



Progenesis QI for proteomics - What's new in the latest release?

Version 4.2 | October 2019

The latest release of Progenesis QI for proteomics helps scientists to overcome challenges in their research by offering some new developments. At the same time, attention has been paid to the usability of Progenesis QI for proteomics.

Host Cell Protein Quantitation

When using Progenesis QI for proteomics for Host Cell Protein (HCP) analysis, you can now choose to use the quantitation method designed specifically for HCP analysis. A new column has been added for greater understanding of your HCP data.

File Experiment Experiment Alignment Fittering Design Setup	Review Peak Peptide Ion Picking Statistics	Identify Peptides QC M	Rafine Identifications	Review Proteins	Protein Statistics	Report	nonline A Waters Comp	
Review Proteins	W No filter applie	a)		0			😧 He	
Ising this screen, you can find the proteins of interest in your experiment.	T	Create	Search	. 24				
Set the quantitation options			Amou	nt (fmai) - A	Amount (fmol) - B Amount ((ng) - A Amount (ng	
If you've not already done so, choose between relative and absolute quantitation, use of Hi-N.	=4 \$V=1		10.6		14.5	0.531	0.728	
protein grouping and more.	4 SV=1		50		50	1.93	1.93	
Protein options	=4.5V=1		12.4	-	18.2	0.178	0.262	
res of property of the little	OP Protein quantitation o	ptions			308	6.31	8.74	
Create a shortlist to review In the table, sort and filter the proteins based	Quantitation method:				26	0.565	0.66	
on their measurements, to generate a shortlist	Absolute Quantitation for HCP using Hi-N				81.4	1.16	1.28	
for further review. How are the measurements calculated?	And a second sec				21.4	0.611	1.19	
To sort the table by a given value, simply click	Requires a calibrant protein to calculate absolute amounts Uses mean calibrant abundance measured across runs Uses the mora shundant Np protes Allows comparison between proteins within a run Relative Quantitation using H-N Uses the most abundant N peptides Allows comparison between proteins within a run				3.55	0.157	0.247	
the relevant column header.				10	31.8	1.18	1.67	
Review the proteins				- 10	22.4	0.703	2.39	
For each protein of interest, review its peptide					19.5	0.571	0.74	
measurements and correlations:					57.7	0.615	0.722	
View peptide measurements	Relative Quantitation				4.31	0.265	0.358	
You can also double-click to review a protein.	Uses only peptides			ications		m		
Export data for further processing By exporting your data to external tools, there's no limit to your analysis.	Allows comparison Relative Quantitation Uses all peptides in	using all peptides dentified as part of a	protein	nte	in GN=CA	WG_00322	2 PE=4 SV=1	
Export to pathways tool	Allows comparison of a single protein across runs Absolute Quantitation for HCP using Hi-N				8			
	 Requires a calibrar 							
Export protein measurements	Ubes calibrated abundance measured per nun ⁺ Ubes the most abundance M peptides Calculates the amount of HOPs per nun in finul and ng 40							
Export peptide measurements								
Export peptide ion measurements								
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Integration with MetaCore, a Cortellis solution for pathway analysis

Progenesis QI for proteomics now integrates with MetaCore, a Cortellis solution that enables precise, actionable answers to specific questions across the R&D lifecycle. MetaCore delivers high-quality systems biology content in the context of comprehensive pathway-based analytics, molecular network building and insightful visualizations.



Improvements to alignment

We are always looking to improve the usability of the software which is why we have made improvements to the alignment for low complexity injections.

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