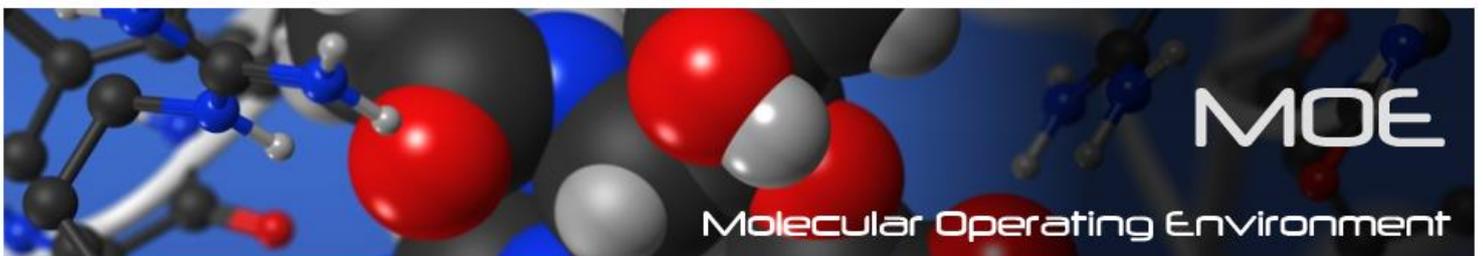


# How to find the right drug?

DRUG DESIGN BASED ON  
PHARMACOPHORE MODELING



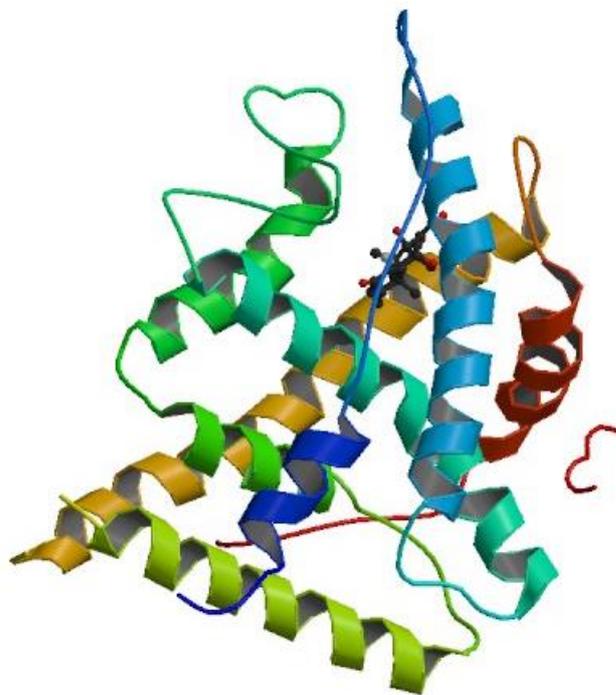
<http://chemcomp.com/>

## OBJECTIVES

- **Search for ligands of glucocorticoid receptor**
  1. **Creating phramacophore queries from database of inhibitors**
  2. **Identifying potential hits in a chemical database**
  3. **Repeating the database query**
  4. **Modifying the pharmacophore and comparing results**

## GLUCOCORTICOID RECEPTOR (GR)

- The receptor to which cortisol and other glucocorticoids bind
- Expressed in almost every cell in the human body
- Regulates genes controlling the development, metabolism and immune response
- Pleiotropic effects in different parts of the body



