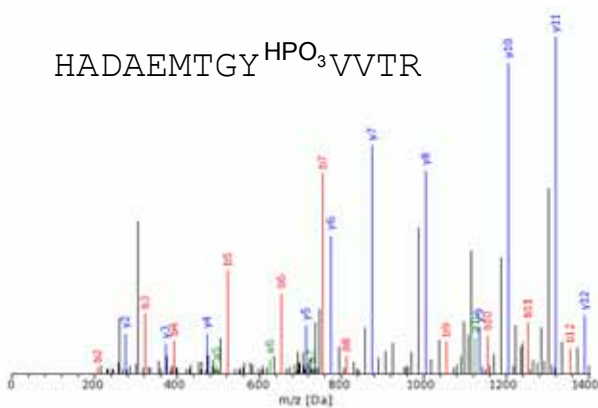


ModiroTM

The PTM-Explorer

Software for discovery of
post-translational modifications



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Mannosylation (C) 162.0528
Hydroxylation (DKNP) 15.9949
Glutathione disulfide (C) 305.3076
Glucosylation (N-term) 162.0528
Glucosylation (KNTWCRY) 162.0528
Gamma-carboxylation (DE) 43.9898
Geranyl-geranyl (C) 272.2504
Formylation (C) 27.9949
Farnesylation (C) 204.1878
Di-methylation (KR) 28.0532
Deamidation (NQ) 0.9840
Citrullination (R) 0.9840
Carbamylation (K) 43.0058
Biotinylation (K) 226.0776
Beta-methylthiolation (D) 45.9877
Amidation (C) -0.9840
Acetylation (K) 42.0106
Acetylation (N-term) 42.0106
Methylation (N-term) 14.0157
Tri-methylation (KR) 42.0797
Sulphone (M) 31.9988
Sulfation (Y) 79.9568
Phosphopantetheine (S) 339.0780
Pyro-glutamine (Q) -17.0305
Pyridoxal phosphate (K) 229.0140
Phosphorylation (STYHCD) 79.9799
Palmitoylation (CKST) 238.2297
O-GlcNAc (NST) 203.0794
N-pyruvic acid 2-iminyl (CVK) 70.0468
N-acyl diglyceride cysteine (C) 788.7258
Myristoylation (N-term) 210.1984
Myristoylation (K) 210.1984
    
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Modiro™ ...the gold standard for identification of PTM from MS/MS data

Modiro™ is a novel software tool enabling rapid, automated detection of true post-translational modifications in your MS/MS datasets.

Modiro™ has been developed to discover PTMs, which cannot be detected by any other software. Explore the large amount of valuable information hidden in your acquired MS/MS data and overcome the tremendous amount of manual analysis time.

Numerous application scenarios

The Software has been developed by Protagen in close cooperation with Bruker Daltonik GmbH, Bremen, a leading worldwide manufacturer of mass spectrometry instruments. Modiro™ does not only reveal a multitude of different post-translational modifications automatically, its application scenarios go far beyond. That might be a detailed primary structure elucidation required for

quality control e.g. of recombinant proteins, searching for phosphorylations in a typical proteome study or even optimization of analytical processes.

