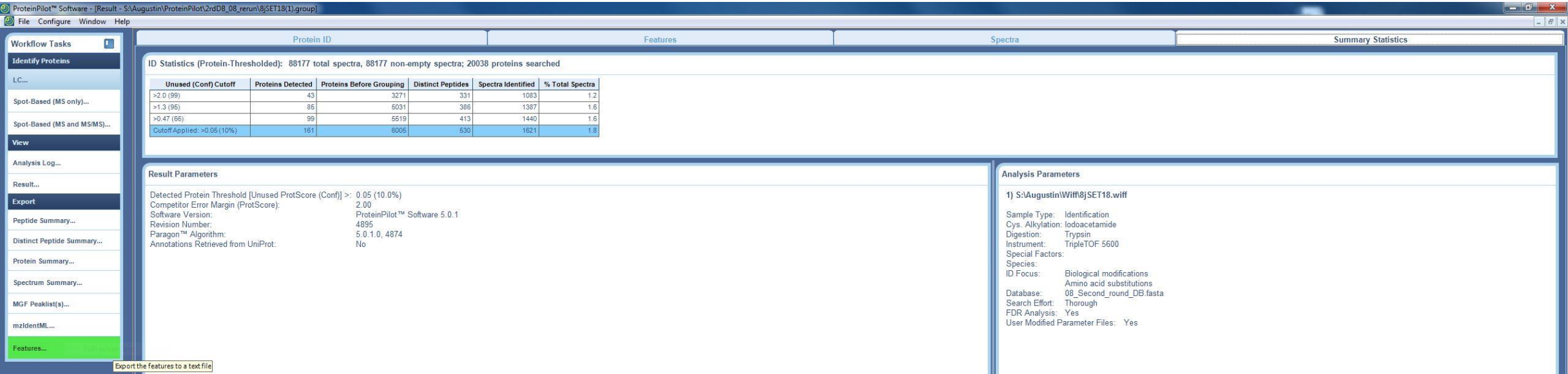
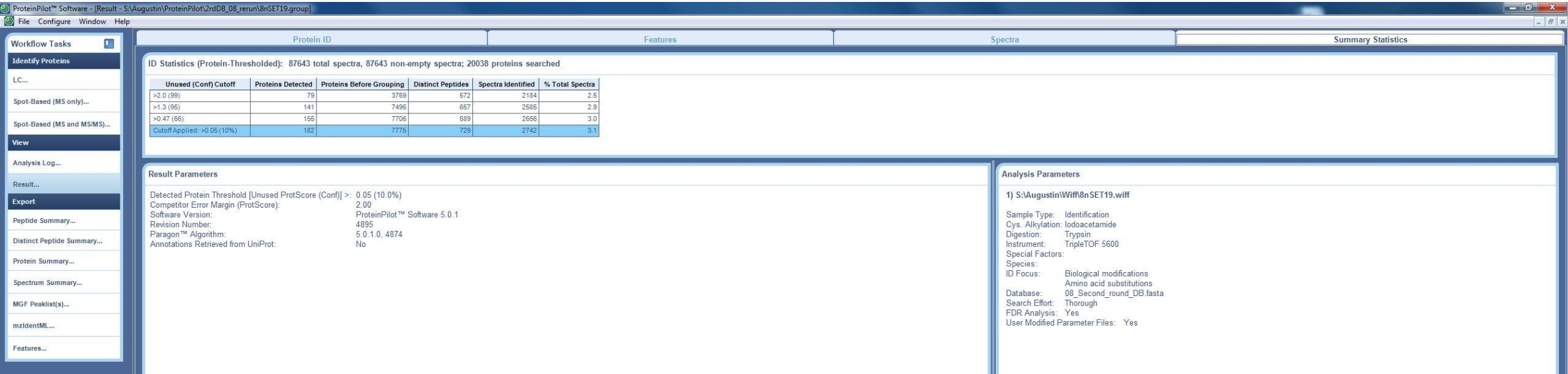


Sample name: 8jSET18 - Metaproteome name: particle-attached day 1



Sample name: 8nSET19 - Metaproteome name: particle-attached night 1



Sample name: 8j2SET110 - Metaproteome name: particle-attached day 2

ProteinPilot™ Software - [Result - S:\Augustin\ProteinPilot2rdDB_08_rerun\8j2SET110.group]

FileConfigureWindowHelp

Workflow Tasks

Identify Proteins

LC...

