

In silico identification of bioisosteric substituents, linkers and scaffolds for medicinal chemists

Peter Ertl, <http://peter-ertl.com>

Novartis Institutes for BioMedical Research, Basel, CH

September 2014

Bioisosteric replacements

The everyday medicinal chemistry challenge:

Molecule has good potency, but has a liability (high clearance, not sufficient solubility, bad selectivity, poor permeability, phototox ...)

Solution:

One has to identify part of the molecule responsible for the liability (what is not easy, sometimes a trial and error procedure is required) and then to replace it by another compatible part that would keep potency but fix the liability.

The big question

How to identify the optimal bioisosteric group?

1. medicinal chemistry experience



validated by numerous examples



subjective, limited in scope

2. examples from literature (“matched molecular pairs”)



broader coverage, validated by experiment



limited only to published examples; “my scaffold” often missing

3. similarity based on calculated group properties



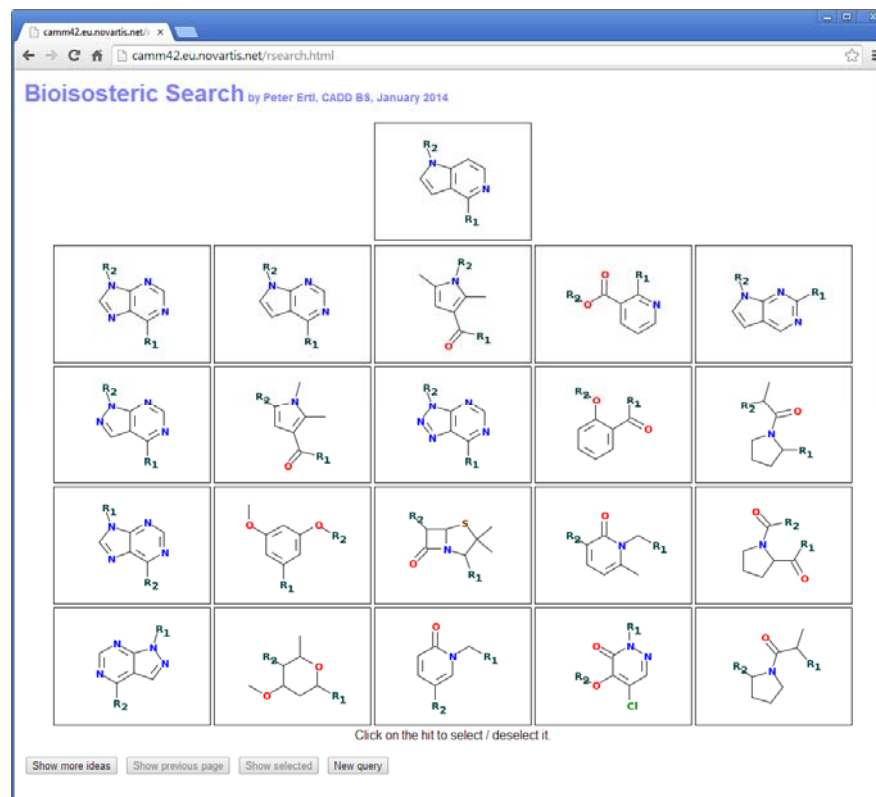
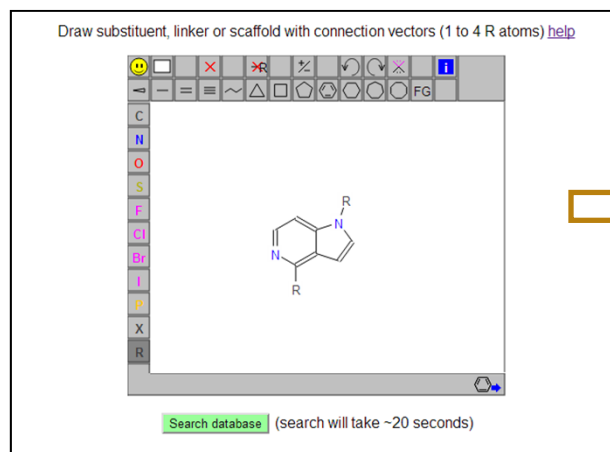
allows to find also novel bioisosteres; practically unlimited scope



not experimentally validated

Interactive web tool for medicinal chemists

Easy to use web tool developed at Novartis allows medicinal chemists to identify bioisosteric groups (substituents, linkers, scaffolds) based on similarity in their properties:



A look under the hood

How does the bioisosteric search tool work

1. creation of the fragment database - extraction of fragments (substituents, linkers, scaffolds) from known bioactive molecules
2. characterization of fragments by medicinal chemistry relevant calculated properties
3. identification of proper search metrics – scaling of properties, fine tuning of property contributions for different user cases

Development of fragment database

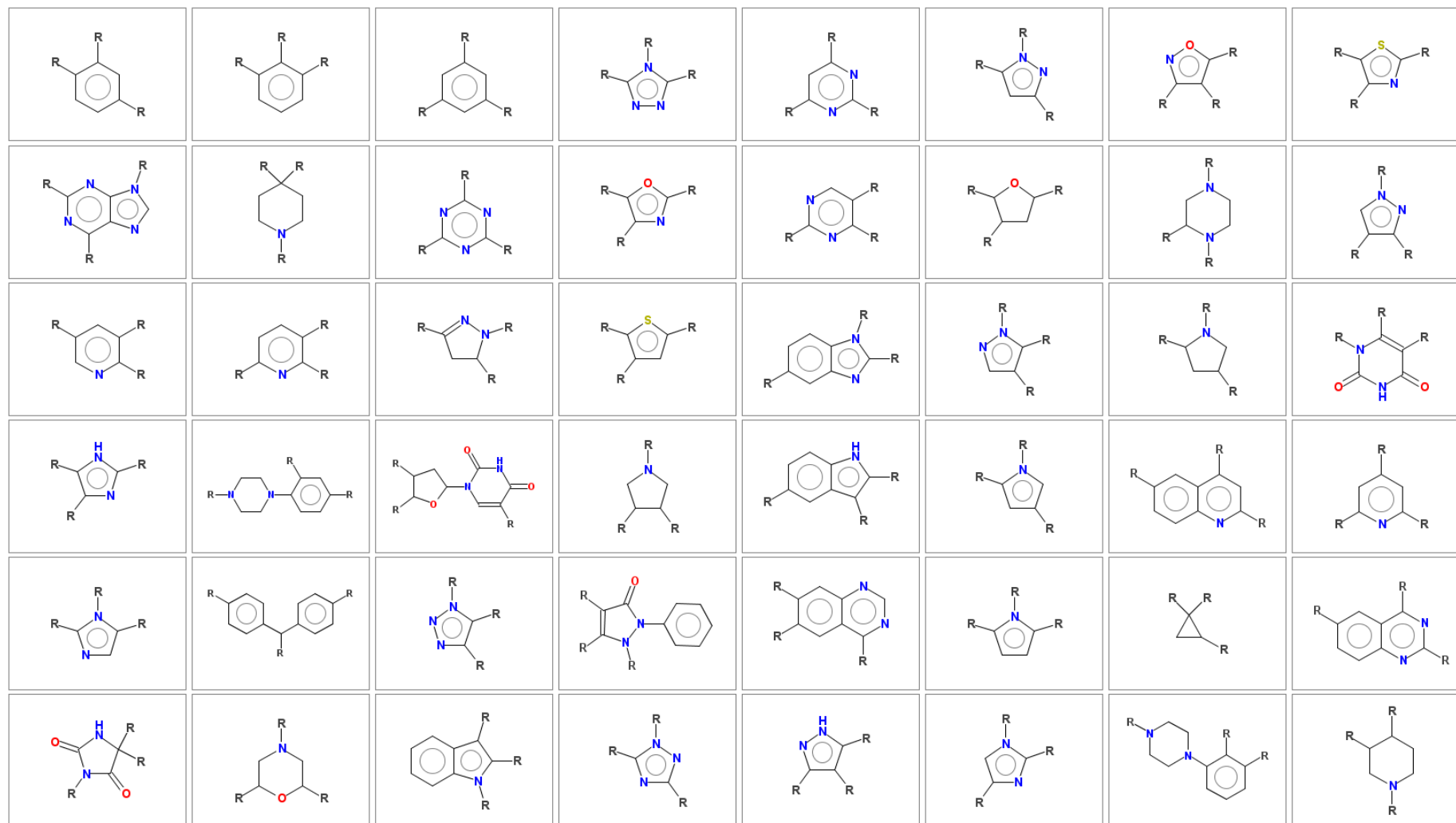


- The ChEMBL database contains about 1.7 million structures extracted from medchem literature together with their bioactivities
