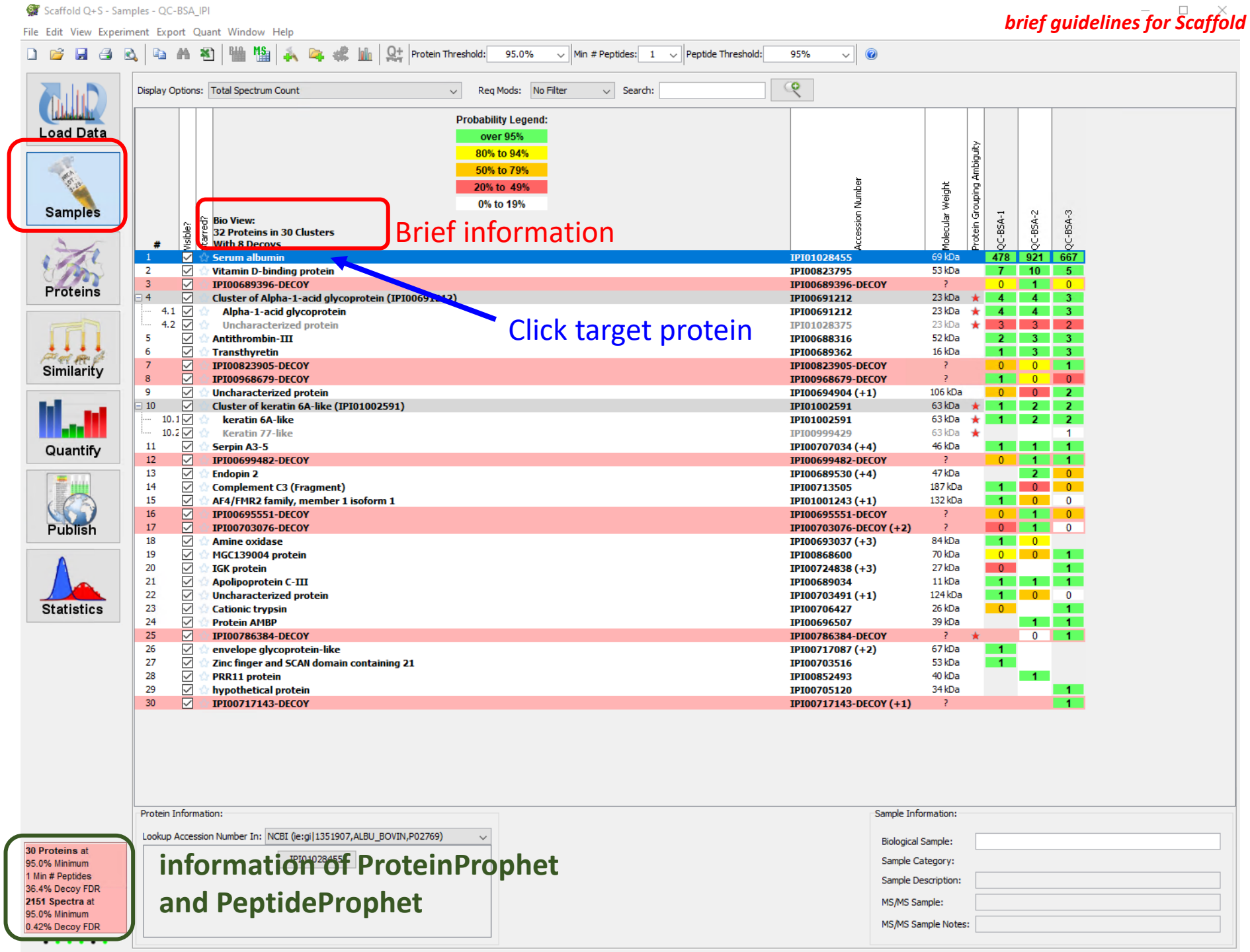
