Supplemental Table 1

Protein/Peptide	**Scaffold Probability**	**SEQUEST Xcorr**	**Mascot Expect**
Hsp90, beta	**100%**		
ADLINNLGTIAK	95%	4.83	6.1 x 10^{-4}
ALLFIPR	95%	1.98	1.8
DLVVLLFETALLSSGFSLEDPQTHSNR	95%	-----	4.4 x 10^{-2}
EDQTEYLEER	95%	3.31	5.3 x 10^{-2}
EGLELPEDEEEK	95%	2.27	5.0 x 10^{-2}
EGLELPEDEEEKK	95%	3.01	1.4 x 10^{-1}
EGLELPEDEEEKKK	95%	3.22	6.8 x 10^{-3}
ELISNASDALDK	95%	3.91	8.0 x 10^{-6}
FYEAFSK	95%	2.28	2.9 x 10^{-2}
GFEVVYMTEPIDEYCVQQLK	95%	-----	1.7 x 10^{-1}
HFSVEGQLEFR	95%	3.36	5.1 x 10^{-3}
HLEINPDHPIVETLR	95%	-----	9.6 x 10^{-5}
HNDDEQYAWESSAGGSFTVR	95%	-----	3.0 x 10^{-4}
HSQFIGYPITLYLEK	95%	-----	3.1 x 10^{-4}
IDIIPNPQER	95%	2.61	2.0 x 10^{-3}
KHLEINPDHPIVETLR	95%	-----	5.6 x 10^{-2}
KHSQFIGYPITLYLEK	95%	-----	1.2 x 10^{-1}
LGIHEDSTNR	95%	2.68	5.0 x 10^{-1}
RAPFDLFENK	95%	3.58	2.7 x 10^{-3}
RAPFDLFENKK	95%	3.26	2.0 x 10^{-3}
SIYYITGESK	95%	3.52	1.5 x 10^{-3}
SLTNDWEDHLAVK	95%	3.7	2.7 x 10^{-1}
TLTLVDTGIGMTK	95%	3.83	5.2 x 10^{-4}
VILHLKEDQTEYLEER	95%	-----	8.8 x 10^{-1}
YESLTDPSK	95%	2.51	4.6 x 10^{-2}
YESLTDPSKLDSGK	95%	3.45	1.4 x 10^{-1}
YHTSQSGDEMTSLSEYVSR	95%	-----	2.9 x 10^{-2}
YIDQEELNK	95%	3.06	6.4 x 10^{-5}
Hsp70 protein 8, isoform 1	**100%**		
DAGTIAGLNVLR	95%	3.53	9.6 x 10-5
GPAVGIDLGTTYSCVGVFQHGK	95%	-----	3.0 x 10-4
HWPFMVVNDAGRPK	95%	3.02	1.1
IINEPTAAAIAYGLDK	95%	-----	1.7 x 10-4
IINEPTAAAIAYGLDKK	95%	-----	5.0 x 10-2
MKEIAEAYLGK	95%	2.78	6.4 x 10-3
MVNHFIAEFK	95%	3.14	6.3 x 10-3
NQVAMNPTNTVFDAK	95%	-----	1.7 x 10-4
NSLESYAFNMK	95%	3.33	6.8 x 10-4
QTQTFTTYSDNQPGVLIQVYEGER	95%	-----	3.4 x 10-1
SINPDEAVAYGAAVQAAILSGDK	95%	-----	6.2 x 10-7
SQIHDIVLVGGSTR	95%	4.71	9.4 x 10-4
STAGDTHLGGEDFDNR	95%	-----	1.2 x 10-3
TTPSYVAFTDTER	95%	3.14	5.3 x 10-4
TVTNAVVTVPAYFNDSQR	95%	-----	5.2 x 10-4
Hsp70 protein 1B	**100%**		
AQIHDLVLVGGSTR	95%	4.34	3.3 x 10-4
ATAGDTHLGGEDFDNR	95%	-----	1.7 x 10-2
DAGVIAGLNVLR	95%	3.58	2.0 x 10-6
IINEPTAAAIAYGLDR	95%	-----	8.2 x 10-5
NQVALNPQNTVFDAK	95%	-----	4.5 x 10-1
SINPDEAVAYGAAVQAAILMGDK	95%	-----	9.9 x 10-5
TTPSYVAFTDTER	95%	3.14	5.3 x 10-4
Hsp70 protein 9 precursor	**100%**		
AQFEGIVTDLIR	95%	4.14	1.3 x 10-3
DAGQISGLNVLR	95%	3.54	5.9 x 10-4
SDIGEVILVGGMTR	95%	2.68	1.3 x 10-1
STNGDTFLGGEDFDQALLR	95%	-----	7.8 x 10-4
TTPSVVAFTADGER	95%	2.47	2.5 x 10-1
VINEPTAAALAYGLDK	95%	-----	2.5 x 10-4
Survivin	**100%**		
AIEQLAAMD	95%	1.04	99
ELEGWEPDDDPIEEHKK	95%	-----	0.048
MAEAGFIHCPTENEPDLAQCFFCFK	95%	-----	0.046
NWPFLEGCACTPER	95%	3.2	4.8

The Scaffold score for peptides and proteins represents the probability of a correct assignment as calculated by PeptideProphet [24] and ProteinProphet [25], respectively. The PeptideProphet probability represents a consensus of SEQUEST, Mascot, and X!Tandem scores when available for a given peptide. The Sequest Xcorr values of greater than 1.73 and 1.97 for single and double charged peptides, respectively, have been empirically shown to represent a 95% probability of a correct assignment [52]. The expected number of hits for each peptide that will occur by random chance during a Mascot search of the database is shown in the last column.