Spot-Based (MS only)...

Spot-Based (MS and MS/MS)...

View

Analysis Log...

Result...

Export

Peptide Summary...

Distinct Peptide Summary...

Protein Summary...

Spectrum Summary...

MGF Peaklist(s)...

mzIdentML...

Features...

Protein IDFeaturesSpectraSummary Statistics

ID Statistics (Protein-Thresholded): 86844 total spectra, 86844 non-empty spectra; 20038 proteins searched

Unused (Conf) Cutoff	Proteins Detected	Proteins Before Grouping	Distinct Peptides	Spectra Identified	% Total Spectra
>2.0 (99)	81	2963	701	3033	3.5
>1.3 (95)	137	6496	786	3424	3.9
>0.47 (66)	150	5920	817	3492	4.0
Cutoff Applied: >0.05 (10%)	197	8746	900	3643	4.2

Result Parameters

Detected Protein Threshold [Unused ProtScore (Conf)] >: 0.05 (10.0%)
Competitor Error Margin (ProtScore): 2.00
Software Version: ProteinPilot™ Software 5.0.1
Revision Number: 4895
Paragon™ Algorithm: 5.0.1.0, 4874
Annotations Retrieved from UniProt: No

Analysis Parameters

1) S:\Augustin\Wiff\8j2SET110.wiff

Sample Type: Identification
Cys. Alkylation: Iodoacetamide
Digestion: Trypsin
Instrument: TripleTOF 5600
Special Factors:
Species:
ID Focus: Biological modifications
Amino acid substitutions
Database: 08_Second_round_DB.fasta
Search Effort: Thorough
FDR Analysis: Yes
User Modified Parameter Files: Yes

Sample name: 8n2SET111 - Metaproteome name: particle-attached night 2

ProteinPilot™ Software - [Result - S:\Augustin\ProteinPilot2rdDB_08_rerun\8n2SET111.group]

FileConfigureWindowHelp

Workflow Tasks

Identify Proteins

LC...

Spot-Based (MS only)...

Spot-Based (MS and MS/MS)...

View

Analysis Log...

Result...

Export

Peptide Summary...

Distinct Peptide Summary...

Protein Summary...

Spectrum Summary...

MGF Peaklist(s)...

mzIdentML...

Features...

Protein IDFeaturesSpectraSummary Statistics

ID Statistics (Protein-Thresholded): 86537 total spectra, 86537 non-empty spectra; 20038 proteins searched

Unused (Conf) Cutoff	Proteins Detected	Proteins Before Grouping	Distinct Peptides	Spectra Identified	% Total Spectra
>2.0 (99)	108	4485	884	3791	4.4
>1.3 (95)	165	6638	977	4251	4.9
>0.47 (66)	188	6964	1018	4359	5.0
Cutoff Applied: >0.05 (10%)	236	7807	1104	4609	5.2

