

Peptide-to-spectrum match (PSM) database	Total proteins	Total unique peptides	Total spectra matched	Decoy FDR <sup>a</sup> percent (peptide level)
(1) <i>Phaeocystis</i> strains transcriptomes <sup>b</sup>	1545 (912)	3816 (2103)	14 088 (8226)	0.6 (0.17)
(2) Ross Sea metatranscriptome <sup>c</sup>	1474 (859)	3210 (1520)	10 154 (4725)	0.1 (0.7)
(3) Antarctic bacterial metagenomes <sup>d</sup>	102 (92)	237 (186)	530 (440)	3.6 (2.3)