

File Edit View Experiment Export Quant Window Help

Protein Threshold: 95.0% Min # Peptides: 1 Peptide Threshold: 95%

Display Options: Total Spectrum Count Req Mods: No Filter Search:

Probability Legend:

- over 95%
- 80% to 94%
- 50% to 79%
- 20% to 49%
- 0% to 19%

Bio View: 32 Proteins in 30 Clusters With 8 Decoys

#	Visible?	Carved?	Protein	Accession Number	Molecular Weight	Protein Grouping Ambiguity	QC-BSA-1	QC-BSA-2	QC-BSA-3
1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Serum albumin	IPI01028455	69 kDa		478	921	667
2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Vitamin D-binding protein	IPI00823795	53 kDa		7	10	5
3	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	IPI00689396-DECOY	IPI00689396-DECOY	?		0	1	0
4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Cluster of Alpha-1-acid glycoprotein (IPI00691212)	IPI00691212	23 kDa	★	4	4	3
4.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Alpha-1-acid glycoprotein	IPI00691212	23 kDa	★	4	4	3
4.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Uncharacterized protein	IPI01028375	23 kDa	★	3	3	2
5	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Antithrombin-III	IPI00688316	52 kDa		2	3	3
6	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Transferrin	IPI00689362	16 kDa		1	3	3
7	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	IPI00823905-DECOY	IPI00823905-DECOY	?		0	0	1
8	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	IPI00968679-DECOY	IPI00968679-DECOY	?		1	0	0
9	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Uncharacterized protein	IPI00694904 (+1)	106 kDa		0	0	2
10	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Cluster of keratin 6A-like (IPI01002591)	IPI01002591	63 kDa	★	1	2	2
10.1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	keratin 6A-like	IPI01002591	63 kDa	★	1	2	2
10.2	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Keratin 77-like	IPI00999429	63 kDa	★			1
11	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Serpin A3-5	IPI00707034 (+4)	46 kDa		1	1	1
12	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	IPI00699482-DECOY	IPI00699482-DECOY	?		0	1	1
13	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Endopin 2	IPI00689530 (+4)	47 kDa			2	0
14	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Complement C3 (Fragment)	IPI00713505	187 kDa		1	0	0
15	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	AF4/FMR2 family, member 1 isoform 1	IPI01001243 (+1)	132 kDa		1	0	0
16	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	IPI00695551-DECOY	IPI00695551-DECOY	?		0	1	0
17	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	IPI00703076-DECOY	IPI00703076-DECOY (+2)	?		0	1	0
18	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Amine oxidase	IPI00693037 (+3)	84 kDa		1	0	
19	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	MGC139004 protein	IPI00868600	70 kDa		0	0	1
20	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	IGK protein	IPI00724838 (+3)	27 kDa		0		1
21	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Apolipoprotein C-III	IPI00689034	11 kDa		1	1	1
22	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Uncharacterized protein	IPI00703491 (+1)	124 kDa		1	0	0
23	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Cationic trypsin	IPI00706427	26 kDa		0		1
24	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Protein AMBP	IPI00696507	39 kDa			1	1
25	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	IPI00786384-DECOY	IPI00786384-DECOY	?	★	0		1
26	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	envelope glycoprotein-like	IPI00717087 (+2)	67 kDa		1		
27	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Zinc finger and SCAN domain containing 21	IPI00703516	53 kDa		1		
28	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	PRR11 protein	IPI00852493	40 kDa			1	
29	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	hypothetical protein	IPI00705120	34 kDa				1
30	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	IPI00717143-DECOY	IPI00717143-DECOY (+1)	?				1

click



Bio View: 32 Proteins in 30 Clusters With 8 Decoys

Brief information

Click target protein

30 Proteins at 95.0% Minimum
 1 Min # Peptides
 36.4% Decoy FDR
 2151 Spectra at 95.0% Minimum
 0.42% Decoy FDR

information of ProteinProphet and PeptideProphet

Protein Information:

Lookup Accession Number In: NCBI (|e:gi|1351907,ALBU_BOVIN,P02769)

IPI01028455

Sample Information:

Biological Sample:

Sample Category:

Sample Description:

MS/MS Sample:

MS/MS Sample Notes:

