

PROTEIN SCIENCES

We Are

- Experts in protein production and characterization
- Flexible and adaptable
- Skilled in solving scientific problems

We Excel

- Optimized transient transfection of CHO or HEK293 cells
- Improved recombinant expression in insect or E. coli cells
- Fast turnaround from gene to final products
- High quality and quantity

Mammalian cells
Baculovirus/insect system
Yeast
E. coli

Molecular
Biology

Expression
Purification

QC

We Provide

- A wealth of experience in molecular biology, protein expression and purification
- A team of highly trained scientists able to progress projects from construct design to protein product in as short as 5-8 weeks.
- Full protein characterization

Antibody Research

- · Large-scale Ab production
- · Novel Ab R&D
- · ADC
- · Pre-clinical evaluation

Integrated Services Support

- Immunization
- · Assay development
- · PK/PD
- · Structural biology

Customized Protein Production

- · Construct optimization
- · Process and formula optimization
- · Folding and refolding
- · Mutation and function
- Labeling

Protein Expression Capabilities

- Efficiency
 - From amino acid sequence to protein in as short as 5 weeks
- Multiple Choices
 - Different epitope tags
 - Various expression systems (mammalian, baculovirus, yeast, E.coli)
 - Specialized protein chromatography columns (affinity, SEC, IEX, HIC)
- Scalepup
 - Up to 300L expression cultures
 - Deliver protein in multi-gram scale
- Quality
 - Full spectrum of analytical techniques (DSF, MST, SEC, UV, MS, SEC-MALS, SDS-PAGE, CE-SDS, RPHPLC, etc.)
 - Quality support in NMR and crystal structure illustration, bioassay development/ screening, compound screening, antibody screening
 - PD-1 mAb epitope mapping by co-crystallization
- Strong performance track record of success

Customized Protein Production

Statistics

	Receptors/Ligands	Cellular Signaling	Enzymes & Complexes
Number of Projects	> 200 per year	> 100	> 600
Quantity (per project)	5-100 mg	5-100 mg	5-200 mg

Example of Quality Improvement

Data Resource	Mass Spec.	X-ray Diffraction
Client's Original Data	Double peaks (poor homogeneity)	8.0 Å
ChemPartner's Optimized Data	Single Peak (good homogeneity)	2.2 Å













Our purification protocol for the client has largely improved homogeneity and helped to obtain high-resolution crystal structure.