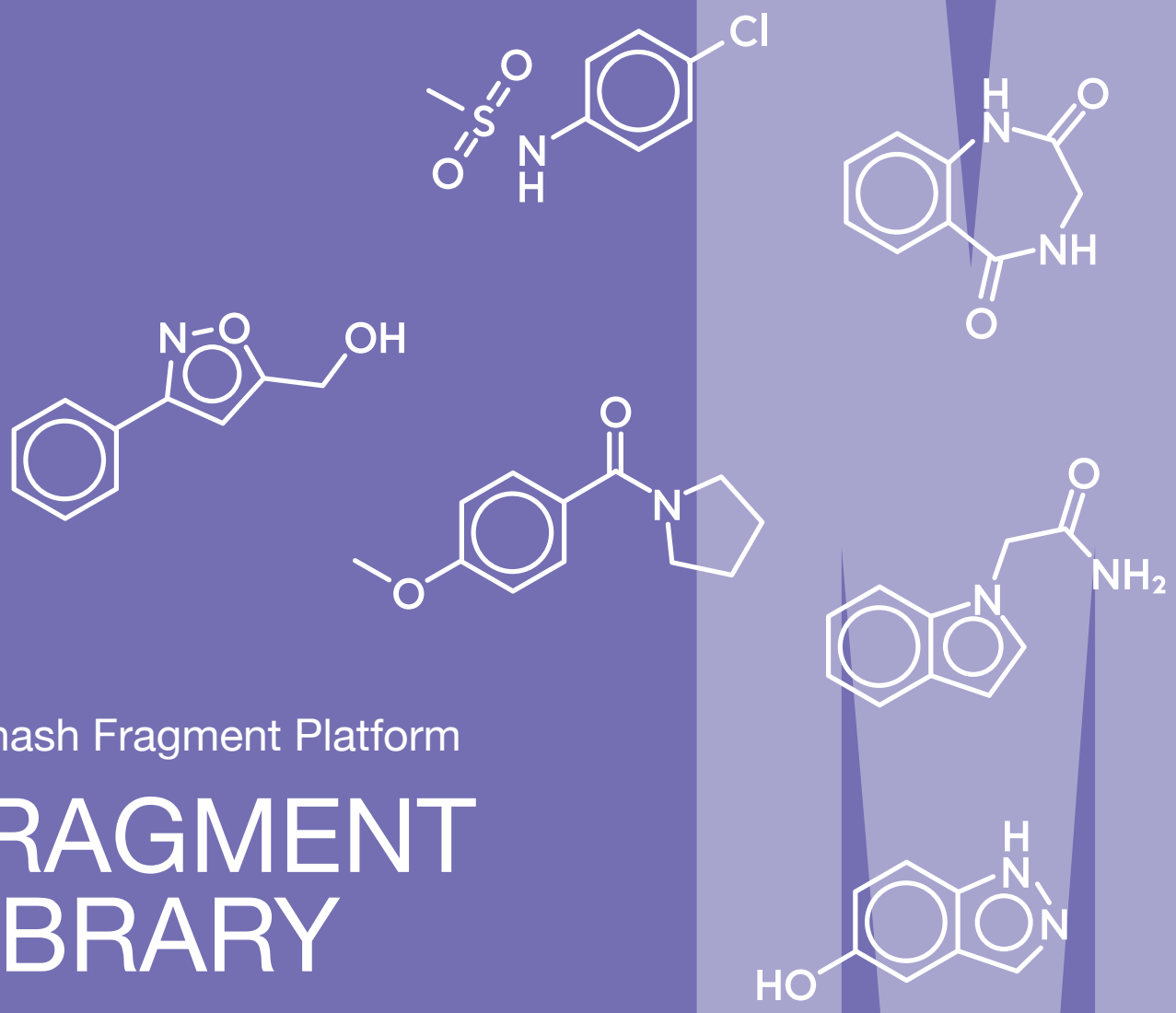


Monash Fragment Platform

FRAGMENT LIBRARY

Fragment-Based Drug Design (FBDD) is a durable and popular approach for drug discovery, identifying ligands of protein targets and generating biologically active small molecules.

The Monash Fragment Platform (MFP) combines pioneering technologies with the know-how of expert scientists to deliver leading-edge research services in FBDD.

We have developed a proprietary fragment library of ~1200 compounds that has broad chemical space coverage, enables rapid analogue access and has excellent quality control for identity, purity, solubility and no aggregation.

We use a variety of biophysical techniques to screen targets against the MFP fragment library. The two most common are: nuclear magnetic resonance (NMR) and surface plasmon resonance (SPR).

