

## Module 2.3

**2.3.S.3 Characterization**

The characterization of KN035 consists of: a) the primary, secondary and higher-order structure; posttranslational modification forms; b) biological activity; c) purity; d) immunochemical properties. The lots used in these studies are 3 lots of GMP DS that are used for nonclinical, reference standard, stability and clinical studies. 3 lots of DP derived from these 3 lots of DS were also used in some characterization studies. The characterization study results are summarized in [Table 2.6](#).

**Table 2.6 Summary of characterization results of KN035**

Characterization	Test method	Results
Amino acid sequence	Reducing peptide mapping with LC-MS/MS after trypsin or chymotrypsin digestion	100% matches to the theoretical sequences for all three lots of DS.
N/C-terminal amino acid sequencing	Reducing peptide mapping with LC-MS/MS	99.7% of N-terminal sequences are blocked by pyroglutamate. Approximately 89.0-93.3% of C terminal has no lysine. The sequence matches the theoretical terminal sequence.
Amino acid composition	LC	Closely matches the theoretical composition with low RSD
Disulfide bond position	Non-reducing LC-MS/MS	Correct disulfide bond formation, and match the theoretical disulfide bonds.
Free thiol content	Colorimetric method	In the range of 0.16- 0.28mol/mol of KN035
N-glycosylation site	Reducing peptide mapping with LC-MS/MS	One N linked glycosylation site is detected at N210 for all 3 lots of DS.
N-glycan	2AB-labeled NP-UPLC-MS/FLD	Mainly G2F and G1F with approximately 30% of sialylated glycans.
Monosaccharide content	IEX-PAD	Fucose, glucosamine, galactosamine, galactose and mannose are detected.
Sialic acid	RP-HPLC	NeuGc < 0.05 mol/mol NeuAc ≤ 0.90 mol/mol
O-linked glycosylation	LC-MS/MS	May present ~ 2.0% of O-linked glycosylation based on MW analysis
Protein secondary and tertiary structure	Circular dichroism (CD)	Has secondary and tertiary structures
Higher order structure	Differential scanning calorimetry (DSC)	KN035 has two melting temperatures at approximately 65°C and 85°C.

## Module 2.3

Apparent molecular weight	SDS-PAGE	100 kD (non-reducing) 50 kD (reducing)
	Western blot	50 kD
Accurate molecular weight	LC- MS	Different MW was obtained for different glycoforms in the range of 82.3 KDa to 84.0KDa.
Charge profile	WCX-HPLC	Acidic peaks 1 and 2, K0, K1 and K2, and other basic peaks (basic peak 1, 2 and 3) are noted.
Size purity	SE-HPLC	> 99.0% monomer with less than 1% of aggregate.
	CE-SDS (reducing)	Monomer > 98.0% and Fragments < 2.0%
Binding affinity	ELISA	EC50 ~ 57 -69 ng/mL
	Octet K2: Binding affinities to PDL1	KD ~ 3 nM
Blocking activity	Competitive ELISA	IC50 ~ 458 -474ng/mL
Binding affinity to FcRn	Fortebio BLI	KD ~ 0.5 $\mu$ M
ADCC/CDC	Cell based assays	No ADCC or CDC activity
Binding to Fc $\gamma$ R	ELISA and cell based assay	No binding to Fc $\gamma$ RI, Fc $\gamma$ RIIa and Fc $\gamma$ RIIIa