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ProteinPilot™ Software

In-depth protein identification
and expression analysis

ONE TOUCH PRODUCTIVITY





The Paragon™ algorithm

The difference is easy to see

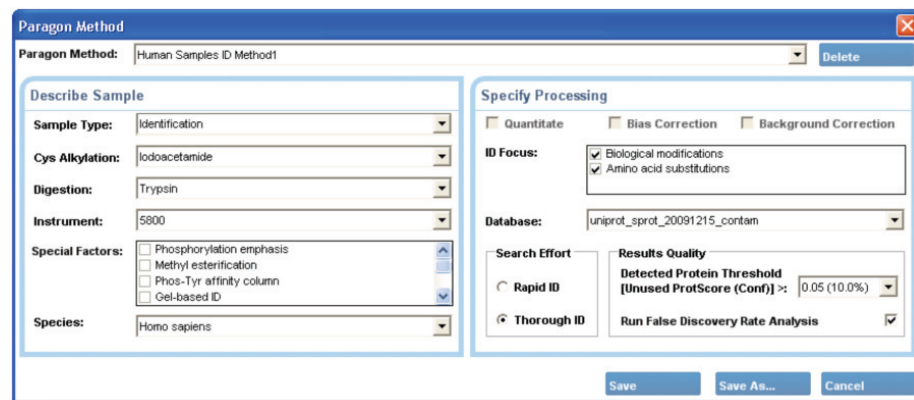


ProteinPilot™ Software has changed the protein identification paradigm with the Paragon™ algorithm. The Paragon algorithm uses a hybrid sequence tag and precursor mass approach to identify hundreds of modifications, substitutions, and unexpected cleavages—simultaneously and without an increase in false positives.

The ProteinPilot™ Software user interface makes it easier than ever to view and navigate protein identification and quantitation results. The Protein ID view displays the proteins detected and the protein-peptide associations for each protein group, including the raw MS/MS spectrum and matching peaks. The Protein Quant view displays each measured protein ratio color-coded by P-value, so you can quickly see changes in expression levels.

Simplified search method creation

You don't have to specify details like mass tolerances, individual modifications, expected fragment ion types, or exceptions to cleavage rules. Simply enter the sample information you know, and the Paragon algorithm automatically optimizes the settings. If you prefer, you control the settings based on your own expertise using the industry standard Mascot search engine.



A faster, easier way to high quality results: Enter the sample information and the Paragon™ algorithm optimizes the settings automatically.

Protein Group 16

Proteins in Group				Peptides in Group						
Unused	Total	Accession #		Contrib	Conf	Sequence	Modifications	Cleavages	ΔMass	Protein MW
17.42	17.42	GSTM1_RUMAN (P94997)	Glutathione	0.00	99	MLLEYDTSYEK	iTRAQ@H-term iTRAQ(R)@13		0.0159	1900.9430
7.87	9.27	GSTM1_RUMAN (P94997)	Glutathione	2.00	99	MLLEYDTSYEK	iTRAQ@H-term iTRAQ(R)@13		0.0078	1900.9350
4.14	11.24	GSTM1_RAT (P98009)	Glutathione	2.00	99	PMTLGYWDR	3in Terminal iTRAQ@H-term Oxidation(M)@7		0.0075	1766.6999
1.70	7.64	GSTM1_CAVPD (P16413)	Glutathione	0.00	99	PMTLGYWDR	iTRAQ@H-term		0.0026	1764.7160
				2.00	99	PMTLGYWDR	iTRAQ@H-term		0.0031	1766.7010
				2.00	99	TLGLDFPILPY	Carbamyl@H-term	cleaved F-T@1 cleav...	0.0446	1791.6909
				0.00	99	TLGLDFPILPY	Carbamyl@H-term	cleaved F-T@1 cleav...	0.0615	1791.7060
				0.00	99	VDLENGLMENR	iTRAQ@H-term		0.0099	1602.8260
				2.00	99	VDLENGLMENR	iTRAQ@H-term		-0.0017	1602.8140
				0.00	99	VDLENGLMENR	iTRAQ@H-term		-0.0011	1602.8150
				0.00	99	YTMGAPDYDR	iTRAQ@H-term		-0.0050	1446.6150
				2.00	99	YTMGAPDYDR	iTRAQ@H-term		-0.0058	1446.6150

Instant comprehension: As shown in the Protein ID view, the Pro Group™ algorithm groups proteins by shared evidence. Click on a protein to highlight all its peptides in yellow. Select a second protein to highlight all its peptides in blue. Peptides shared by both proteins are highlighted in green.

Powerful workflow support

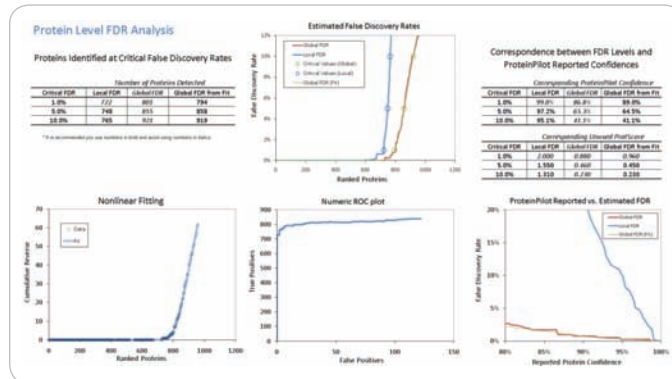
ProteinPilot™ Software includes an automatic false discovery rate (FDR) analysis that gives you a rigorous defense of the quality of your results, using both conventional FDR analysis as well as novel extensions. If your typical workflow is gel-based analysis, you can submit PMF and PMF-combined searches on TOF/TOF data to Mascot for identification of gel spots.

The ultimate in flexibility and control

Search data from any instrument. ProteinPilot™ FDR analysis supports instruments from several manufacturers. An open parameter control function allows you to add support for instruments not already included. You can also control parameters such as new modifications, instrument settings, and digest agents.



Navigate quantitative results with ease: In the Protein Quant view, color-coded protein ratios highlight differentially expressed proteins. With a single click, you can also view the MS or MS/MS quantitation evidence for each peptide.



A detailed FDR analysis report provides graphs and tables that rigorously justify the number of proteins, peptides, and spectra identified at critical local or global error rates. Essential for journal publications today.

You invest in our technology. We invest in your success.

As the world leader in mass spectrometry, AB SCIEX solutions are backed by the industry's most extensive service and support organization. With a network of service professionals, experienced compliance specialists, and over 150 PhD application scientists worldwide, we are dedicated to supporting your technical needs and helping you get the most out of your AB SCIEX systems.

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