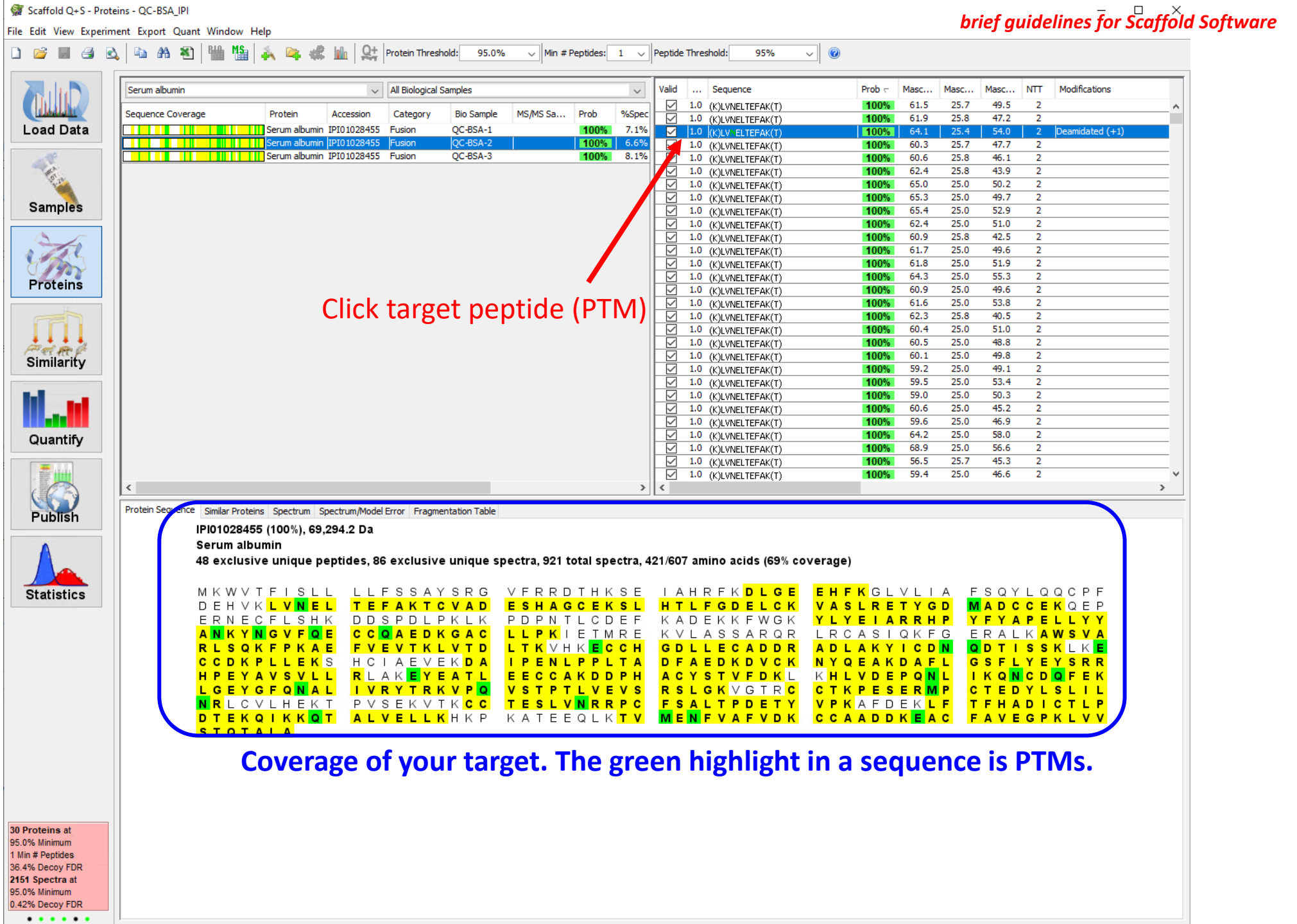


