

Table 2. Number of PR molecules in various types of PRP bacteria.

Bacterial taxa	Region	Method	PR per cell	Reference
SAR86	Pacific coast	Spectroscopic	24 000	Béjà and colleagues (2001)
<i>Pelagibacter</i>	Pure culture	Spectroscopic	10 000	Giovannoni and colleagues (2005a)
Bacteria ^a	S. Atlantic	Metaproteomics	2 189	This study
<i>Alphaproteobacteria</i>	S. Atlantic	Metaproteomics	2 728	This study
HTCC2225	S. Atlantic	Metaproteomics	3 393	This study
<i>Pelagibacter</i>	S. Atlantic	Metaproteomics	337	This study
<i>Bacteroidetes</i>	S. Atlantic	Metaproteomics	576	This study
<i>Polaribacter</i>	S. Atlantic	Metaproteomics	11 434	This study
		Average of Metaproteomics	3 443	

a. Protein fragments for Bacteria, *Alphaproteobacteria* and *Bacteroidetes* could be not classified at a finer taxonomic level. For the metaproteomic-based estimates, we used data from Morris and colleagues (2010) and assumed that the percentage of PR making up total membrane protein mass for a given taxonomic group was equal to the percentage of PR-derived mass spectra relative to the total number of spectra collected from the membrane fraction. This percentage was converted to numbers of PR molecules by assuming 13 fg protein cell⁻¹ with 28% of that protein as membrane protein and an average mass per PR monomer of 26 953 g mol⁻¹.