Result Parameters

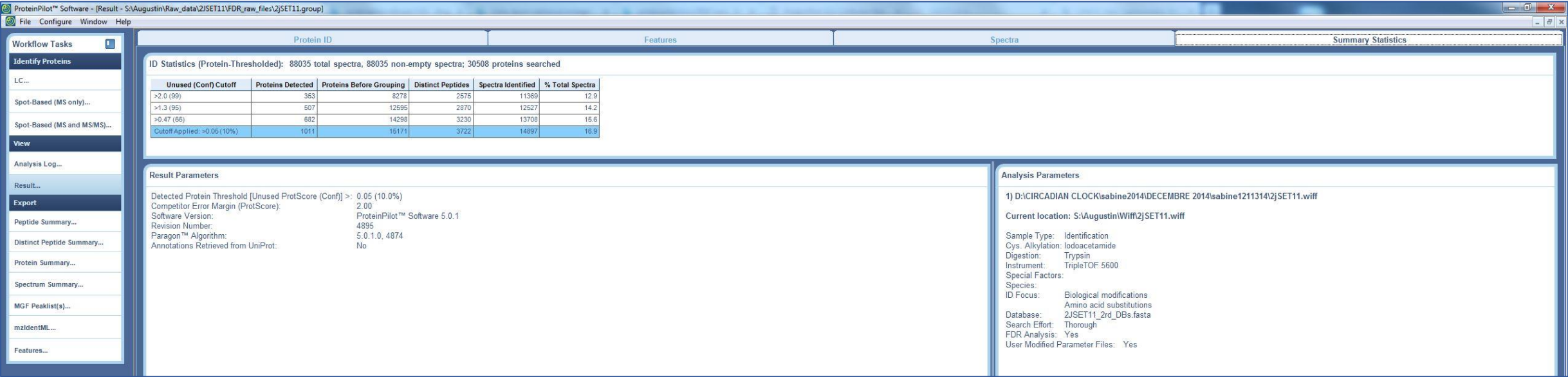
Detected Protein Threshold [Unused ProtScore (Conf)] >: 0.05 (10.0%)
Competitor Error Margin (ProtScore): 2.00
Software Version: ProteinPilot™ Software 5.0.1
Revision Number: 4895
Paragon™ Algorithm: 5.0.1.0, 4874
Annotations Retrieved from UniProt: No

Analysis Parameters

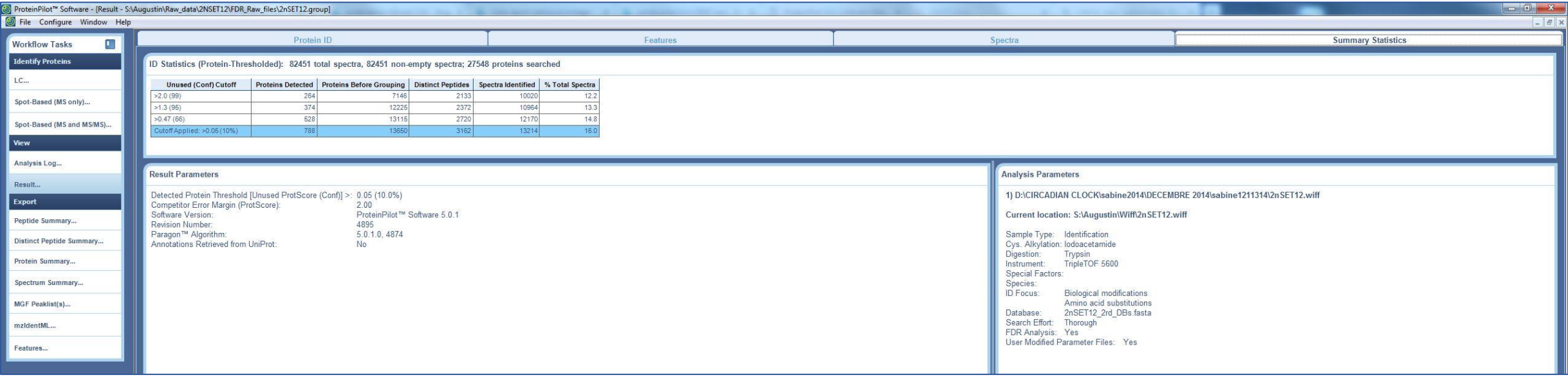
1) S:\Augustin\Wiff\8n2SET111.wiff

Sample Type: Identification
Cys. Alkylation: Iodoacetamide
Digestion: Trypsin
Instrument: TripleTOF 5600
Special Factors:
Species:
ID Focus: Biological modifications
Amino acid substitutions
Database: 08_Second_round_DB.fasta
Search Effort: Thorough
FDR Analysis: Yes
User Modified Parameter Files: Yes

Sample name: 2jSET11 - Metaproteome name: free-living day 1



Sample name: 2nSET12 - Metaproteome name: free-living night 1



Sample name: 2j2SET13 - Metaproteome name: free-living day 2

Workflow Tasks

Identify Proteins

LC...