#	Visible?	Starred?	Bio View: 32 Proteins in 30 Clusters With 8 Decoys	Accession Number	Molecular Weight	Protein Grouping Ambiguity	QC-BSA-1	QC-BSA-2	QC-BSA-3
1	☑	☆	Serum albumin	IPI01028455	69 kDa		478	921	667
2	☑	☆	Vitamin D-binding protein	IPI00823795	53 kDa		7	10	5
3	☑	☆	IPI00689396-DECOY	IPI00689396-DECOY	?		0	1	0
4	☑	☆	Cluster of Alpha-1-acid glycoprotein (IPI00691212)	IPI00691212	23 kDa	★	4	4	3
4.1	☑	☆	Alpha-1-acid glycoprotein	IPI00691212	23 kDa	★	4	4	3
4.2	☑	☆	Uncharacterized protein	IPI01028375	23 kDa	★	3	3	2
5	☑	☆	Antithrombin-III	IPI00688316	52 kDa		2	3	3
6	☑	☆	Transthyretin	IPI00689362	16 kDa		1	3	3
7	☑	☆	IPI00823905-DECOY	IPI00823905-DECOY	?		0	0	1
8	☑	☆	IPI00968679-DECOY	IPI00968679-DECOY	?		1	0	0
9	☑	☆	Uncharacterized protein	IPI00694904 (+1)	106 kDa		0	0	2
10	☑	☆	Cluster of keratin 6A-like (IPI01002591)	IPI01002591	63 kDa	★	1	2	2
10.1	☑	☆	keratin 6A-like	IPI01002591	63 kDa	★	1	2	2
10.2	☑	☆	Keratin 77-like	IPI00999429	63 kDa	★			1
11	☑	☆	Serpin A3-5	IPI00707034 (+4)	46 kDa		1	1	1
12	☑	☆	IPI00699482-DECOY	IPI00699482-DECOY	?		0	1	1
13	☑	☆	Endopin 2	IPI00689530 (+4)	47 kDa			2	0
14	☑	☆	Complement C3 (Fragment)	IPI00713505	187 kDa		1	0	0
15	☑	☆	AF4/FMR2 family, member 1 isoform 1	IPI01001243 (+1)	132 kDa		1	0	0
16	☑	☆	IPI00695551-DECOY	IPI00695551-DECOY	?		0	1	0
17	☑	☆	IPI00703076-DECOY	IPI00703076-DECOY (+2)	?		0	1	0
18	☑	☆	Amine oxidase	IPI00693037 (+3)	84 kDa		1	0	
19	☑	☆	MGC139004 protein	IPI00868600	70 kDa		0	0	1
20	☑	☆	IGK protein	IPI00724838 (+3)	27 kDa		0		1
21	☑	☆	Apolipoprotein C-III	IPI00689034	11 kDa		1	1	1
22	☑	☆	Uncharacterized protein	IPI00703491 (+1)	124 kDa		1	0	0
23	☑	☆	Cationic trypsin	IPI00706427	26 kDa		0		1
24	☑	☆	Protein AMBP	IPI00696507	39 kDa			1	1
25	☑	☆	IPI00786384-DECOY	IPI00786384-DECOY	?	★		0	1
26	☑	☆	envelope glycoprotein-like	IPI00717087 (+2)	67 kDa		1		
27	☑	☆	Zinc finger and SCAN domain containing 21	IPI00703516	53 kDa		1		
28	☑	☆	PRR11 protein	IPI00852493	40 kDa			1	
29	☑	☆	hypothetical protein	IPI00705120	34 kDa				1
30	☑	☆	IPI00717143-DECOY	IPI00717143-DECOY (+1)	?				1