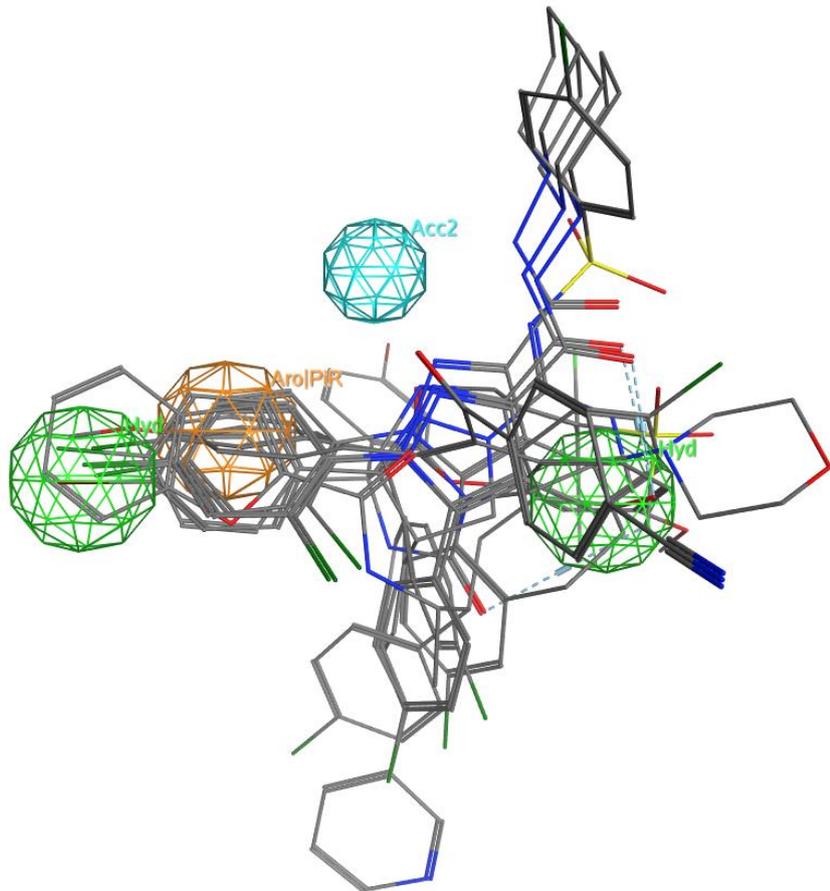
# 1. CREATING PHRAMACOPHORE QUERIES FROM DATABASE OF INHIBITORS

- Open Inhibitor Database
  - Raise the Open panel  
**MOE | RHS | Open**
  - Select the database file - **inhibitors.mdb**
  - Open the database  
**OK**

	mol	CB1 Ki (nM)	name	CB2 Ki (nM)
1		0.0003	NESS 0327	21.0000
2		1.9800	rimonabant	1000.0000
3		5.8000	Compd4	2321.0000
4		7.8000	SLV 319	7943.0000
5		70.3000	Compd3	
6		100.0000	Compd1	
7		141.0000	LY 320135	10000.0000
8		100.0000	Compd2	

- Generating Pharmacophores with the Elucidator
  - Open the Pharmacophore Elucidation panel
    - DBV | Compute: Pharmacophore: Elucidate...**
      - Database of inhibitors appears as the input
      - Change the output database name and directory
      - Set saving of the generated conformations for future elucidation runs by toggling
        - Save Conformations**
        - Set the conformation method
          - Conformations – Conformation Import**
          - Reduce the total number of conformations and the size of the search
            - Conformations – Clustered**
            - Set the Activity Field
              - Activity Field – CB1 Ki**
    - Leave the other options at the defaults and start the elucidation
      - OK**
    - Explore the output database opened in a database viewer

- Browsing Elucidation Results
  - Open the Database Browser
    - DBV | File | Browse...**
    - View the elucidated queries in the MOE window
    - Database Browser: < >**
    - Note the similarity of the top queries



- Saving the top query
  - Load the top query into MOE, load the query into the Pharmacophore Query Editor
    - Database Browser: Edit**
    - Save the query to the MOE pharmacophore file format (\*.ph4 file)
    - Pharmacophore Query Editor: Save...**
    - Set the directory, Enter the filename and save the file
    - OK**

- Saving a modified query
  - Deselect everything by clicking empty space in the MOE main window
  - Add new feature of pharmacophore – Ligand Shape volume

