

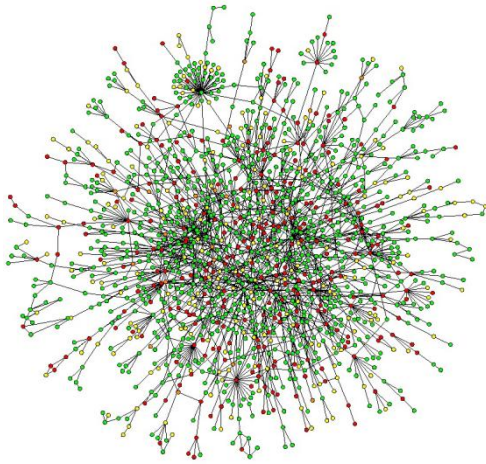
Dualsystems Biotech



Let **us** capture **your** interactors.

CaptiVate™ Interactor Analysis
Protein Complex ID by Mass Spectrometry.

Identify native protein complexes directly from mammalian cells



The majority of proteins exert their biological functions not as isolated molecules but rather in the context of macromolecular complexes. Often, these complexes change dynamically in response to various intracellular or extracellular stimuli. To understand the protein interactions involved and their contribution to signalling and metabolic effects within the cell, the analysis of protein complexes is essential.

CaptiVate™ is a state-of-the-art mass spectrometry-based detection platform developed to identify the composition of protein complexes involving your protein of interest.

Advantages

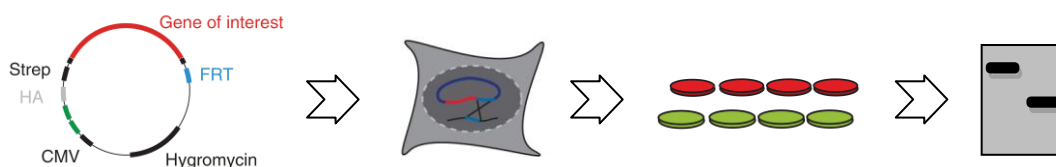
- Low level expression of the bait ensures physiological conditions
- Highly efficient and specific purification of native protein complexes
- Exhaustive analysis of complex partners by LC-MS/MS
- Elimination of non-specific background
- Interactors are ranked according to confidence

Custom Services Outline

Part I

Establishment of a stable cell line expressing your protein of interest

- You provide us with a cDNA encoding your protein of interest
- Cloning of the cDNA into the integration vector
- Stable integration of construct into the genome of the host cell by a highly specific Flp-In procedure
- Establishment of a stable cell line expressing the bait
- Detection of the bait protein by Western blotting



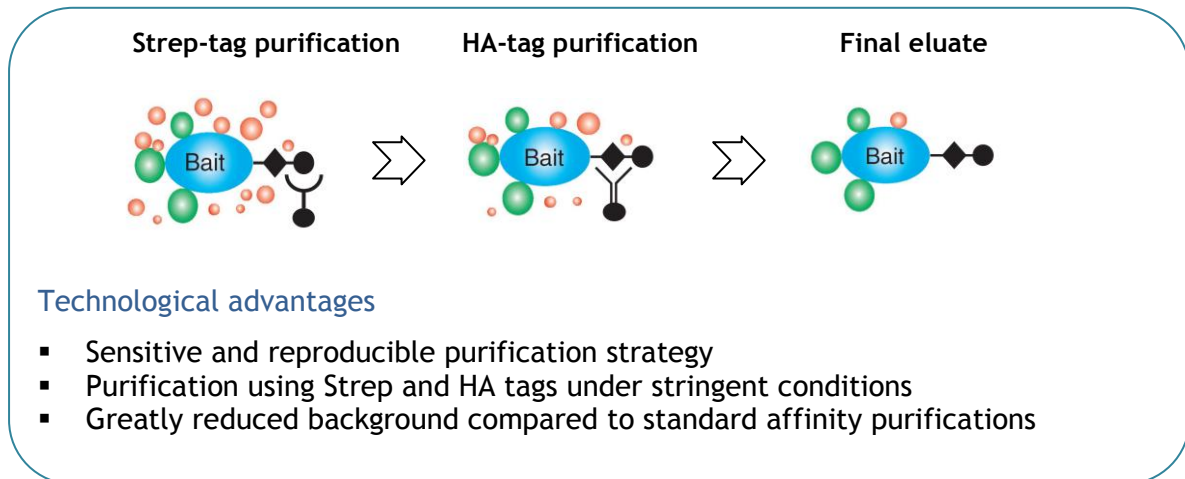
Key features

- Isogenic cell line yields uniform expression levels across the cell population
- Bait expression close to physiological levels
- HEK293 cell line available (additional cell lines will be available soon)

Part II

Double-tag affinity purification of the bait protein complex

- First purification step: Strep-tag
- Second purification step: HA-tag



Part III

Protein complex analysis by liquid chromatography coupled mass spectrometry (LC-MS/MS)

- Sample preparation and analysis by direct LC-MS/MS
- Hits are analyzed using several search algorithms and statistical evaluation programs
- Extensive data analysis and annotation
- You receive a complete report and a list of interactors ranked according to confidence

Technological advantages

- State-of-the-art LTQ Orbitrap mass spectrometer for peptide sequencing
- Comprehensive and accurate identification of proteins
- Data filtering against a proprietary contaminant database
- MS performance assessment by regular runs of protein standards
- More than 5 years of AP/MS experience



Interested?

CaptiVate™ services will become available in the second half of 2009. Please inquire for further information:

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