- about 500,000 of these molecules are reported to be “active” (activity < 10 μM)
- all substituents, linkers and scaffolds with up to 4 connections were extracted from these bioactive molecules and top 10,000 from each class stored in the database

The most common organic substituents

The most common scaffolds with 3 connections

Symmetry needs to be considered



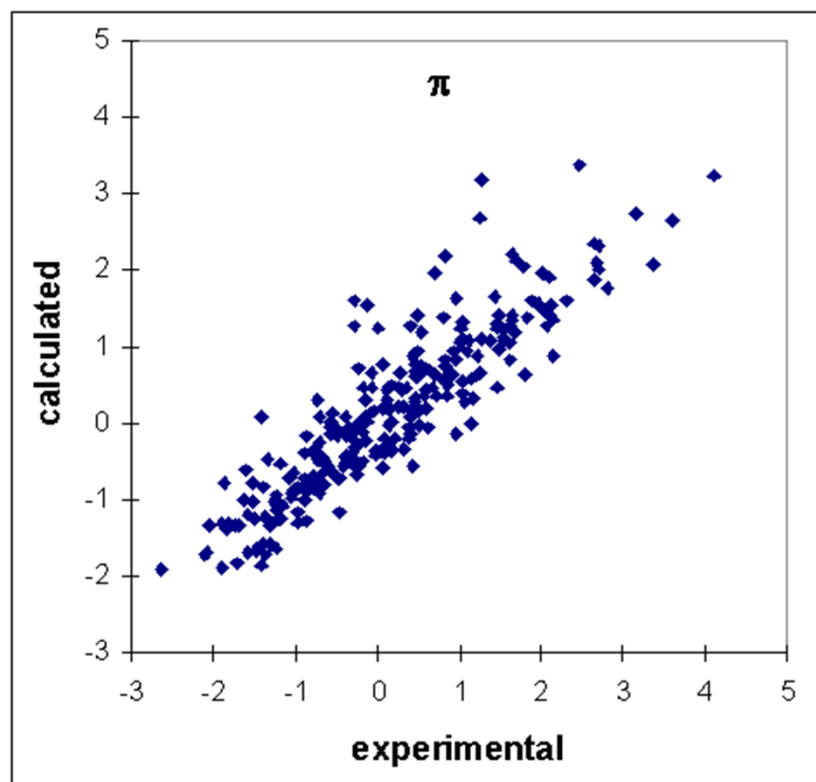
Descriptors relevant to medicinal chemistry

Descriptors used in search should cover all properties playing a role in ligand receptor interactions:

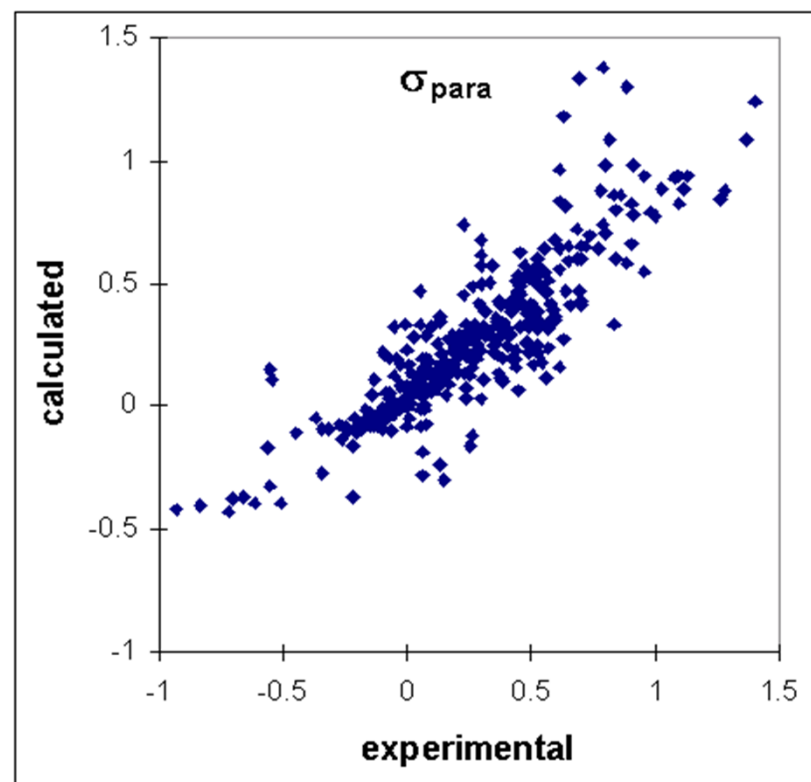
- hydrophobicity
- polarity; electron accepting- / donating-strength
- pharmacophore features
- size and shape

Hydrophobic and electronic substituent properties

Hydrophobicity (π constant)



