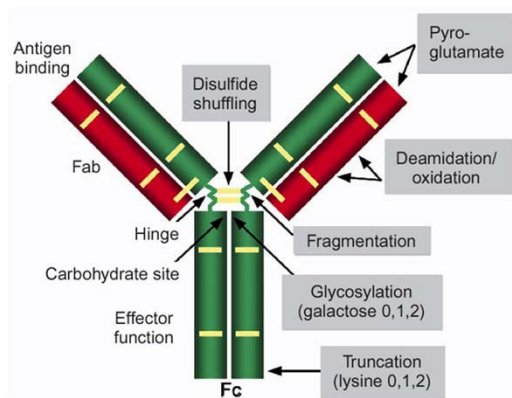


(G) 利用質譜鑑定抗體藥物



- Physical-chemical properties characterization
 - Intact molecular weight determination
 - Full sequence characterization
 - Identification of post-translation modification
 - Disulfide bond
 - Glycosylation
 - Phosphorylation
 - Other modifications
 - Amino acid substitution
 - Side product and impurity analysis

- Clone selection, cell culture optimization
- Comparability test
- QC (lot to lot)

IgG	Heavy Chain	Light Chain
Deglycosylated Protein Sequence Coverage (%)	100	100
Glycosylated Protein Sequence Coverage (%)	90.47~100	98.6~100
Disulfided Protein Sequence Coverage (%)	90~100	100
Disulfide Linkage Sites Coverage (%)	88~100	100

Normally, a sequence coverage of 5-20% is enough to confirm a protein. But ~100% is generally required for a protein product to be commercialized.

Protein View

Match to: CCC Score: 17791

Found in search of D:\AS exp\Service\ LTQ-Orbitrap

Nominal mass (M_n): CCC Calculated pI value: 7.77

NCBI BLAST search of [Abgn-L](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Variable modifications: Carbamidomethyl (C), Deamidated (NQ), Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 99%

Matched peptides shown in **Bold Red**

```

1  KRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
51  KRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
101 KRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
151 KRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
201 KRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
    
```

LTQ-Orbitrap