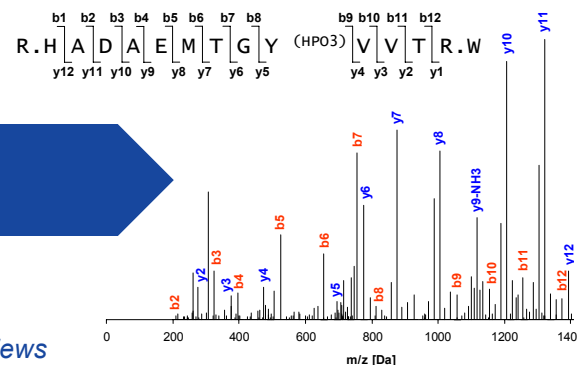
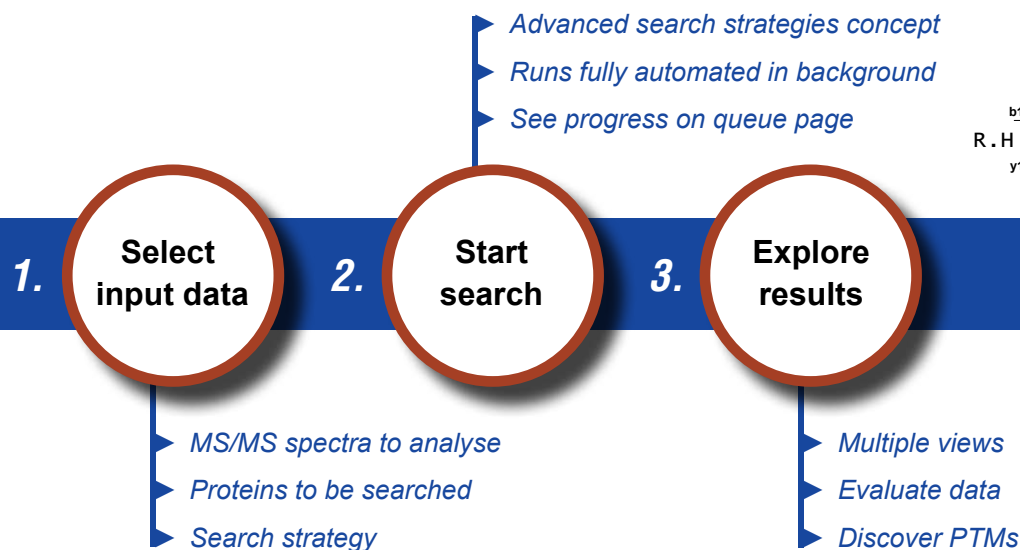
By supporting various evaluation strategies and different views on the results Modiro™ is the benchmark if you want to gain the most information from your MS/MS data.

Simply submit protein sequences of interest and screen simultaneously in one single step for:

- ▶ *Post-translational modifications,*
- ▶ *Unknown mass shifts,*
- ▶ *Isoform detection,*
- ▶ *Unspecific enzymatic cleavage,*
- ▶ *Enzymatic transpeptidation products.*

Ease of operation

Modiro™



Modiro™ utilizes mass spectrometry data from all leading instrument manufacturers



Select the MS/MS spectra you want to analyze. That can be a single spectrum or thousands of spectra (e.g. LC-MS/MS).

Modiro™ is designed to extract all statistically significant information of MS/MS data and to deliver optimum results whatever the source of the data.

Modiro™ outperforms any other search engine by using the advanced concept of search strategies, describing peptide modifications, cleavage rules, sequence patterns, and other search parameters for matching the experimental spectra with candidate peptides.

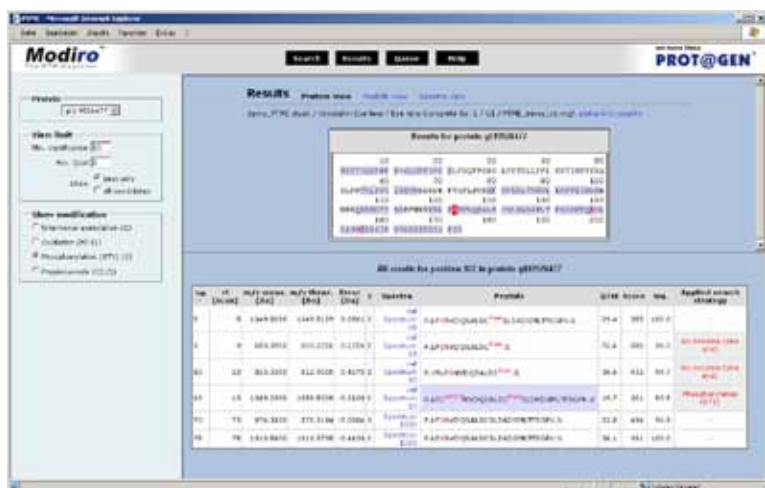
Modiro™ parameter input form

Simply specify the search strategies of interest, define additional search options and start the evaluation. Modiro performs the analysis in the background without hampering the user. Jobs can be easily tracked on Modiro's queue page.