Coverage of your target. The green highlight in a sequence is PTMs.

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%

Load Data

Samples

Proteins

Similarity

Quantify

Publish

Statistics

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

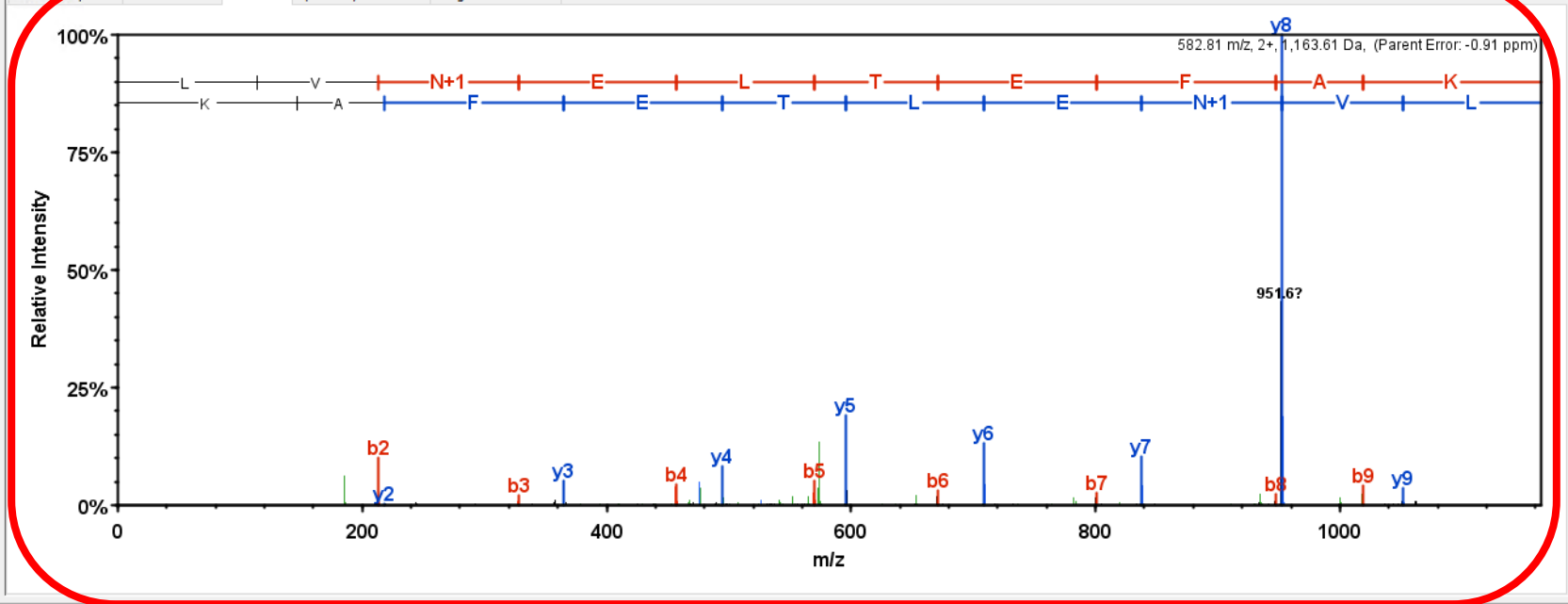
Serum albumin | All Biological Samples

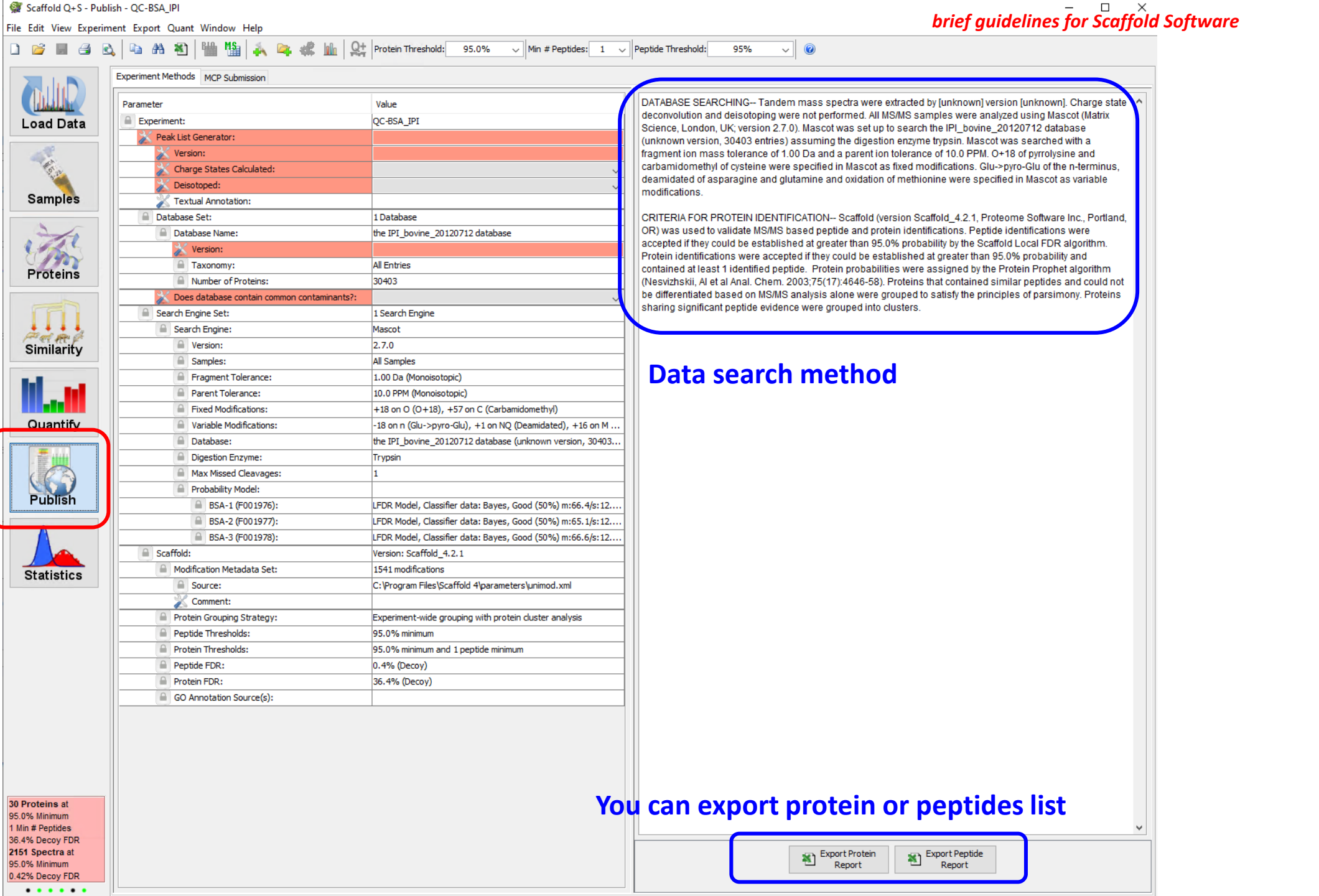
Sequence Coverage	Protein	Accession	Category	Bio Sample	MS/MS Sa...	Prob	%Spec
	Serum albumin	IPI01028455	Fusion	QC-BSA-1		100%	7.1%
	Serum albumin	IPI01028455	Fusion	QC-BSA-2		100%	6.6%
	Serum albumin	IPI01028455	Fusion	QC-BSA-3		100%	8.1%

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

PTM Spectrum for publication

Protein Sequence | Similar Proteins | Spectrum | Spectrum/Model Error | Fragmentation Table

