



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

# 8 TYPES

Providing eight types of secondary structure information

# GxP

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

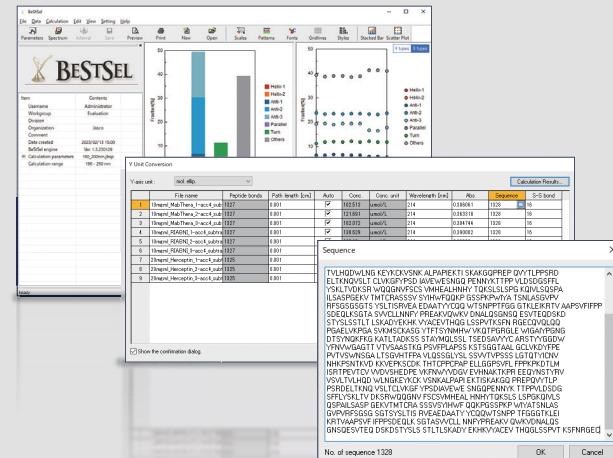
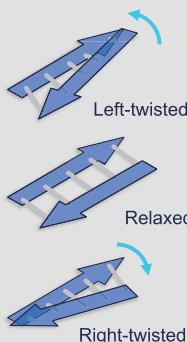
#### Turn

Turn, as defined by DSSP

#### Others

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

Secondary structure information obtained by BeStSel algorism

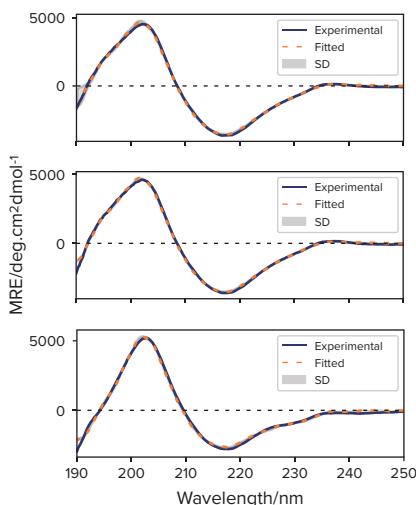


Automatic Y-axis conversion and concentration calculation by amino acid sequence and absorption

### APPLICATION

### Secondary structure prediction of therapeutic antibodies

#### CD spectra of antibodies



**MABTHRA**  
(F. Hoffmann-La Roche AG)

NRMSD  
= 0.02

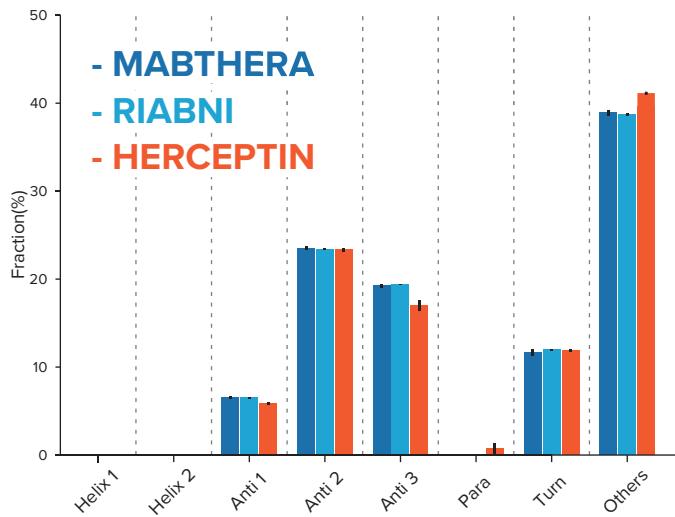
**RIABNI**  
(Amgen Inc.)

NRMSD  
= 0.01

**HERCEPTIN\***

NRMSD  
= 0.02

#### Secondary structure prediction



\* HERCEPTIN is a trademark of Genentech, Inc.

This program utilizes 'BeStSel engine', which is an algorism 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

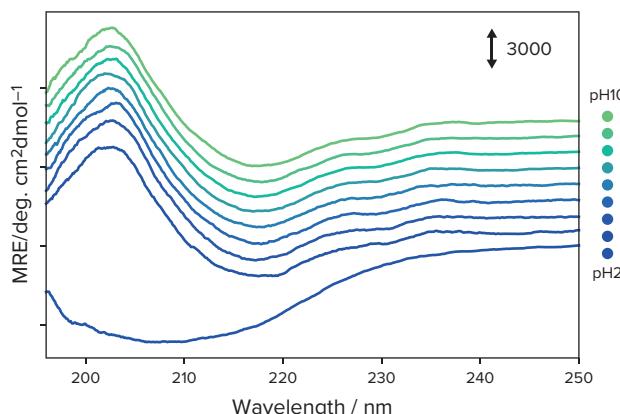
Here, we report the results of a comprehensive analysis of the secondary structure of antibody drugs under various pH conditions utilizing a seamless workflow that combines the automated CD/Absorbance(Abs)/Fluorescence(FL) measurement system HTCD Plus and Spectra Manager BeStSel.