Modiro™ ... specialized for PTM discovery

Features	Benefits
Unique, high-performance identification algorithm for post-translational modifications (PTM) of large MS/MS data sets in one single step	<ul style="list-style-type: none"> ▶ Get results quickly and save time ▶ Get value from your already acquired MS/MS data
Numerous search strategies in a single, integrated package to discover unsuspected and unknown mass shifts, sequence errors (isoforms), unspecific enzymatic cleavage, and transpeptidation products	<ul style="list-style-type: none"> ▶ Gain knowledge from unidentified and previously unusable spectra ▶ Reveal hidden PTM with maximum specificity ▶ Customize search strategies e.g. to your own proprietary protein chemistry
Accepts mass spectrometry data from all leading instrument manufacturers	<ul style="list-style-type: none"> ▶ Independence of spectra source ▶ Future-proof ▶ Comparative analysis possible
Advanced validation and unique visualisation of results	<ul style="list-style-type: none"> ▶ Less false positives while maintaining maximum sensitivity ▶ Easy interpretation with intuitive visualisation minimizes evaluation time
Easy operation and installation	<ul style="list-style-type: none"> ▶ Short period to get started ▶ Only one server installation, multiple users
Plug-in capability with ProteinScape™ (by Bruker Daltonik GmbH and Protagen AG)	<ul style="list-style-type: none"> ▶ Comfortable use within proteomics warehousing system
Proven track-record and in-house expertise based on numerous successful identifications for analytical customers for your support	<ul style="list-style-type: none"> ▶ Quick and competent answers to your questions

Exploring results – the effective way



Search results in protein view

Modiro™ saves your time organizing and sharing your data by easily exporting results e.g. into Microsoft® Excel.

The results are visualized and evaluated via a unique interface, delivering three alternative views on your results, namely “Spectra View”, “Peptide View” and “Protein View”. That generates maximum flexibility, depending on your specific application scenario and needs.

System Requirements

Desktop

- ▶ Intel Pentium III 800 MHz or better
- ▶ 256 MB RAM
- ▶ 500 MB available hard disk space
- ▶ Microsoft Windows Operating System (e.g. XP or 2000)

Web Server

- ▶ Intel Pentium IV 2.4 GHz or better
- ▶ 500 MB RAM
- ▶ 1 GB available hard disk space
- ▶ Microsoft Windows Operating System (e.g. 2000 or 2003 ServerXP or 2000)

How to order

Product	Licence	Cat. No.	Description
Modiro™ v1.0	perpetual	1201-1000	Software for PTM discovery, including full support and all updates for one year

We offer special prices for academic customers, please inquire.

References:

- Gaining knowledge from previously unexplained spectra-application of the PTM-Explorer software to detect PTM in HUPO BPP MS/MS data; Chamrad D.C., Korting G., Schafer H., Stephan C., Thiele H., Apweiler R., Meyer H.E., Marcus K., Bluggel M.; Proteomics, 2006 Sep, 6 (18): 5048-58.
- Study of posttranslational modifications in lenticular α A-Crystallin of mice using proteomic analysis techniques; H. Schaefer, Chamrad D.C., Herrmann M., Stuwe J., Becker G., Klose J., Bluggel M., Meyer H.E., Marcus K.; Biochim Biophys Acta, Epub 2006, Oct 14.
- Identification of phosphorylation and acetylation sites in alphaA-crystallin of the eye lens (mus musculus) after two-dimensional gel electrophoresis; Schaefer H., Marcus K., Sickmann A., Herrmann M., Klose J., Meyer H.E.; Anal Bioanal Chem., 2003 Aug, 376 (7): 966-72. Epub 2003 Jul 10.

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we move ideas

PROT@GEN®

Contact

Protagen AG
Otto-Hahn-Str. 15
44227 Dortmund
Germany

T +49 231 9742 6300
F +49 231 9742 6301
info@protagen.de
www.protagen.de