

Supplement S3: MS-Dictionary based database search for short and long peptides

<i>TotalProbability</i>	IDs(target)	IDs(decoy)	FDR	New Peptides
1e-9	651(4486)	16(27)	0.024	71(62)
1e-10	273(1314)	2(2)	0.007	17(17)
5e-11	191(885)	2(2)	0.010	10(10)
2e-11	149(556)	0(0)	0	8(8)

Table 1: Similar to Table 3 in the manuscript, for peptides of average length 8 (spectra in the parent mass range of 882 to 978 Da). One of the 149 peptides identified at zero error rate matches a “one-hit-wonder” while others match to proteins confirmed by multiple peptides in *Shewanella*.

<i>TotalProbability</i>	IDs(target)	IDs(decoy)	FDR	New Peptides
1e-9	444(4544)	0(0)	0	17(17)
1e-10	444(4544)	0(0)	0	17(17)
5e-11	444(4544)	0(0)	0	17(17)
2e-11	444(4544)	0(0)	0	17(17)

Table 2: Similar to Table 3 in the manuscript, for peptides of average length 14 (spectra in the parent mass range of 1447 to 1656 Da). The numbers of identifications are same for all values of *TotalProbability* considered here since for this length, the number of reconstructions exceeds the limit of 100,000 allowed per spectrum. Of the 444 peptides identified, 4 peptides mapped to proteins that did not have any InsPecT identifications.