diglycidyl ether during the production of epoxy resins. Half of the samples of canned fish in oil collected in April 2010 contained cyclo-diBA with an average concentration of 1025 $\mu\text{g}/\text{kg}$ and a maximum of 1980 $\mu\text{g}/\text{kg}$. The majority of the canned meat products contained cyclo-diBA at a mean concentration of 477 $\mu\text{g}/\text{kg}$ and a maximum of 1050 $\mu\text{g}/\text{kg}$. All prepared meals, such as ravioli or soups, contained cyclo-diBA with a mean at 287 $\mu\text{g}/\text{kg}$. In canned tomatoes, peas and other vegetables in water or fruits in syrup, no cyclo-diBA was detected ($<25 \mu\text{g}/\text{kg}$). Since no experimental toxicity data are available except for its cytotoxicity, an *in silico* hazard profiling was performed. Cyclo-diBA seems to be stable and of low reactivity. There is indication for considerable oral bioavailability and for the potential to accumulate in the human body. Cyclo-diBA can be metabolized into cyclic and acyclic compounds.



Zusammenarbeit mit Dr. Beat Brüschweiler, BAG



Cyclo-diBA: Mutanten können für Toxizität verantwortlich sein



Bindung von Cyclo-diBA an CYP450 3A4: Erklärt Mutanten M5 und M6

Compound	Isomers	ToxPot	Target
----------	---------	--------	--------

Parent compound

Cyclo-diBA	2	cis = 0.477 trans = 0.377	GR PR
------------	---	------------------------------	----------

Cyclic metabolites

M1	1	0.380	PR
M4	4	0.339–0.621	ER β
M5	4	0.371–0.625	GR
M6	4	0.267–0.295	GR
M7	1	0.369	3A4

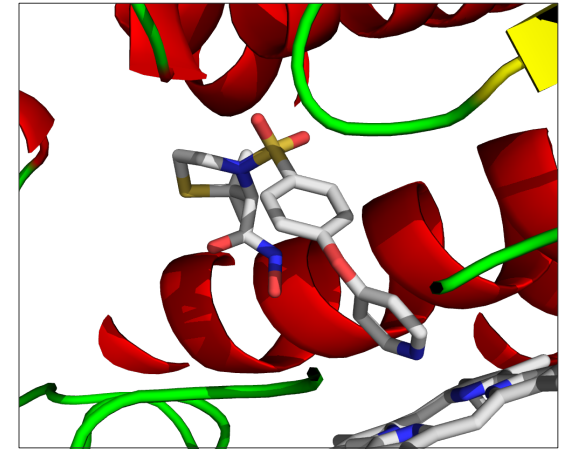
Acyclic metabolites

M2	4	0.359–0.587	PR
M3	4	0.420–0.641	GR

Reference compound

Bisphenol A	1	0.474	ER β ¹
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¹ Calculated binding affinity = 67 nM (exp. = 93 nM)



de-CYP-her

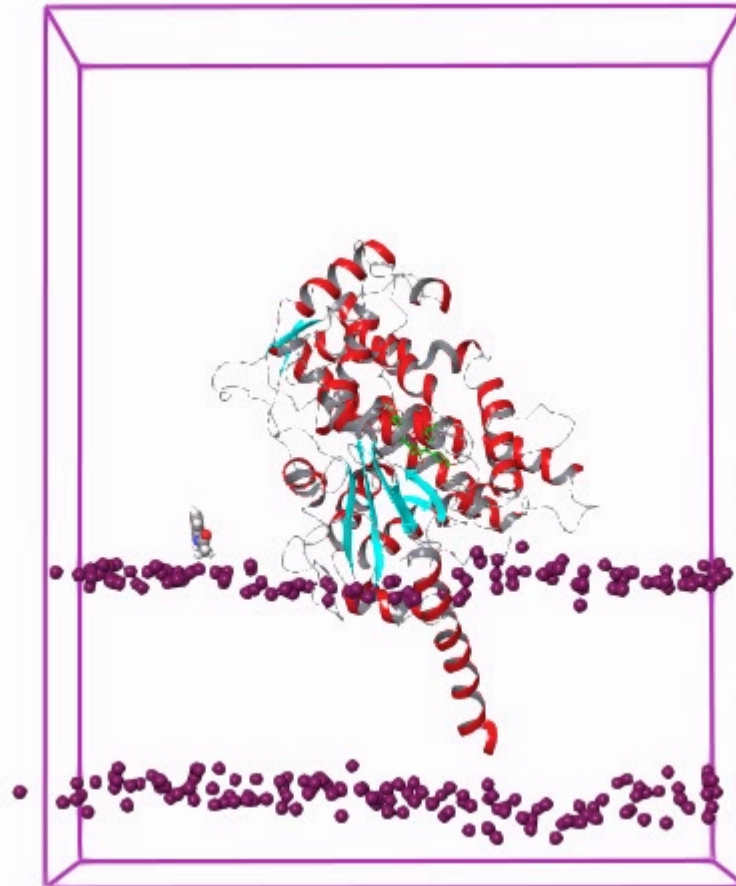
deciphering cytochrome issues in drug design

- molecular docking & scoring (VTL analogue)
- (post processing) microsecond scale MD simulations (GPU accelerated)
- structural and functional effects in (single nucleotide) polymorphs / variants
- substrate entrance / exit channels and their function
- residence time, mode of action
- substrate (incl. site of metabolism) / inhibitor prediction