Hammett σ parameter

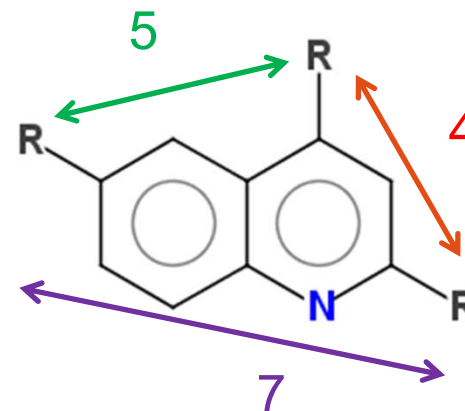


Calculated vs experimental substituent properties
for 300 common substituents

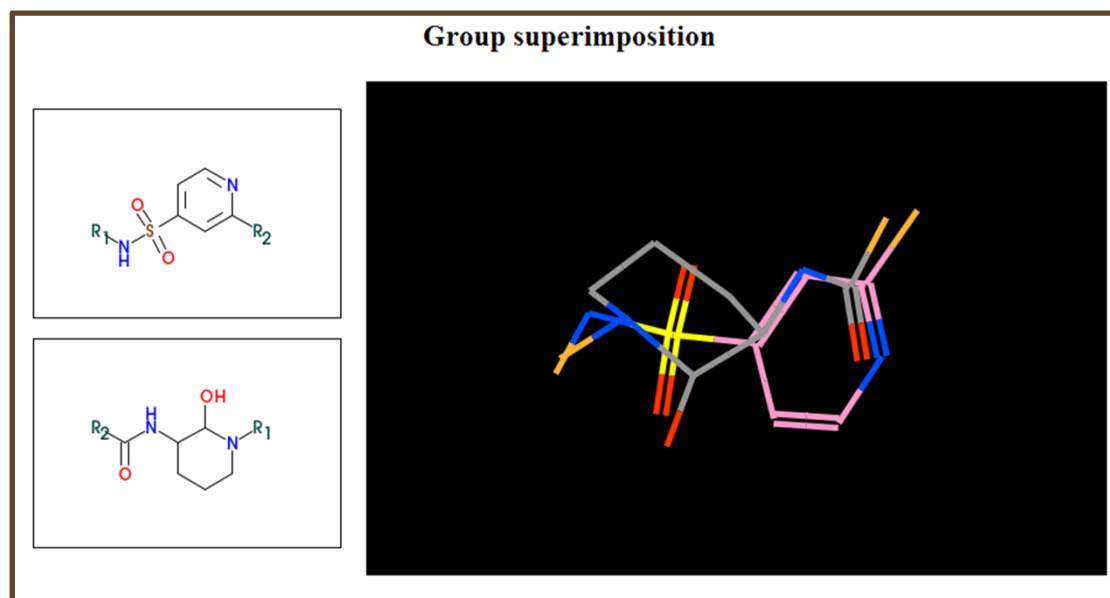
Size and shape properties

Which descriptors are used in search depends on the search scope

Topological size and shape properties + distances between connection points (R atoms)



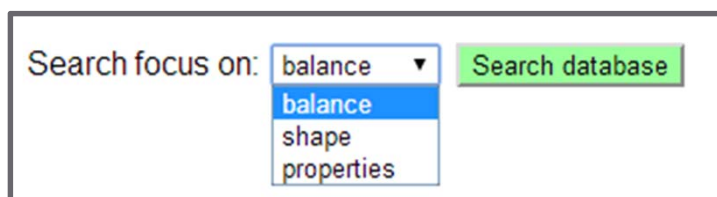
3D shape match and exact superimposition of exit vectors



Fine-tuning of the search procedure

Different users have different requirements on the bioisosteric replacements - selection of proper search scope is important.

- to find an alternative to the existing solubilizing group
- modification of a group affecting electronic properties (charge) on a neighboring atoms
- find an alternative to the central heterocyclic system
- replacement of the linker connecting two parts in the exactly same angle



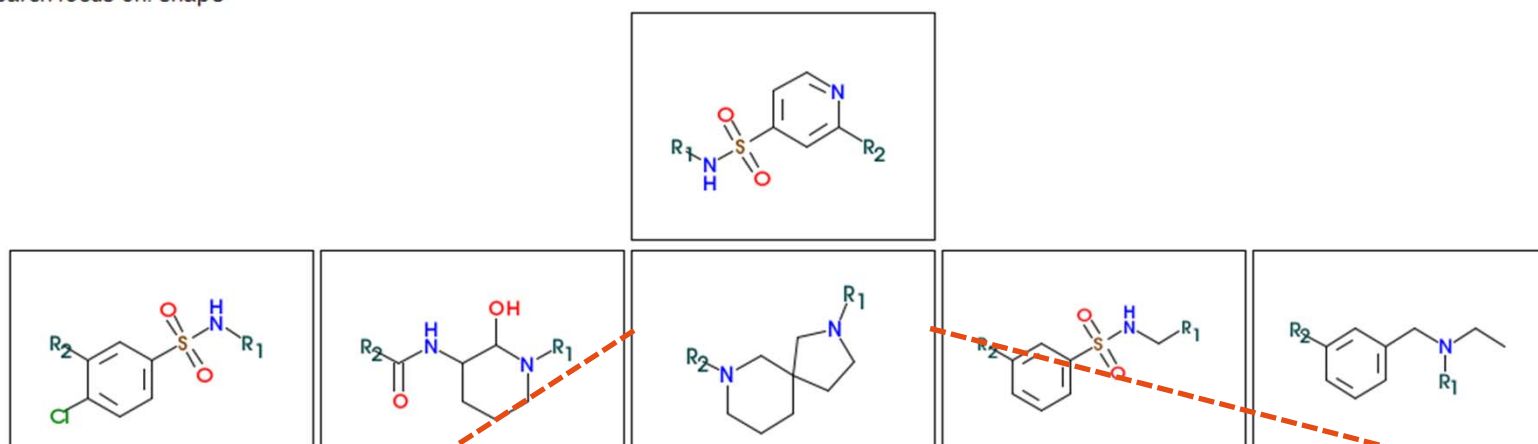
Search focus on: balance ▼ Search database

balance
shape
properties

Menu with 3 search options offered

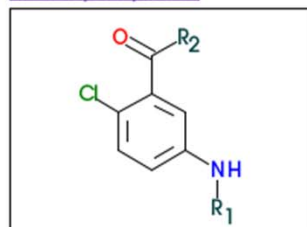
Shape match search

Search focus on: shape

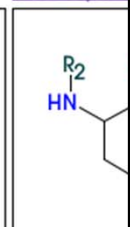


[show superimposition](#)

