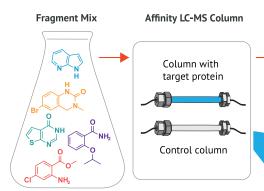
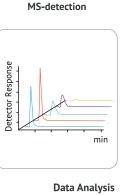
Fragment Screening in Lead Discovery by Weak Affinity Chromatography





Protein Silica Fragments Binding

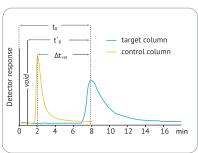




Schematic representaion of screening using WAC™

 $K_{\rm D} = B_{\rm tot}/(\Delta t_{\rm ret} \times {\rm flow \ rate})$

Affinity constant $(K_{\scriptscriptstyle D})$ is calculated from the retention time difference $(\Delta t_{\scriptscriptstyle \rm ret})$ for the compounds on target and blank columns.



WAC™ Facts

- Screening and binding assay in one experiment
- Measure fragment affinity to immobilized protein
- Built-in quality control (MS)

WAC™ Key Advantages

- Robust and accurate (validated against NMR and X-ray)
- Quick set-up and workflow (3 weeks turnaround)
- High throughput (>5000 cmpds/week)
- Low material consumption (<5 mg protein)
- Find mM hits by screening fragments at low concentration (1-5 μ M)
- Hit rates from 1% to 20%, (avg 6%)
- Output High quality data for MedChem

WAC™ Applications

- Screen for novel chemical starting points
- Assess druggability of new targets
- Find differentiated backups in mature projects
- Rescue mode for challenging targets (PPI etc.)

WAC™ Fragment Screen

- In-house collection or client fragments
- Two step milestone process:
 - 1 Feasibility and set-up
 - 2 Full screen

Description

- · Feasibility using client's reference cmpds
- Client supply protein or protein production included
- Preparation of column with immobilized protein
- Screening in duplicates
- Optional validation of hits using NMR or TSA

Deliverables

- List of hits sorted after Δt_{res}
- · Report with results

Follow-up Activities

Opportunity for rapid fragment hit expansion by accessing our integrated lead discovery platform (medicinal chemistry, computational chemistry, X-ray crystallography, biophysical validation, biochemical and cell-based screening, *in vitro* ADME etc.)