**Pharmacophore Editor: Volume – Ligand Shape**

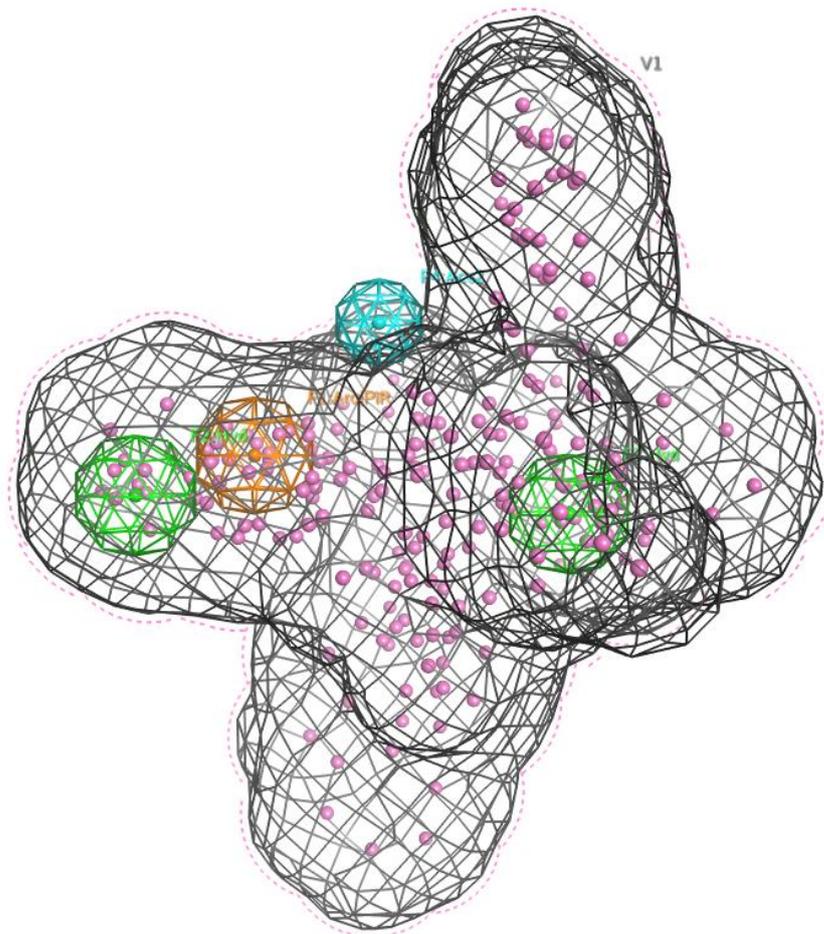
- Save the modified query to the MOE pharmacophore file format (\*.ph4 file)

**Pharmacophore Query Editor: Save...**

- Set the directory, Enter the different filename and save the file

**OK**

- Close the Database Browser and Query Editor



## 2. IDENTIFYING POTENTIAL HITS IN A CHEMICAL DATABASE

- Launch the Pharmacophore Search panel
  - a) from the Pharmacophore Editor
    - Open query  
**MOE | RHS | Open**
      - Select the pharmacophore query and open query  
**OK**
    - Open Search panel  
**Pharmacophore Editor: Search...**
      - Supply a list of search databases
      - Select database to search **searchdatabase.mdb**
  - b) from the database of conformations to be searched
    - Open searched database  
**MOE | RHS | Open**
      - Select database to search **searchdatabase.mdb**  
**OK**
    - Open Search Panel  
**DBV | Compute | Pharmacophore | Search**
      - Set the query

- Searching the database with the query
  - Pharmacophore Search**
    - Select the database to search
    - Input: searchdatabase.mdb**
    - Subrange searched molecules by toggling **Subrange**
    - Set the subrange to **Start: 1 End: 10000**
    - Set the output the hits to a database by pressing
    - Results – Conformations**
    - Set the output database
    - Browse...**
    - Go with the defaults and search with the current query
    - Search**
  - Wait till the search is complete
    - Check in the status line the number of hits and total molecules searched when the search is finished

<b>query</b>	<b>number of hits</b>	<b>total molecules searched</b>
query1		
query2		

