

Consensus Rows (first row in the .xls and .pdf files)	
Reference	Displays the alphanumeric reference for the <i>.dta</i> file, which is the header information from the Fasta database that describes the entry.
P (pro)	Displays only when a unified search (<i>.srf</i>) file is loaded. This entry displays the probability of finding a match as good or better than the observed match by chance. The value displayed for the protein is the probability of the best peptide match (the peptide with the lowest score).
Sf	Displays only if you have selected the Calculate The Sf Scores During The SEQUEST Search option in the Configuration dialog box - SEQUEST Search page . The Sf score for each peptide is calculated by a neural network algorithm that incorporates the Xcorr, DeltaCn, Sp, RSp, peptide mass, charge state, and the number of matched peptides for the search. The protein Sf score is the sum of peptide Sf scores for all the peptides associated with that protein. The higher the value of the Sf score, the better the protein match.
Score	<p>Displays a score for the SEQUEST results; the higher the score, the better the match to the searched sequence.</p> <p>If you have selected a Unified Score filter in the Search Results Options dialog box, this is the Unified Score. The unified score is calculated by: $\text{Score} = (10,000 \times ((\text{DeltaCn}^2) + \text{Sp})) \times \text{XCORR}$</p> <p>If you have not selected a Unified Score filter in the Search Results Options dialog box, this score is calculated by multiplying the first entry in the Hits column by 10, the second entry by 8, the third by 6, the fourth by 4, and the fifth by 2, and then summing these values. The higher the number, the better the match to your search.</p>
Coverage	Displays the coverage of the protein, which is the percentage of the protein sequence covered by the identified peptides.
MW	Displays the molecular weight of the protein.
Accession	Displays the Accession number of the protein.
Peptides (Hits)	Displays total number of peptide matches, and the number of proteins that were found to be related to that entry in parentheses. The first number is the number of proteins that have been identified with the first hit and corresponds to the first entry in the <i>.out</i> file. The second number is the number of proteins that have been identified with the second hit and corresponds to the second entry in the <i>.out</i> file, and so on.
% Area or % Height	<p>Displays the percent area or the percent height of the protein, depending on which option you selected when performing the peak area/height calculation.</p> <p>This value is calculated by reading the MH+ value from the <i>.dta</i> file and calculating the precursor mass. A reconstructed ion chromatogram (RIC) is</p>

	<p>generated using the precursor mass, is smoothed, and the integrated height of the peaks are calculated.</p> <p>Displays only if you have set the parameters in the Protein Area/Height Calculation dialog box, which you access by choosing Actions > Protein Area/Height Calculation.</p>
Ratios	Displays the average value of the ratio for the protein. This column is displayed only if you have set the parameters in the ICAT Parameters dialog box, which you access by choosing Actions > PepQuan .
% TIC	Displays the %TIC for the protein. To display this column, right-click in the results table and choose Display > TIC Value from the shortcut menu.
Summary Rows (second row in the protein/peptide table of the .pdf file)	
Scans	Lists the scans corresponding to the current row of data.
Sequence	<p>Displays the peptide sequence of each .dta file that matches a portion of the searched sequence.</p> <p>If SEQUEST determines that a peptide has a differential modification, then it adds one of the following characters after that amino acid in the peptide sequence displayed in the Sequence column:</p> <p>* First ~ Fifth # Second \$ Sixth @ Third] N term ^ Fourth [C term</p> <p>For example, AS*EDLKK means that S was modified by the first differential modification listed in the SEQUEST Search Parameters dialog box - Modifications page.</p>
MH+	Displays the molecular weight for each .dta file.
z	Displays the charge of each .dta file.
Type	Displays the activation type.
P (pep)	Displays only when a unified search (.srf) file is used. This column displays the probability of finding a match as good or better than the observed peptide match by chance.
Sf	Displays only if you have selected the Calculate The Sf Scores During The SEQUEST Search option in the Configuration dialog box - SEQUEST Search page . The Sf score for each peptide is calculated by a neural network algorithm that incorporates the Xcorr, DeltaCn, Sp, RSp, peptide mass, charge state, and the number of matched peptides for the search. The higher the value of the Sf score, the better the peptide match.
XC	Displays the XCorr value for the given scan.
Delta Cn	Displays the Delta Cn value for the given scan.

Sp	Displays the Sp value for the given scan.
RSp	<p>Displays the RSp value for the given scan.</p> <p>The RSp column is displayed by not selecting Unified Score as a filter in the Search Results Options dialog box.</p>
Ions	Displays the number of ions matched for each <i>.dta</i> file.
Count	Displays the number of duplicate entries found for each <i>.dta</i> file. If a number is reported in this column, then it does not include the initial reporting of the sequence.
Peak Area or Peak Height	<p>Displays the peak area or the peak height of the protein, depending on which option you selected when performing the peak area/height calculation.</p> <p>This value is calculated by reading the MH⁺ value from the <i>.dta</i> file and calculating the precursor mass. A reconstructed ion chromatogram (RIC) is generated using the precursor mass, is smoothed, and the integrated height of the peaks are calculated.</p> <p>Displays only if you have set the parameters in the Protein Area/Height Calculation dialog box, which you access by choosing Actions > Protein Area/Height Calculation.</p>
TIC	Displays the TIC for the peptide. To display this column, right-click in the results table and choose Display > TIC Value from the shortcut menu.