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.

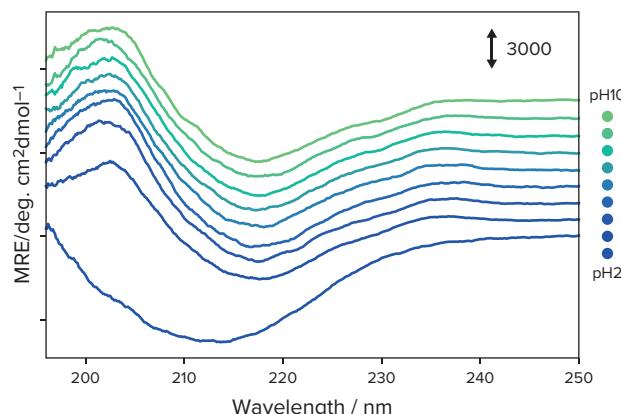
Spectra Manager BeStSel is a powerful tool for structural analysis of a wide range of proteins, **HTCD Plus**  
including antibody drugs.



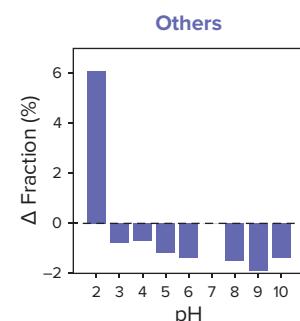
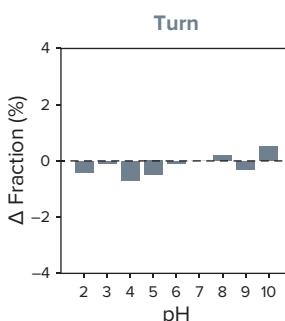
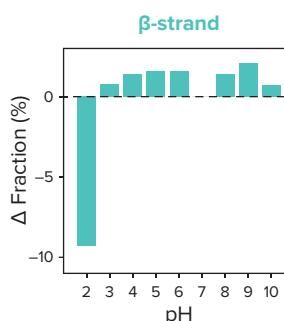
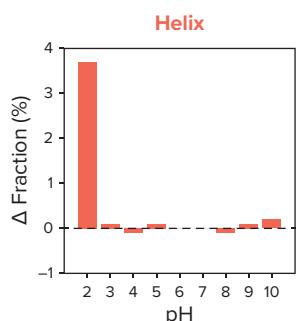
High-Throughput Circular Dichroism Measurement System



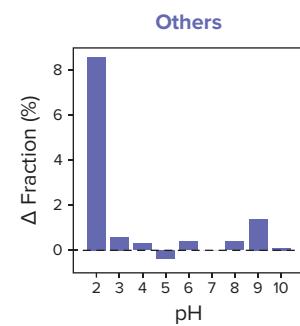
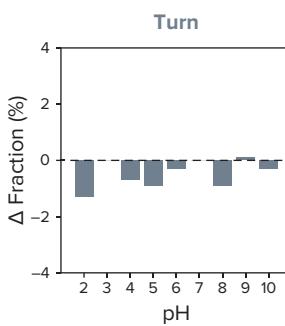
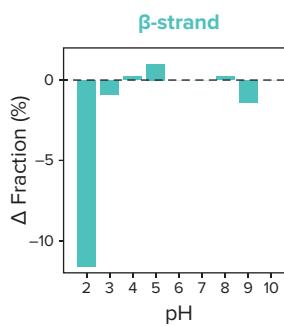
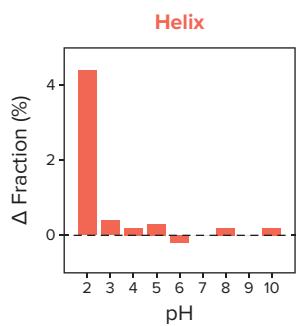
CD spectrum of Trastuzumab



CD spectrum of Rituximab



Secondary structure analysis results of Trastuzumab



Secondary structure analysis results of Rituximab

\*JWBeStSel-532 is available for J-1000 series with Spectra Manager 2.5 only.

\*JWBeStSel-532-CFR is available for J-1000 series with Spectra Manager 2.5 CFR only.

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