



High estimation accuracy for a wide range of proteins including  $\beta$ -structure-rich -proteins such as antibodies.



Providing eight types of secondary structure information



We also offer CFR version that complies with the data management standards of 21 CFR Part 11.

### Secondary structure

#### Helix 1 – regular $\alpha$ -helix

The middle part of  $\alpha$ -helices

#### Helix 2 – distorted $\alpha$ -helix

2-2 residues at the ends of  $\alpha$ -helices

#### Anti 1 – left-twisted $\beta$ -strand

Left-hand twisted antiparallel  $\beta$ -sheet

#### Anti 2 – relaxed $\beta$ -strand

Relaxed (slightly right-hand twisted) antiparallel  $\beta$ -sheet

#### Anti 3 – right-twisted $\beta$ -strand

Right-hand twisted antiparallel  $\beta$ -sheet

#### Parallel $\beta$ -strand

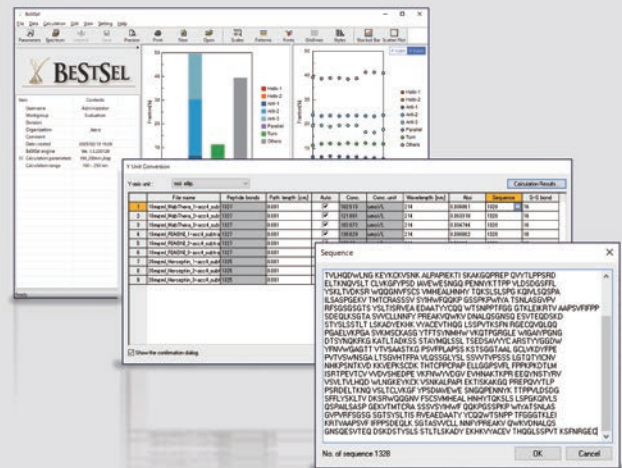
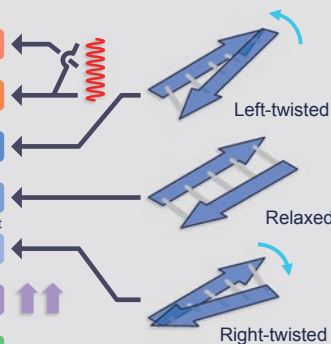
Parallel  $\beta$ -sheet

#### Turn

Turn, as defined by DSSP

#### Others

3<sub>10</sub>-helix,  $\pi$ -helix,  $\beta$ -bridge, bend, loop/irregular and invisible regions of the structure



Secondary structure information obtained by BeStSel algorithm

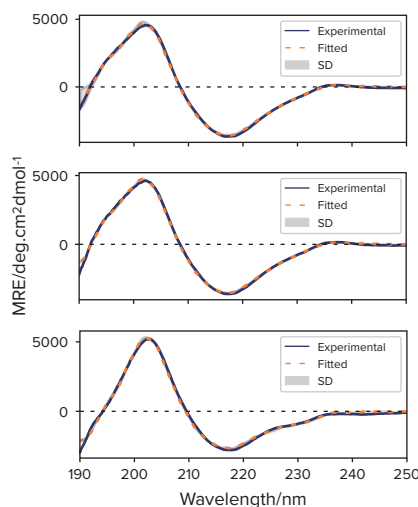
Automatic Y-axis conversion and concentration calculation by amino acid sequence and absorption

## APPLICATION

## Secondary structure prediction of therapeutic antibodies

### CD spectra of antibodies

### Secondary structure prediction



#### MABTHRA

(F. Hoffmann-La Roche AG)

NRMSD

= 0.02



#### RIABNI

(Amgen Inc.)

NRMSD

= 0.01



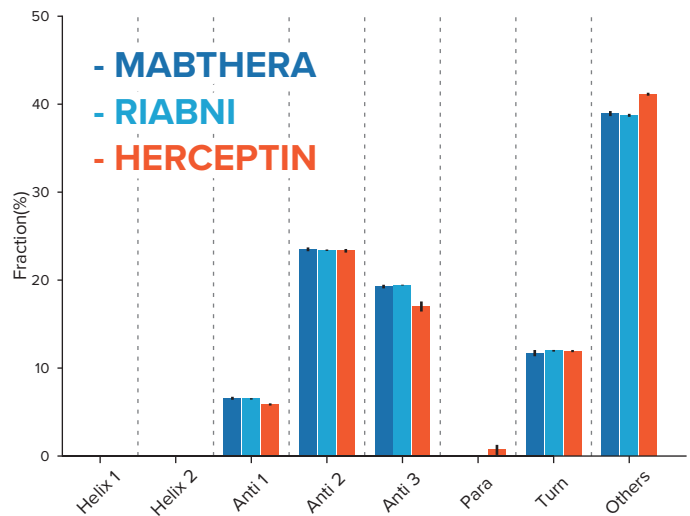
#### HERCEPTIN\*

NRMSD

= 0.02



\* HERCEPTIN is a trademark of Genentech, Inc.



This program utilizes 'BeStSel engine', which is an algorithm developed by Dr. József Kardos and Dr. András Micsonai, et. al. at ELTE (Eötvös Loránd University, Hungary).



