Development of a successful drug candidate requires extensive characterization and comparability assays. This work describes the application of static and dynamic light scattering techniques for the characterization of a recombinant protein as a drug candidate.

**RESULTS**

**ABSTRACT**

The protein consists of 532 amino acid residues (Mw 56264 Da) and is in monomeric form (peak#2) under the given conditions. Peak#1 is a dimer, peaks #3 and #4 appear to be degradants. The presence of monomer, dimer and degradants was confirmed in all three domains. The data on particle sizes and their distribution in given protein samples measured by DLS and SEC-MALLS are very close.

**BACKGROUND**

- The presence of monomer, dimer and degradants was confirmed in all three domains. The data on particle sizes and their distribution in given protein samples measured by DLS and SEC-MALLS are very close.

**METHODS**

- Size exclusion chromatography with on-line light scattering detection
- Dynamic light scattering analysis

**SUMMARY**

- The presence of monomer, dimer and degradants was confirmed in all three domains. The data on particle sizes and their distribution in given protein samples measured by DLS and SEC-MALLS are very close.

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- Elena Severina

**REFERENCES**

- Agilent 1100 FPLC System with diode array detector (UV) was connected to DAWN HELEOS light scattering instrument with integrated Wyatt Wyatt Software, version 5.1.9.1 (Wyatt Technology, Santa Barbara, CA). The detectors were connected in the following order: DLS, SEC-MALLS. TSK-Gel G3000SWxl 7.8mm x 30cm (TOSOH Corporation) was used with a mobile phase of 20 mM Tris-HCl, 150 mM NaCl, pH 7.4.
- The presence of monomer, dimer and degradants was confirmed in all three domains. The data on particle sizes and their distribution in given protein samples measured by DLS and SEC-MALLS are very close.