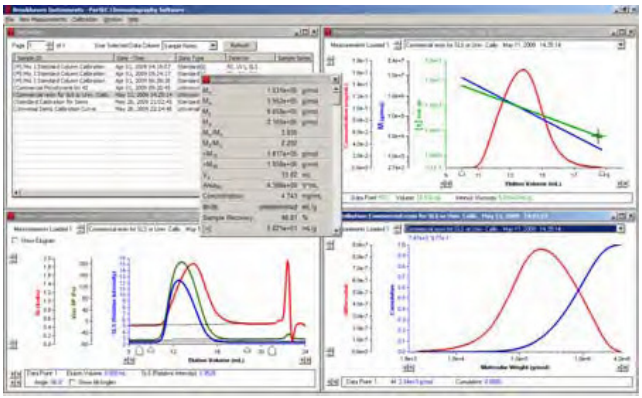
Brookhaven Instruments

ParSEC

Software Suite

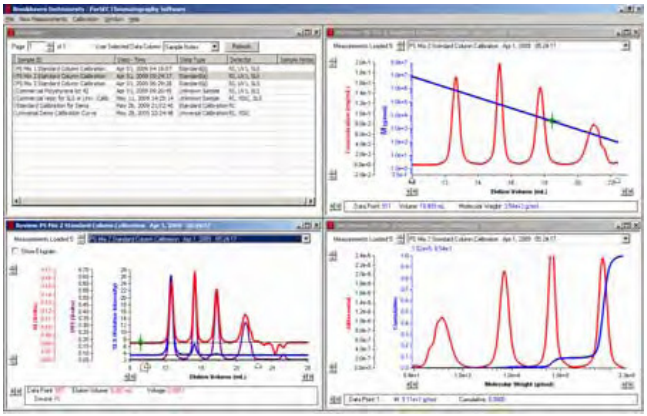
ParSEC is a powerful new suite of software for multi-detector, macromolecular characterization and represents the most significant development in GPC/SEC analysis. **ParSEC** is compatible with ALL GPC/SEC systems and detectors. Many attractive and practical features have been written into the new software for the benefit of chromatographers, including "function specific" views, ensuring the uncluttered display of information relevant to the task at hand, customizable display and annotation options for all graph types, plus a database approach for practical storage and archiving of data and results associated with any application. Two versions are available:

ParSEC - Enhanced



Advanced Macromolecular Characterization

- Intuitive, comprehensive, & flexible
- Calibration options available: Standard & universal
- Absolute molecular weight determination
- Multi-detector capabilities: RI, UV, MALS, DLS, and viscometery
- Protein aggregation and protein-protein interactions using DLS
- "Smart Tile" feature arranges all open windows to be viewed conveniently



ParSEC - Enhanced software provides complete software solution for polymer characterization with multi-detector GPC.

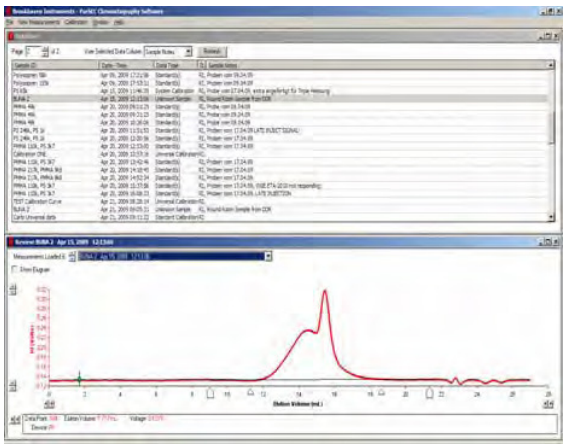
ParSEC - Enhanced software is designed to acquire and analyze data from GPC systems fitted with virtually any combination of refractive index, light scattering, and viscosity detectors. All operating conditions, raw data files, analysis methods, related calibrations, results, and sample information are stored in a database for easy archiving and retrieval.

All the expected and necessary functions are where they should be

ParSEC

ParSEC - Standard

Conventional Macromolecular Characterization using Polymer Standards



ParSEC software provides a complete software solution for polymer characterization when using a GPC system fitted with concentration detectors and using polymer standards for calibration.

All operating conditions, raw data files, analysis methods, related calibrations, and sample information are stored in a database for easy retrieval.

Calculates molecular weight averages: M_W, M_N, M_Z and PDI (M_W/M_N)

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