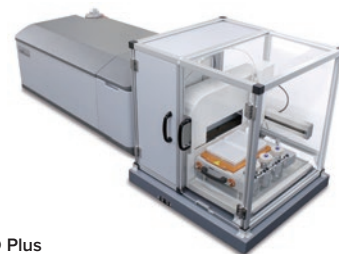
ELTE EÖTVÖS LORÁND UNIVERSITY

## Evaluation of the Structural Stability of Antibody Drugs

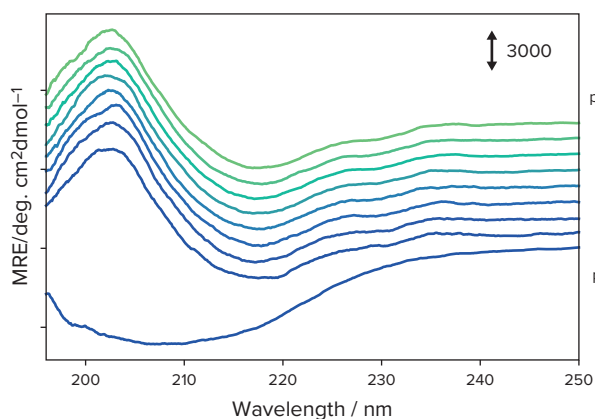
Here, we report the results of a comprehensive analysis of the secondary structure of antibody drugs under various pH conditions utilizing a seamless workflow that combines the automated CD/Absorbance(Abs)/Fluorescence(FL) measurement system HTCD Plus and Spectra Manager BeStSel.

Results of SSE showed that both Herceptin and RIABNI retained their secondary structure down to pH 3, but the ratio of Helix,  $\beta$ -strand, and Others changed significantly at pH 2.

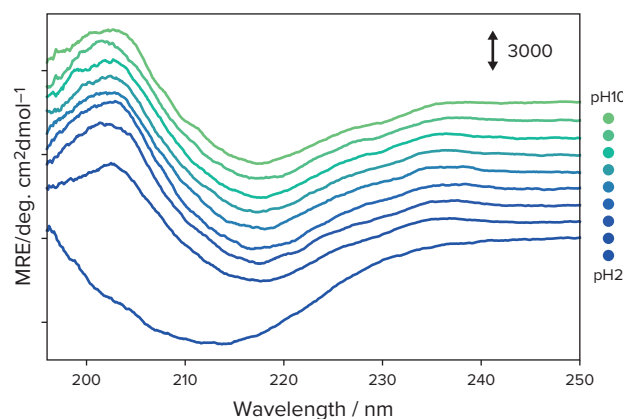
Spectra Manager BeStSel is a powerful tool for structural analysis of a wide range of proteins, including antibody drugs.



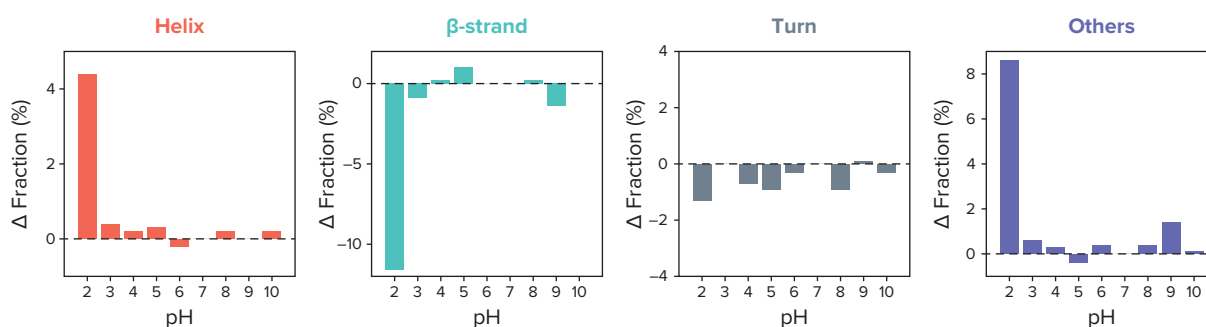
**HTCD Plus**  
High-Throughput Circular Dichroism Measurement System



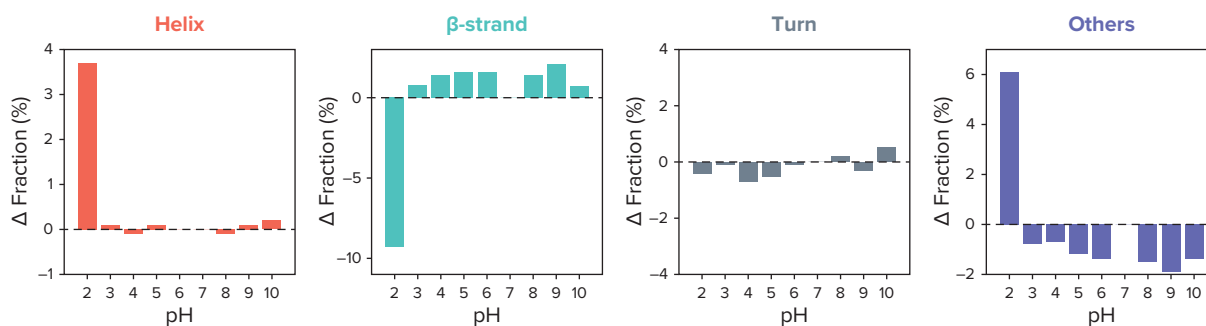
**CD spectrum of Trastuzumab**



**CD spectrum of Rituximab**



**Secondary structure analysis results of Trastuzumab**



**Secondary structure analysis results of Rituximab**

The contents of this material are for reference and illustrative purposes only. Information, descriptions, and specifications in this publication are subject to change without notice. JASCO assumes no responsibility and will not be liable for any errors or omissions contained herein or for incidental, consequential damages or losses in connection with the furnishing, performance or use of this material.



**JASCO CORPORATION**

2967-5, Ishikawa-machi, Hachioji-shi, Tokyo 192-8537 Japan

Tel: +81-42-649-5177 Fax: +81-42-646-4515

Web: [www.jasco-global.com](http://www.jasco-global.com)



Products described herein are designed and manufactured by ISO-9001 and ISO-14001 certified JASCO Corporation