



## **Metaproteome of the viral concentrates from the deep chlorophyll maximum of the South China Sea**

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Viral concentrates (VCs) have been commonly used for studying viral diversity, viral metagenomics and virus-host interactions in the natural ecosystem. However, the protein characteristics of VCs have not been explored. Here, we applied shotgun proteomics to characterize the proteins of VCs collected from the oligotrophic deep chlorophyll maximum of the South China Sea. We found that 34% of the identified proteins were assigned to the viruses, mainly being those of SAR11 related bacteria, cyanobacteria and picophytoeukaryotes. The remaining 66% were non-viral proteins mostly originating from diverse bacteria, such as SAR324, SAR11 and the Alteromonadales, and were functionally dominated by transport, translation, sulfur metabolism and one-carbon metabolism. Among the non-viral proteins, 28% were extracellular proteins and 10% were identified exclusively in the VCs, suggesting that non-viral entities might exist in the VCs. This study demonstrated that metaproteomics provides a valuable avenue to explore not only the diversity and structure of a viral community but also the novel ecological functions affiliated with microbes in the natural environment.