



# Diversity Matters

## Target your research with the HitFinder™ collection of screening compounds

### Maximize quality hits from your screens

- The HitFinder™ collection includes 14,400 premier compounds representing the drug-like diversity of the Maybridge Screening Collection, offering easy and rapid lead identification.
- Selections are made using a clustering algorithm employing standard daylight fingerprints with the Tanimoto similarity index clustering at 0.71 similarity.\*

### Reduced time to optimize any hit

- All screening compounds fit Lipinski guidelines for 'Drug-likeness', and all have purity greater than 90%.\*\*
- Compounds have generally been selected to be non-reactive, ensuring fewer false-positives and higher quality results.
- When you are ready to enhance your drug lead, use over 6,000 advanced novel Maybridge building blocks to easily synthesize the ideal design.



All Hitfinder plates are securely sealed and carry both a clear plate number and barcode for convenient use and storage.

### Ready to screen

- Preformatted as dry films for easy storage and use.
- Pre-plated as 1µmol per compound and 80 compounds per plate.
- Each competitively-priced plate contains a diverse subset of compounds.
- Plate map provided in several formats (pdf, sd, excel) for convenience.
- Plates barcoded for automated systems.
- Off-the-shelf availability of any number of plates, from 1 to the complete set of 180.
- Reserve stock of compounds available for follow-up work when required.

### This pre-selected diverse screening library makes identifying potential drug leads easy and convenient.

To download and view the HitFinder™ compound database visit [www.maybridge.com](http://www.maybridge.com).

To order HitFinder™ or any of the other Maybridge discovery products please contact us at [enquiries@maybridge.com](mailto:enquiries@maybridge.com), by telephone on +44 (0)1840 770567 or contact your local representative.

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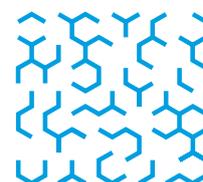
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**MAYBRIDGE**

**Bringing Life to  
Drug Discovery™**

\* J.Chem.Inf.Comput.Sci., 1999,39,747-750

\*\* ClogP <=5, H-bond acceptors <=10, H-bond donors <=5, Molecular Weight <=500