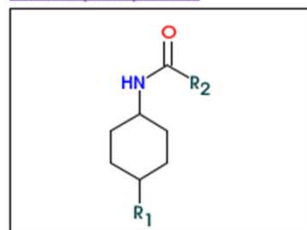
[show superimposition](#)



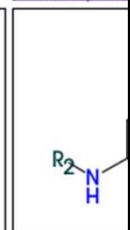
[show superimposition](#)



[show superimposition](#)

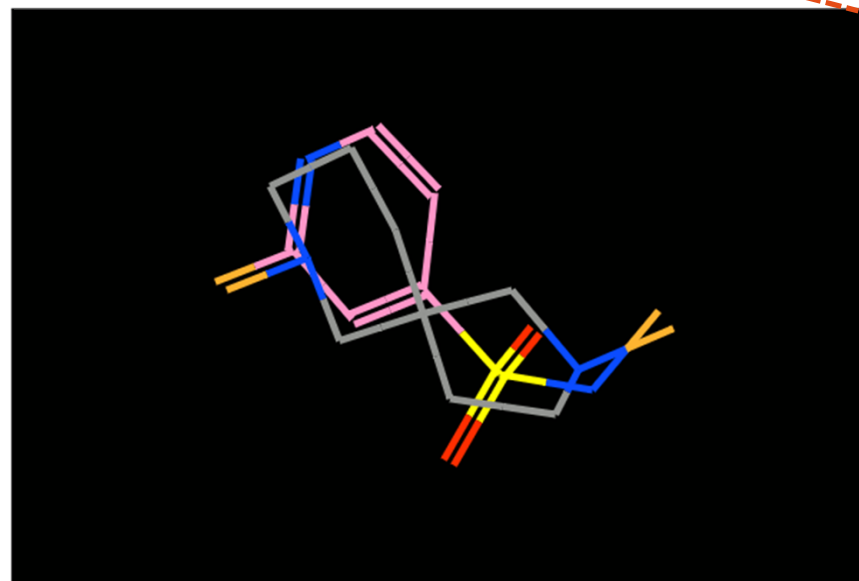
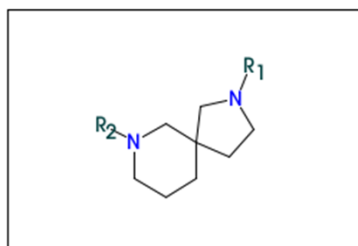
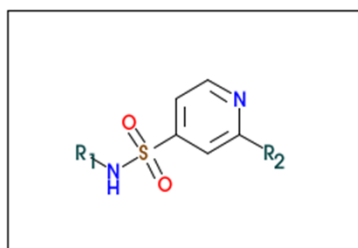


[show superimposition](#)



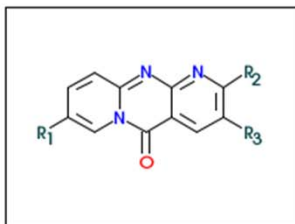
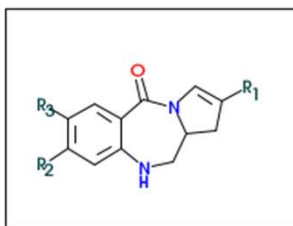
[show superimposition](#)

Group superimposition

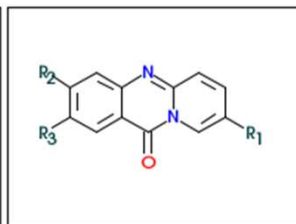


Central ring system replacement

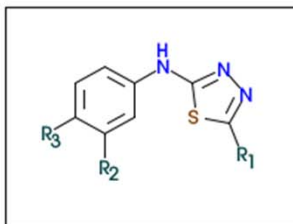
Search focus on: balance



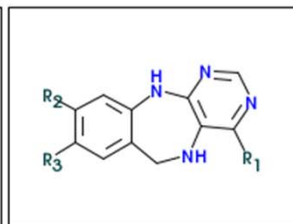
[show superimposition](#)



