

# MUSE

## Inspiration for New Ideas

Muse™ is a *de novo* design workflow designed to accelerate the identification and optimization of lead candidates. With Muse, CADD scientists and medicinal chemists identify novel structures, scaffolds, or side-chains that meet specific design objectives. Use for lead hopping, scaffold hopping or inventing new R-Groups around a fixed scaffold. Generate ideas that meet multiple design criteria. Easily integrate in-house or 3rd party scoring methods for use as design criteria.

### FEATURES

- Intuitive and easy to use for medicinal chemists, casual modelers and expert computational chemists
- Design new candidates that mimic the shape and pharmacophore features of your lead structures
- Generate ideas based on multiple design criteria you choose by integrating Muse with other scoring tools (e.g. docking, ADME prediction, etc.)
- Rich and complete palette of chemical structure mutation operators ensures drug-like structures are suggested
- Never produces chemically invalid structures and chemically reactive or undesirable groups are automatically filtered out
- Choose to preserve either scaffolds or R-groups during design

Muse addresses issues faced by discovery scientists every day:

***How do you generate new ideas that meet many different design objectives?***

***What do you do when you've searched your existing compounds and you've run out of ideas?***

***What if filtering virtual screening results leaves you with nothing that meets your design objectives?***

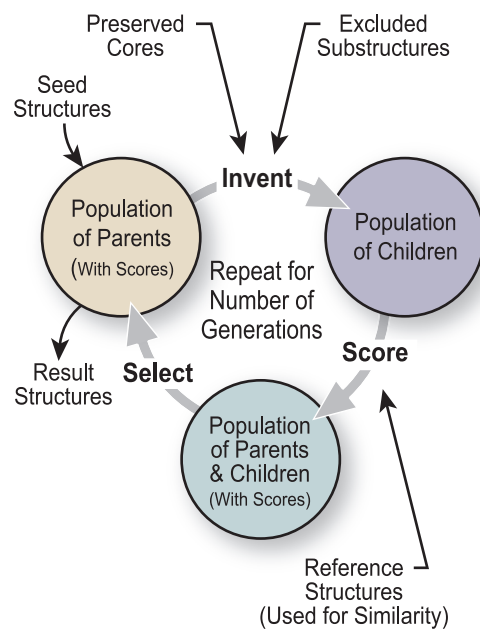
Muse is a *de novo* design workflow that allows you to address all of organic chemistry to get more ideas. As provided, Muse uses ligand-based scoring to generate ideas that optimize the shape and pharmacophoric similarity to a set of lead structures.

A successful drug design candidate has to take a lot of parameters into consideration - potency at the target, selectivity, good ADME properties, toxicity. Muse allows you to generate new ideas that satisfy multiple drug design parameters.

With Muse, you're also empowered to integrate additional computed properties and use them to optimize design ideas. These properties can be derived from literally any in-house or third-party scoring function you have available (blood brain barrier, ADME, toxicity, docking...), allowing easy generation of ideas that meet multiple design criteria.

Muse uses a molecular evolution process to create generations of ideas.

Starting with a set of structures you're interested in or one provided by Muse, sets of parent structures are mutated into children using any of the 28 evolutionary molecular operators.



Muse's evolutionary operators generate design ideas which are scored before choosing those ideas which optimize the design criteria. Multiple iterations continuously improve each generation.

Each generation of children produced are scored, with only the highest scoring surviving, until the number of generations or structures specified by the user has been reached.

The ideas generated by Muse are drug-like and evocative and are often directly synthesizable.

Structures that contain reactive or undesirable groups are automatically rejected by Muse, and the user can tailor these filters to add their own.

Powered by Tripos' Pantheon platform, Muse provides ease of use and an intuitive interface medicinal chemists, casual and expert computational chemists will find accelerate the pace of idea generation.

#### Publications:

- EAI-TupletScore, a Pharmacophore and Shape Driven Ligand-Based De-novo Design Program**  
BB Masek, RD Clark, T Mansley, EA Abrahamian, S Nagy, & KM Smith  
J. Chem. Inf. Model., Submitted
- The use of ligand-based design for scaffold hopping and side-chain optimization: Two case studies**  
M Feher, Y Gao, JC Baber, WA Shirley, and J Saunders  
Bioorg. Med. Chem., 2008, 16, 422-427
- A Tagged Fragment Method for Evolutionary Structure-Based de novo Lead Generation and Optimization**  
Q. Liu, B. Masek, K. Smith & J. Smith  
J. Med. Chem., 2007, 50, 5392-5402
- Sharing Chemical Information without Sharing Chemical Structure**  
BB Masek, L Shen, KM Smith, and RS Pearlman  
J. Chem. Inf. Model., 2008, 48 (2), 256 -261

#### Hardware requirements

Windows: XP or Vista

Linux: RHEL 4 or 5 (coming soon)

#### Complementary software

Pantheon™ (coming soon)

KNIME™ with Tripos Chemistry Extensions

Surflex-Dock™

POWERED BY



The New  
Tripos™

The Tripos logo consists of a stylized blue and white graphic element resembling a mountain peak or a chemical structure, followed by the word "Tripos" in a bold, sans-serif font.