Microsecond-scale MD Simulations

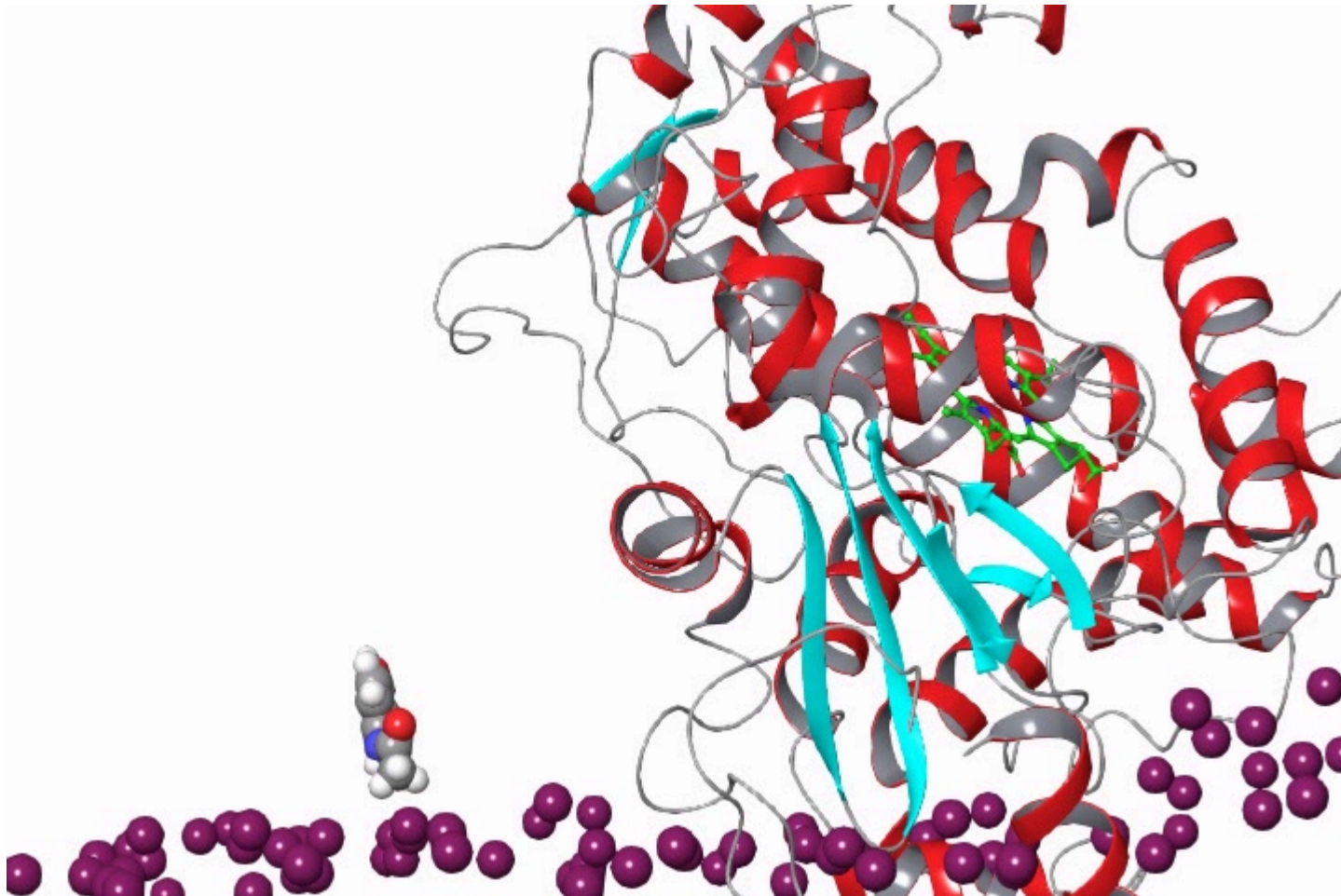
- periodic boundary system with a membrane (80 x 100 x 130 Å)
- cytochrome 2D6 anchored in the membrane
- small-molecule ligand(s) interacting with the protein, membrane, channels...
- software: Desmond, hardware: nVidia Titan X (80 ns / day)





Microsecond-scale MD Simulations

- close-up on *paracetamol* entering the active site of the enzyme (heme colored green)
- huge amount of data generated (structure, mechanistic effects, function, theories...)





Was bring die Zukunft?

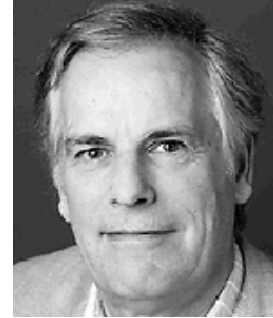
- bessere (akkurate) Kraftfelder, schnellere und schlaue Algorithmen
- noch mehr detaillierte und komplexere Simulationen (grössere Systeme)
- neue Targets (idealerweise: alle relevante Humane Makromoleküle und ihre Komplexe)
- längere Simulationszeiten bei der MDs → grössere Datenmengen
- Personalised Medicine – genetische Information wird in der Computersimulation berücksichtigt
- akkurate Simulationen → sichere Voraussagen → sichere Substanzen



Acknowledgements



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Universität Basel &
BiografikLabor 3R



Professor Max Dobler
Emeritus ETH Zürich
Software-Entwicklung

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Universität Basel

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Gazan Stiftung, Zug
Doerenkamp-Zbinden Stiftung, Zürich
Biografiklabor 3R, Basel

nVidia Academic Grant Support