

| Attribute | Characterization Methods |
|--|---|
| Biochemical Characterization | |
| Primary Structure | <ul style="list-style-type: none"> • Peptide map/MS/MS using different enzymes |
| Oxidized variants and deamidated species | <ul style="list-style-type: none"> • Sites and amounts of oxidized and deamidated species by peptide map/MS/MS • Total deamidation (isoAsp) by IsoQuant Assay • Oxidized Mabs by hydrophobic interaction HPLC |
| Aggregates/Association States | <ul style="list-style-type: none"> • Quantitation and assessment of reversibility by SEC • Characterization by SEC-MALLS detection* • Analytical Ultracentrifugation* • Dynamic Light Scattering* • SDS-PAGE reduced/non-reduced (Coomassie Stained) |
| Fragments | <ul style="list-style-type: none"> • Size exclusion HPLC • SDS-PAGE reduced/non-reduced • Intact and reduced mass to verify MW and deduce structure • N-terminal sequencing of bands cut from gel to deduce identity* |
| Glycovariants | <ul style="list-style-type: none"> • Intact mass distribution of glycovariants • Glycan maps of PNGaseF-released N-glycans • Sialic acid content (NANA and NGNA) • N-linked and O-linked glycans by peptide map/MS • Site-specific glycan analysis |
| Disulfide linkage analysis | <ul style="list-style-type: none"> • Peptide map/MS ± reducing and carboxymethylating agents • Free thiol content by DTNB colorimetric assay. • MS analysis of Fabricator cleaved Fc and Fab segments of Mabs and fusion proteins. |
| Charge variants (chemical or physical) | <ul style="list-style-type: none"> • Ion exchange HPLC • cIEF* |
| Biophysical Characterization | |
| Secondary structure | <ul style="list-style-type: none"> • Far UV CD spectroscopy with data fitting* • FTIR* |
| Tertiary structure | <ul style="list-style-type: none"> • Near UV CD spectroscopy* • Fluorescence spectroscopy* |
| Melting temperature (structural stability) | <ul style="list-style-type: none"> • T_m and ΔH by differential scanning calorimetry |
| Impurities | |
| Residual Host cell proteins | <ul style="list-style-type: none"> • ELISA • 2D SDS-PAGE and Mass Spec analysis of coverage • Mass fingerprint of HCPs |
| Residual Host cell DNA | <ul style="list-style-type: none"> • qPCR |
| Column resin leachate | <ul style="list-style-type: none"> • e.g. Protein A (ELISA), residual heparin, etc. |
| Process additives | <ul style="list-style-type: none"> • RP-HPLC, quantitative MS (depending on the type of additive) |

| | |
|--------------------------------------|---|
| Product-related Variants/Impurities | <ul style="list-style-type: none"> • SDS-PAGE (Silver stained) |
| Biological Activity | |
| Ligand binding (as appropriate) | <ul style="list-style-type: none"> • ELISA • Biacore • Label-free binding kinetics by ForteBio |
| Potency | <ul style="list-style-type: none"> • Product-specific cell based bioassays • ADCC & CDC (for antibodies) |
| Fc γ binding (for antibodies) | <ul style="list-style-type: none"> • CHO-expressed Fc receptor cell based binding assay (FACS) |
| FcRn binding (for antibodies) | <ul style="list-style-type: none"> • CHO-expressed FcRn cell based binding assay (FACS) |
| Safety | |
| Immunogenicity | <ul style="list-style-type: none"> • Cytokine release from PBMCs or in whole blood or specific cells |
| Particulates | <ul style="list-style-type: none"> • Subvisible particles by light obscuration and microflow imaging* • Visual appearance test for color, clarity, and particles. |