Scaffold Q+S - Proteins - QC-BSA_IPI

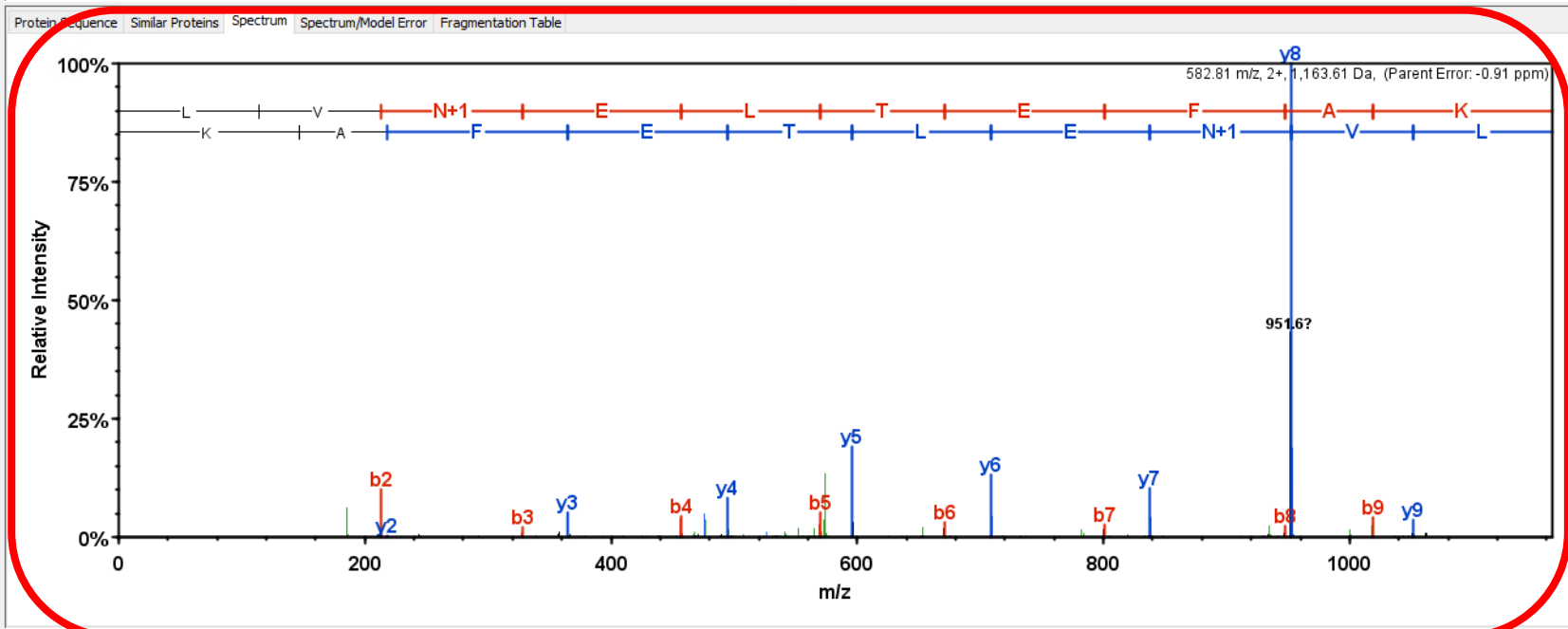
File Edit View Experiment Export Quant Window Help

Protein Threshold: 95.0% Min # Peptides: 1 Peptide Threshold: 95%

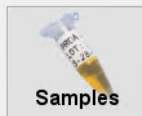
Sequence Coverage	Protein	Accession	Category	Bio Sample	MS/MS Sa...	Prob	%Spec
	Serum albumin	IP101028455	Fusion	QC-BSA-1		100%	7.1%
	Serum albumin	IP101028455	Fusion	QC-BSA-2		100%	6.6%
	Serum albumin	IP101028455	Fusion	QC-BSA-3		100%	8.1%