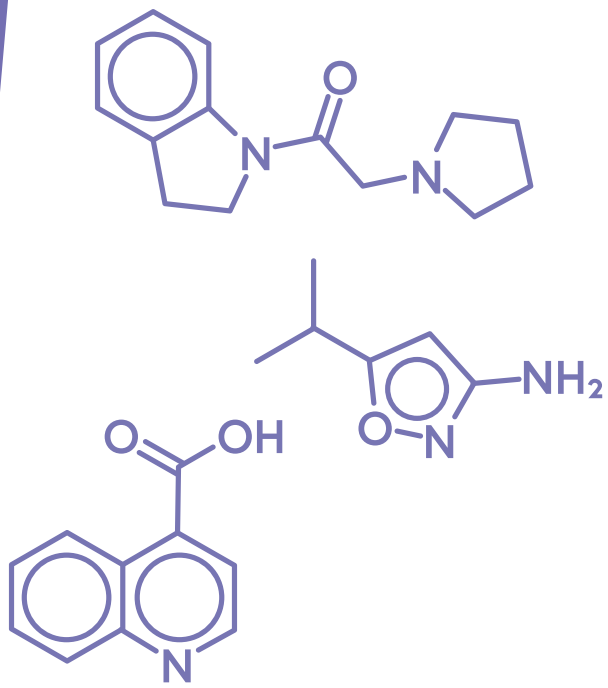
monash.edu/researchinfrastructure/mfp

MONASH University

Monash Fragment Platform

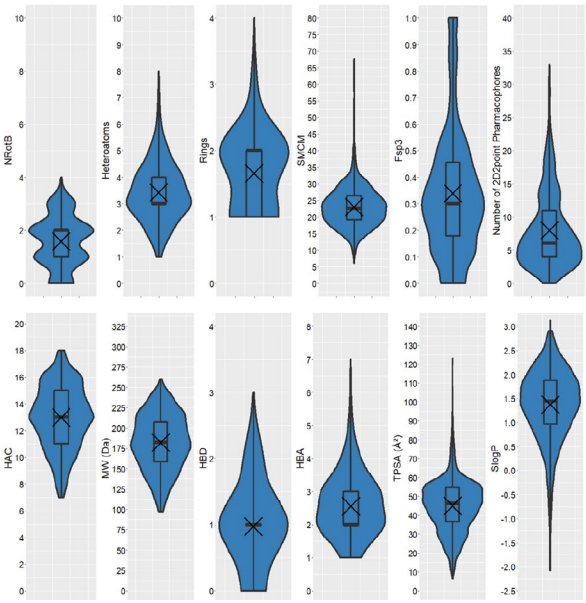
LIBRARY FEATURES

- NMR set is 1148 fragments and SPR set is 1280 fragments
- Filtered by a refined set of PAINS, alert and reactive functional groups to balance diversity and undesirable functional groups
- Measured solubility at 1 mM in aqueous buffer by ^{1}H NMR and Water LOGSY NMR
- Screened against 5 common SPR surfaces to eliminate problematic compounds
- Purity > 90 % and spectral data available for all compounds
- Designed to have > 10 commercially available analogues for quick follow up of validated hits



PROPERTIES AND DIVERSITY

- Molecular Weight (MW) 97-259 Da
- Number of Hydrogen Bond Donors (HBD) 0-3
- Number of Hydrogen Bond Acceptors (HBA) 1-7
- Octanol/Water Partition Coefficient (CLogP) -2.1 – 3.1
- Number of Rotatable Bonds (NRotB) 0-4
- Topological Polar Surface Area (TPSA) 6-123 Å^{2}
- Number of Rings 1-4
- 414 unique Murcko scaffolds
- Covers 96 % of 2D 2-point pharmacophores
- Covers 36 % of 2D 3-point pharmacophores
- Covers 89 % of common functional groups and ring systems across all fragment sizes
- Designed into a set of 249 mixtures suitable for ligand detect NMR screening with minimal spectral overlap



Monash Fragment Platform
Monash Institute of Pharmaceutical Sciences (MIPS)
Monash University, 381 Royal Parade,
Parkville campus, Melbourne

Director, Professor Martin Scanlon
Martin is an expert in NMR and structural biology and the founder of FBDD at MIPS
T +61 (3) 9903 9540
E martin.scanlon@monash.edu

Senior Scientist, Dr Bradley Doak
Brad is a medicinal chemist who specialises in the chemoinformatics and medicinal chemistry of FBDD.
T +61 (3) 9903 9117
E bradley.doak@monash.edu

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References on our library design and QC:

Doak, B. C., Morton, C. J., Simpson, J. S. and Scanlon, M. J. Assembly of Fragment Screening Libraries: Property and Diversity Analysis. Applied Biophysics for Drug Discovery, 2017, p.263-283.

Taylor, A., Doak, B. C. & Scanlon, M. J. Design of a Fragment-Screening Library. Methods in Enzymology, 2018, 610, p.97–115.