

Native Target Discovery™

Our New Native Target Discovery™ platform has the potential to overcome the limitations of traditional methods (i.e. analytical detection of secreted proteins and/or related genomic information) such as flawed bioinformatics, insufficient expression of the target, low antigen immunogenicity, antibodies missing the functional epitope, incorrect or unknown localization of the target RNA or protein, insensitive functional assays, antigen structural requirement for antibody generation, sample mixture complexity issues, and the general inability to localize antigens due to limitations in visualization technologies.

With BioAtla's proprietary novel target discovery platform, you can explore the dark matter of target discovery.

FEATURES

- Discover novel, unexplored targets
- Use any cells and/or biomaterials in target screen, such as whole cells, primary tissue or blood
- Discover novel targets from membrane bound antigens, low concentration antigens, antibody "druggable" antigens, processed antigens, antigens with or without signal sequences, naturally presented antigens
- Simultaneously discover low, medium and high binding affinity antibodies
- Identify multiple different antibodies that bind weakly and/or strongly to multiple different epitopes on a target
- Select for morphological endpoints, stem-cell modulation and cell apoptosis; other selections include:
 - Serum (normal and stressed individuals)
 - Tumor cells (normal and tumor)
 - Immune cells (closely-related or distantly-related)
- Applicable to many antigens simultaneously
- Endotoxin-free systems avoid false negatives or positives in assays
- Available for collaboration

BENEFITS

Potential to overcome the deficiencies of traditional approaches of target discovery, allowing exploration of a multitude of completely novel targets

Simultaneously discover multiple antibodies to multiple targets

Save time with integrated target validation system adapted to a wide range of assays types

Discover targets that are missed by genomics, RNA mapping and proteomics!

RESULTS / DATA

Example of in vitro target identification