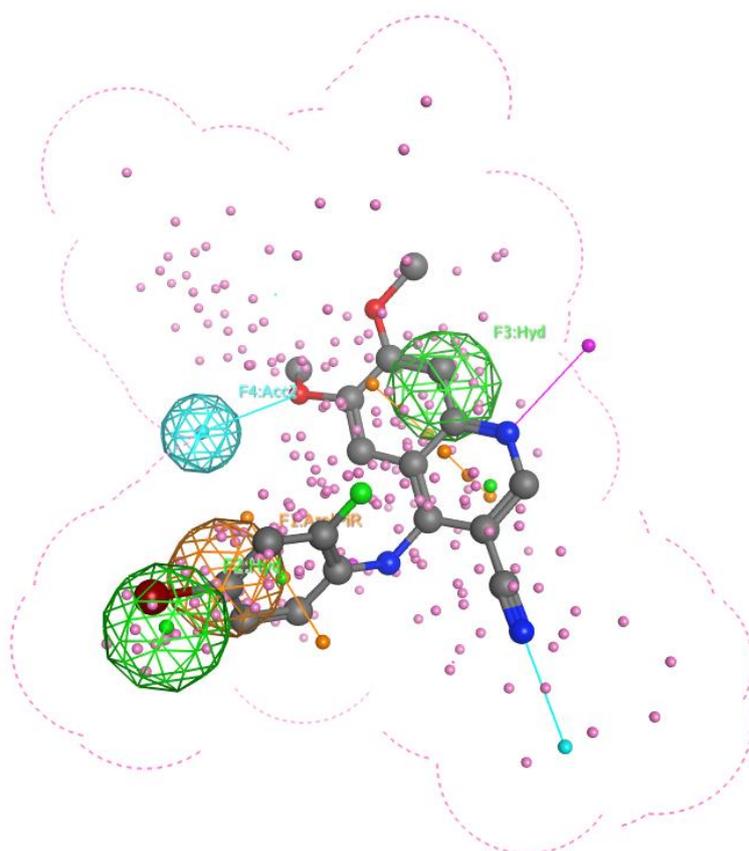
#### 4. REPEATING THE DATABASE QUERY

- Repeat the searching process with the second query
  - Open a new query into the editor panel
    - Pharmacophore Editor: Open...**
    - Select the second query – doubleclick will load it
  - Search again in the same database as previously
    - Set a different name of the output database
  - When the second search is done, fill the results in the table and open the output database
    - Pharmacophore Search - Results: Open...**

### 3. MODIFYING THE PHARMACOPHORE AND COMPARING RESULTS

- To get more hits reduce the excluded volume radii or increase the feature radii
  - Open the Pharmacophore Editor for editing  
**Pharmacophore Search: Edit...**
  - Edit the features
- To get fewer hits decrease feature radii or increase excluded volume radii
  - Open the Pharmacophore Editor for editing  
**Pharmacophore Search: Edit...**
  - Edit the features
- Compare results

- Viewing Pharmacophore Search Results
  - Open a Database Viewer and view the hit molecules aligned to the query
  - Pharmacophore Search - Results: Open...**
  - Launch the Database Browser from the output database **DBV | File | Browse...**
  - Open the System Manager popup panel **MOE | RHS | System**
    - The browsed molecule will appear as the last item
    - Set the rendering of the browser atoms **Atoms: Ball-and-Stick**
  - To compare results to the query open the query **MOE | RHS | Open**
    - Select the exterior volume in the query editor and hide it **Pharmacophore Editor: V1 – hiding eye button**
  - Scroll through the hit structures and visually compare them to the pharmacophore query **Database Browser: < | >**



- Closing the system
  - Close the Database Browser  
**Database Browser - Close**
  - Close the Pharmacophore Editor  
**Pharmacophore Editor - Close**
  - Close the Pharmacophore Search panel  
**Pharmacophore Search - Close**
  - Delete all objects from the MOE system  
**MOE | RHS | Close**  
**OK**

## Used Abbreviations:

### **MOE**

The MOE Window, which is primary interface window of graphical MOE, containing the 3D rendering area

### **DBV**

A Database Viewer, used for examining the contents of MOE databases. More than one can be open at any given time.

### **MOE | RHS**

The Right Hand Side button bar of the MOE window

### **REFERENCE:**

*Molecular Operating Environment (MOE)*, 2013.08; Chemical Computing Group Inc., 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7, 2015.

### **Acknowledgement:**

We kindly acknowledge the Chemical Computing Group for providing us with the MOE educational licenses in successful completion of the workshop.