

We claim:

1. A method for identifying glucuronylation of a protein drug product comprising deglycosylating the protein drug product;
treating the deglycosylated protein drug product to produce one Fc* fragment comprising two identical Fc/2 fragments bound together through non-covalent interactions, and one Fab2 fragment comprising one Fab2 fragment;
separating the Fc* and Fab2 complexes using ion exchange chromatography into acidic fractions of Fc* and Fab2;
drying and denaturing the acidic fractions;
alkylating the acidic fractions;
digesting the acidic fractions with trypsin to form a non-reduced sample;
incubating a portion of the non-reduced sample with NaBH₄ to form a reduced sample;
and
subjecting the reduced sample to reverse phase liquid chromatography/mass spectroscopy analysis to identify glucuronylation of the protein drug product.
2. The method of claim 1, further comprising the step of comparing mass spectroscopy analysis between the reduced sample and the non-reduced sample to identify mass differences between the reduced sample and the non-reduced sample.
3. The method of claim 1 or 2, wherein the protein drug product comprises a monoclonal antibody.
4. The method of any one of claims 1-3, wherein the Fc* and Fab₂ fragments are formed using a recombinantly modified form of IdeS from *Streptococcus pyogenes*.
5. The method of any one of claims 1-4, wherein the ion exchange chromatography is strong cation exchange chromatography.
6. The method of anyone of claims 1-5, wherein the acidic fractions are alkylated with iodoacetamide.