Valid	Sequence	Prob	Masc...	Masc...	Masc...	NTT	Modifications
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	61.5	25.7	49.5	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	61.9	25.8	47.2	2	
<input checked="" type="checkbox"/>	1.0 (K)LV ELTEFAK(T)	100%	64.1	25.4	54.0	2	Deamidated (+1)
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	60.3	25.7	47.7	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	60.6	25.8	46.1	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	62.4	25.8	43.9	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	65.0	25.0	50.2	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	65.3	25.0	49.7	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	65.4	25.0	52.9	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	62.4	25.0	51.0	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	60.9	25.8	42.5	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	61.7	25.0	49.6	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	61.8	25.0	51.9	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	64.3	25.0	55.3	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	60.9	25.0	49.6	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	61.6	25.0	53.8	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	62.3	25.8	40.5	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	60.4	25.0	51.0	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	60.5	25.0	48.8	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	60.1	25.0	49.8	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	59.2	25.0	49.1	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	59.5	25.0	53.4	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	59.0	25.0	50.3	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	60.6	25.0	45.2	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	59.6	25.0	46.9	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	64.2	25.0	58.0	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	68.9	25.0	56.6	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	56.5	25.7	45.3	2	
<input checked="" type="checkbox"/>	1.0 (K)LVNELTEFAK(T)	100%	59.4	25.0	46.6	2	

PTM Spectrum for publication



30 Proteins at 95.0% Minimum
 1 Min # Peptides
 36.4% Decoy FDR
 2151 Spectra at 95.0% Minimum
 0.42% Decoy FDR



click

Experiment Methods | MCP Submission

Parameter	Value
Experiment:	QC-BSA_IPI
Peak List Generator:	
Version:	
Charge States Calculated:	
Deisotoped:	
Textual Annotation:	
Database Set:	1 Database
Database Name:	the IPI_bovine_20120712 database
Version:	
Taxonomy:	All Entries
Number of Proteins:	30403
Does database contain common contaminants?:	
Search Engine Set:	1 Search Engine
Search Engine:	Mascot
Version:	2.7.0
Samples:	All Samples
Fragment Tolerance:	1.00 Da (Monoisotopic)
Parent Tolerance:	10.0 PPM (Monoisotopic)
Fixed Modifications:	+18 on O (O+18), +57 on C (Carbamidomethyl)
Variable Modifications:	-18 on n (Glu->pyro-Glu), +1 on NQ (Deamidated), +16 on M ...
Database:	the IPI_bovine_20120712 database (unknown version, 30403...
Digestion Enzyme:	Trypsin
Max Missed Cleavages:	1
Probability Model:	
BSA-1 (F001976):	LFDR Model, Classifier data: Bayes, Good (50%) m:66.4/s:12....
BSA-2 (F001977):	LFDR Model, Classifier data: Bayes, Good (50%) m:65.1/s:12....
BSA-3 (F001978):	LFDR Model, Classifier data: Bayes, Good (50%) m:66.6/s:12....
Scaffold:	Version: Scaffold_4.2.1
Modification Metadata Set:	1541 modifications
Source:	C:\Program Files\Scaffold 4\parameters\unimod.xml
Comment:	
Protein Grouping Strategy:	Experiment-wide grouping with protein cluster analysis
Peptide Thresholds:	95.0% minimum
Protein Thresholds:	95.0% minimum and 1 peptide minimum
Peptide FDR:	0.4% (Decoy)
Protein FDR:	36.4% (Decoy)
GO Annotation Source(s):	

DATABASE SEARCHING-- Tandem mass spectra were extracted by [unknown] version [unknown]. Charge state deconvolution and deisotoping were not performed. All MS/MS samples were analyzed using Mascot (Matrix Science, London, UK; version 2.7.0). Mascot was set up to search the IPI_bovine_20120712 database (unknown version, 30403 entries) assuming the digestion enzyme trypsin. Mascot was searched with a fragment ion mass tolerance of 1.00 Da and a parent ion tolerance of 10.0 PPM. O+18 of pyrrolysine and carbamidomethyl of cysteine were specified in Mascot as fixed modifications. Glu->pyro-Glu of the n-terminus, deamidated of asparagine and glutamine and oxidation of methionine were specified in Mascot as variable modifications.