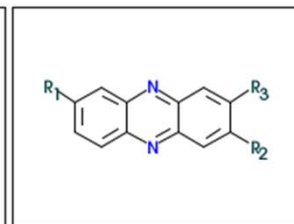
[show superimposition](#)



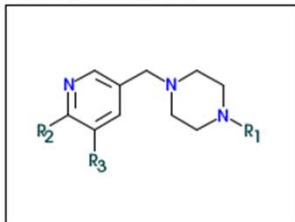
[show superimposition](#)



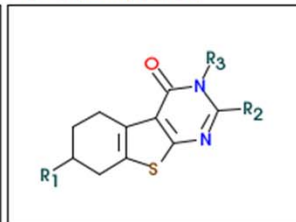
[show superimposition](#)



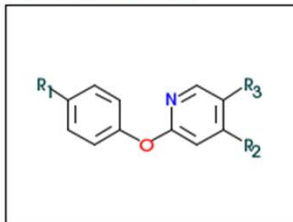
[show superimposition](#)



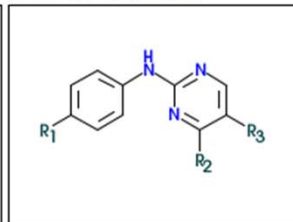
[show superimposition](#)



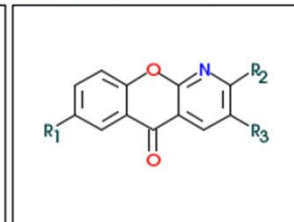
[show superimposition](#)



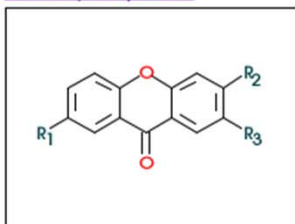
[show superimposition](#)



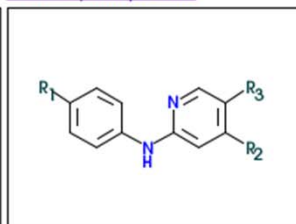
[show superimposition](#)



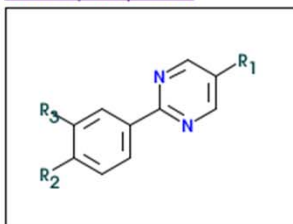
[show superimposition](#)



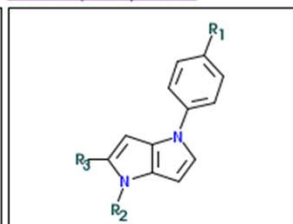
[show superimposition](#)



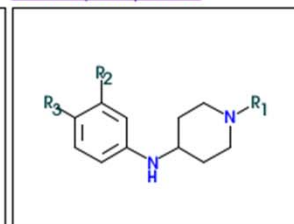
[show superimposition](#)



[show superimposition](#)



[show superimposition](#)



