

Multivariate SSE Program

Introduction

Proteins, biological polymers composed of amino acids, have primary structures indicating the sequence of amino acids and higher three-dimensional order structures as well. The structure of proteins defines their biological functionality and CD spectroscopy is commonly used in the study of proteins and oligopeptide applications. Using secondary structure estimation (SSE) software, the helix, sheet and random coil contents of unknown proteins can be quantitatively estimated from CD spectra.

SSE software has been applied mainly in academic or research studies of protein structure. JASCO now offers the new SSE Program based on the PLS/PCR method of multivariate analysis, to cope with expanding usage of protein studies across a wide range of fields, such as biopharmaceutical.

Keywords: Protein, Secondary structure estimation, PLS, PCR

Features

1. Versatile PLS and PCR multivariate analysis applied to SSE
 - Enhanced accuracy and robustness
 - Easy validation of calibration models
 - F test certification
 - GLP/GMP compliant
2. Operational flexibility
 - Selectable reference sets
 - Editable secondary structure fractions
3. Reference CD Spectra of 26 proteins (260 – 176 nm) provided as standard.

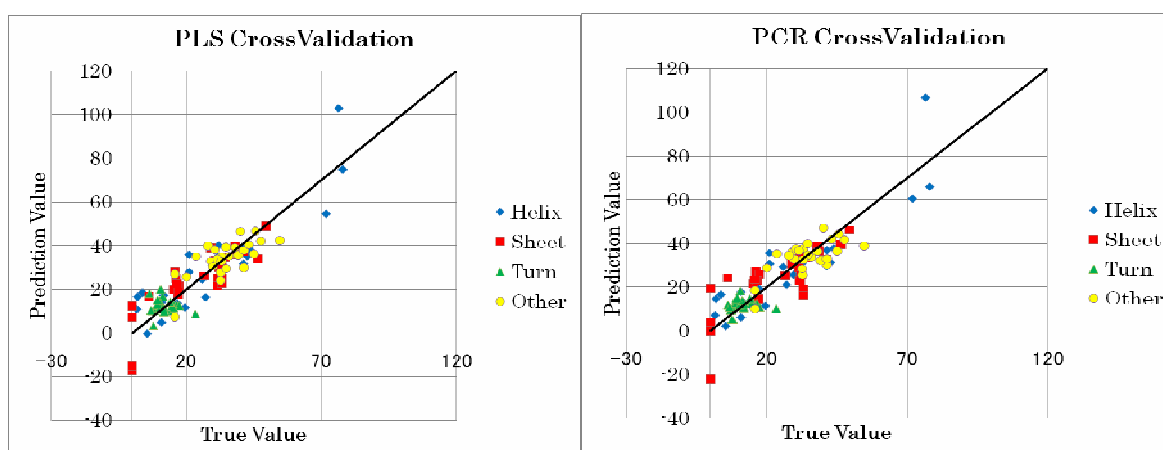


Fig. 1 Cross Validation of Multivariate SSE Program