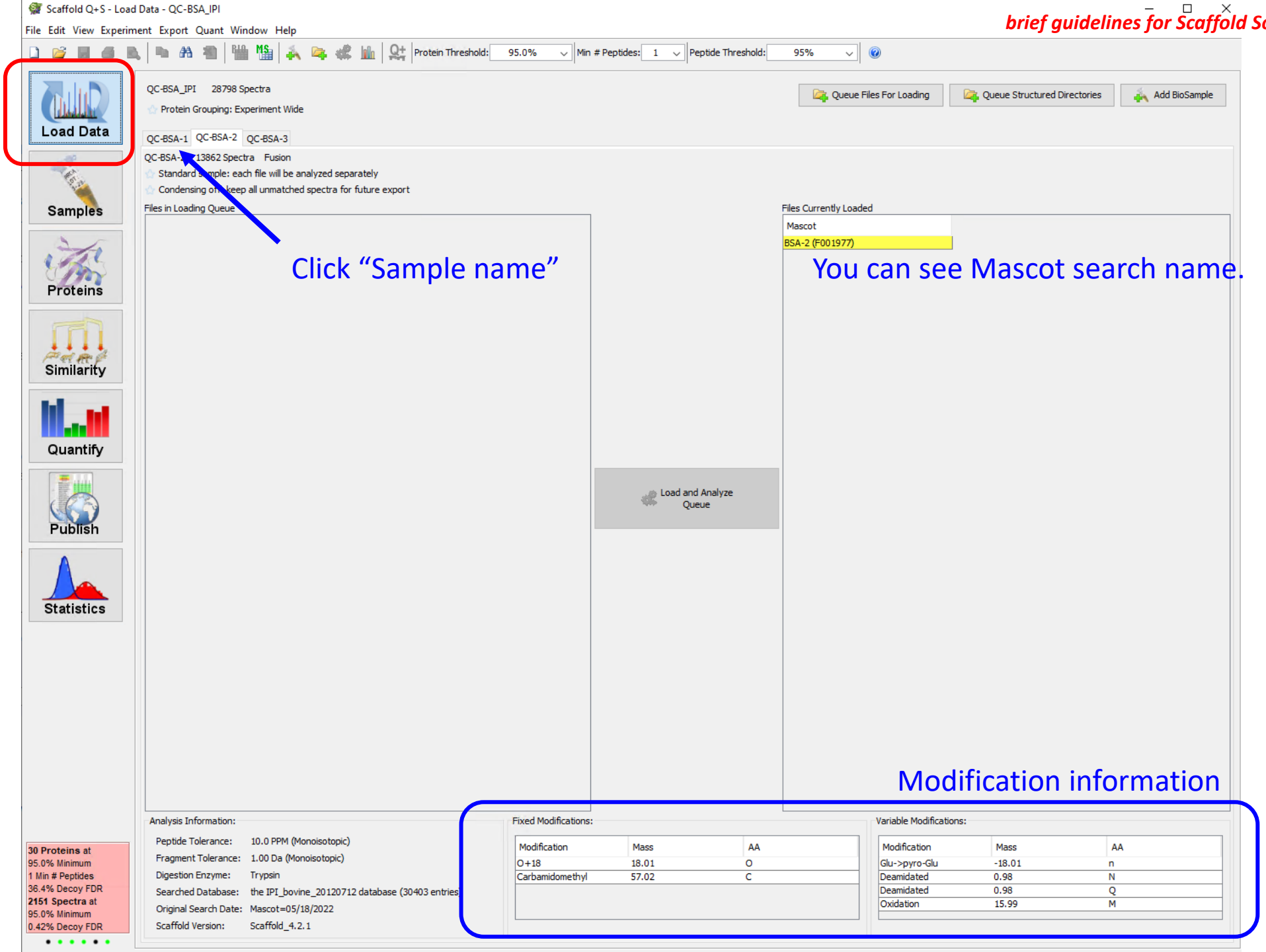




click

Data search method

You can export protein or peptides list


click
Scaffold Q+S - Load Data - QC-BSA_IPI
File Edit View Experiment Export Quant Window Help
Protein Threshold: 95.0%
Min # Peptides: 1
Peptide Threshold: 95%
Load Data
Samples
Proteins
Similarity
Quantify
Publish
Statistics
QC-BSA_IPI 28798 Spectra
Protein Grouping: Experiment Wide
Queue Files For Loading
Queue Structured Directories
Add BioSample
QC-BSA-1
QC-BSA-2
QC-BSA-3
13862 Spectra Fusion
Standard sample: each file will be analyzed separately
Condensing off: keep all unmatched spectra for future export
Files in Loading Queue
Files Currently Loaded
Mascot
BSA-2 (F001977)
Click “Sample name”
You can see Mascot search name.
Load and Analyze Queue
Modification information
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:
Modification Mass AA
O+18 18.01 O
Carbamidomethyl 57.02 C
Variable Modifications:
Modification Mass AA
Glu->pyro-Glu -18.01 n
Deamidated 0.98 N
Deamidated 0.98 Q
Oxidation 15.99 M
30 Proteins at
95.0% Minimum
1 Min # Peptides
36.4% Decoy FDR
2151 Spectra at
95.0% Minimum
0.42% Decoy FDR