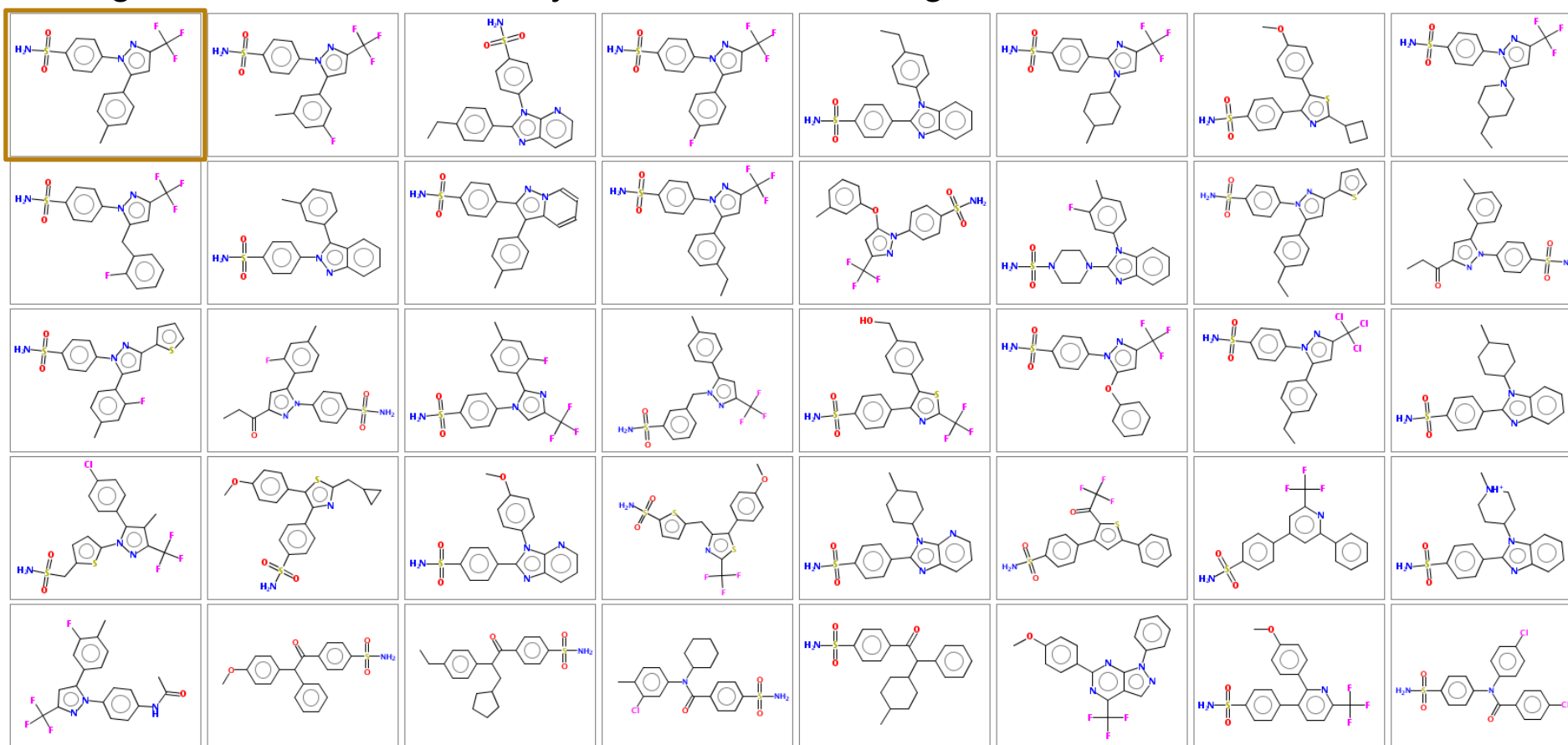
[show superimposition](#)

Click on the hit to select / deselect it.

Exploration of novel chemical space

Automatic analog generator (with Celecoxib as an example)

This concept may be extended to the whole molecules. The template has to be dissected into pieces, analogs for every piece found and combinatorially combined. The generated molecules may be ranked according to desired criteria.



Additional technology details

Database of bioactive ring systems with calculated properties and its use in bioisosteric design and scaffold hopping

Peter Ertl

Bioorganic & Medicinal Chemistry 20, 5436-5442 (2012)

IADE: a system for intelligent automatic design of bioisosteric analogs

Peter Ertl and Richard Lewis

J. Comp. Aided Mol. Design, 26, 1207-1215 (2012)

Bioisosteric Replacement and Scaffold Hopping in Lead Generation and Optimization

Sarah R. Langdon, Peter Ertl, Nathan Brown

Molecular Informatics, 29, 366-385 (2010)

Simple quantum-chemical parameters as an alternative to the Hammett sigma constants in QSAR studies.

Peter Ertl

Quantitative Structure-Activity Relationships 16, 377-382 (1997)