Spot-Based (MS only)...

Spot-Based (MS and MS/MS)...

View

Analysis Log...

Result...

Export

Peptide Summary...

Distinct Peptide Summary...

Protein Summary...

Spectrum Summary...

MGF Peaklist(s)...

mzIdentML...

Features...

Protein ID

Features

Spectra

Summary Statistics

ID Statistics (Protein-Thresholded): 75910 total spectra, 75910 non-empty spectra; 37008 proteins searched

Unused (Conf) Cutoff	Proteins Detected	Proteins Before Grouping	Distinct Peptides	Spectra Identified	% Total Spectra
>2.0 (99)	323	9120	2112	9270	12.2
>1.3 (95)	472	14535	2391	10325	13.6
>0.47 (66)	613	17231	2641	11289	14.9
Cutoff Applied: >0.05 (10%)	881	17627	3017	12169	16.0

Result Parameters

Detected Protein Threshold [Unused ProtScore (Conf)] >: 0.05 (10.0%)
Competitor Error Margin (ProtScore): 2.00
Software Version: ProteinPilot™ Software 5.0.1
Revision Number: 4895
Paragon™ Algorithm: 5.0.1.0, 4874
Annotations Retrieved from UniProt: No

Analysis Parameters

1) D:\CIRCADIAN CLOCK\isabine2014\DECEMBRE 2014\isabine1211314\2j2SET13.wiff

Current location: S:\Augustin\Wiff\2j2SET13.wiff

Sample Type: Identification
Cys. Alkylation: Iodoacetamide
Digestion: Trypsin
Instrument: TripleTOF 5600
Special Factors:
Species:
ID Focus: Biological modifications
Amino acid substitutions
Database: 2j2SET13_2rd_DBs.fasta
Search Effort: Thorough
FDR Analysis: Yes
User Modified Parameter Files: Yes

Sample name: 2n2SET14 - Metaproteome name: free-living night 2

Workflow Tasks

Identify Proteins

LC...

Spot-Based (MS only)...

Spot-Based (MS and MS/MS)...

View

Analysis Log...

Result...

Export

Peptide Summary...

Distinct Peptide Summary...

Protein Summary...

Spectrum Summary...

MGF Peaklist(s)...

mzIdentML...

Features...

Protein ID

Features

Spectra

Summary Statistics

ID Statistics (Protein-Thresholded): 72101 total spectra, 72101 non-empty spectra; 30876 proteins searched

Unused (Conf) Cutoff	Proteins Detected	Proteins Before Grouping	Distinct Peptides	Spectra Identified	% Total Spectra
>2.0 (99)	284	9789	2070	9729	13.5
>1.3 (95)	420	13691	2344	10721	14.9
>0.47 (66)	554	14470	2636	11533	16.0
Cutoff Applied: >0.05 (10%)	837	15288	3085	12643	17.4

Result Parameters

Detected Protein Threshold [Unused ProtScore (Conf)] >: 0.05 (10.0%)
Competitor Error Margin (ProtScore): 2.00
Software Version: ProteinPilot™ Software 5.0.1
Revision Number: 4895
Paragon™ Algorithm: 5.0.1.0, 4874
Annotations Retrieved from UniProt: No

Analysis Parameters

1) D:\CIRCADIAN CLOCK\isabine2014\DECEMBRE 2014\isabine1211314\2n2SET14.wiff

Current location: S:\Augustin\Wiff\2n2SET14.wiff

Sample Type: Identification
Cys. Alkylation: Iodoacetamide
Digestion: Trypsin
Instrument: TripleTOF 5600
Special Factors:
Species:
ID Focus: Biological modifications
Amino acid substitutions
Database: 2n2SET14_2rd_DBs.fasta
Search Effort: Thorough
FDR Analysis: Yes
User Modified Parameter Files: Yes