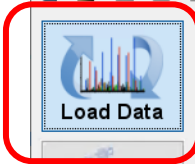
CRITERIA FOR PROTEIN IDENTIFICATION-- Scaffold (version Scaffold_4.2.1, Proteome Software Inc., Portland, OR) was used to validate MS/MS based peptide and protein identifications. Peptide identifications were accepted if they could be established at greater than 95.0% probability by the Scaffold Local FDR algorithm. Protein identifications were accepted if they could be established at greater than 95.0% probability and contained at least 1 identified peptide. Protein probabilities were assigned by the Protein Prophet algorithm (Nesvizhskii, Al et al Anal. Chem. 2003;75(17):4646-58). Proteins that contained similar peptides and could not be differentiated based on MS/MS analysis alone were grouped to satisfy the principles of parsimony. Proteins sharing significant peptide evidence were grouped into clusters.

Data search method

You can export protein or peptides list

30 Proteins at
95.0% Minimum
1 Min # Peptides
36.4% Decoy FDR
2151 Spectra at
95.0% Minimum
0.42% Decoy FDR

click



Load Data

Samples

Proteins

Similarity

Quantify

Publish

Statistics

QC-BSA_IPI 28798 Spectra

Protein Grouping: Experiment Wide

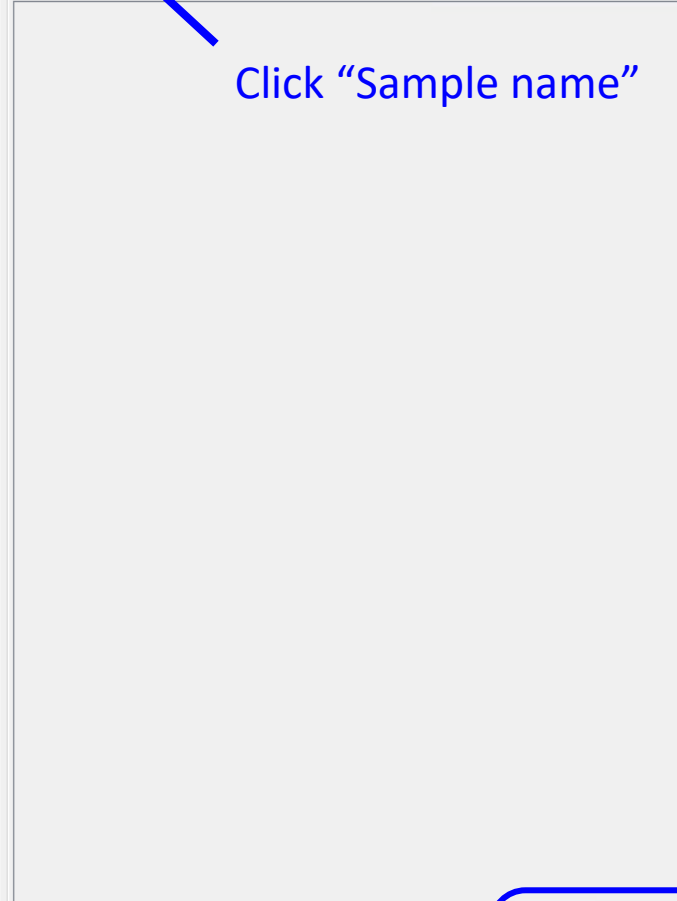
QC-BSA-1 QC-BSA-2 QC-BSA-3

QC-BSA-1 13862 Spectra Fusion

Standard Sample: each file will be analyzed separately

Condensing on keep all unmatched spectra for future export

Files in Loading Queue



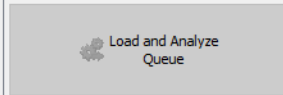
Click "Sample name"

Files Currently Loaded

Mascot

BSA-2 (F001977)

You can see Mascot search name.



Modification information

30 Proteins at 95.0% Minimum 1 Min # Peptides 36.4% Decoy FDR 2151 Spectra at 95.0% Minimum 0.42% Decoy FDR

Analysis Information:

Peptide Tolerance: 10.0 PPM (Monoisotopic)
Fragment Tolerance: 1.00 Da (Monoisotopic)
Digestion Enzyme: Trypsin
Searched Database: the IPI_bovine_20120712 database (30403 entries)
Original Search Date: Mascot=05/18/2022
Scaffold Version: Scaffold_4.2.1

Fixed Modifications:

Table with 3 columns: Modification, Mass, AA. Rows include O+18, Carbamidomethyl.

Variable Modifications:

Table with 3 columns: Modification, Mass, AA. Rows include Glu->pyro-Glu, Deamidated, Oxidation.