

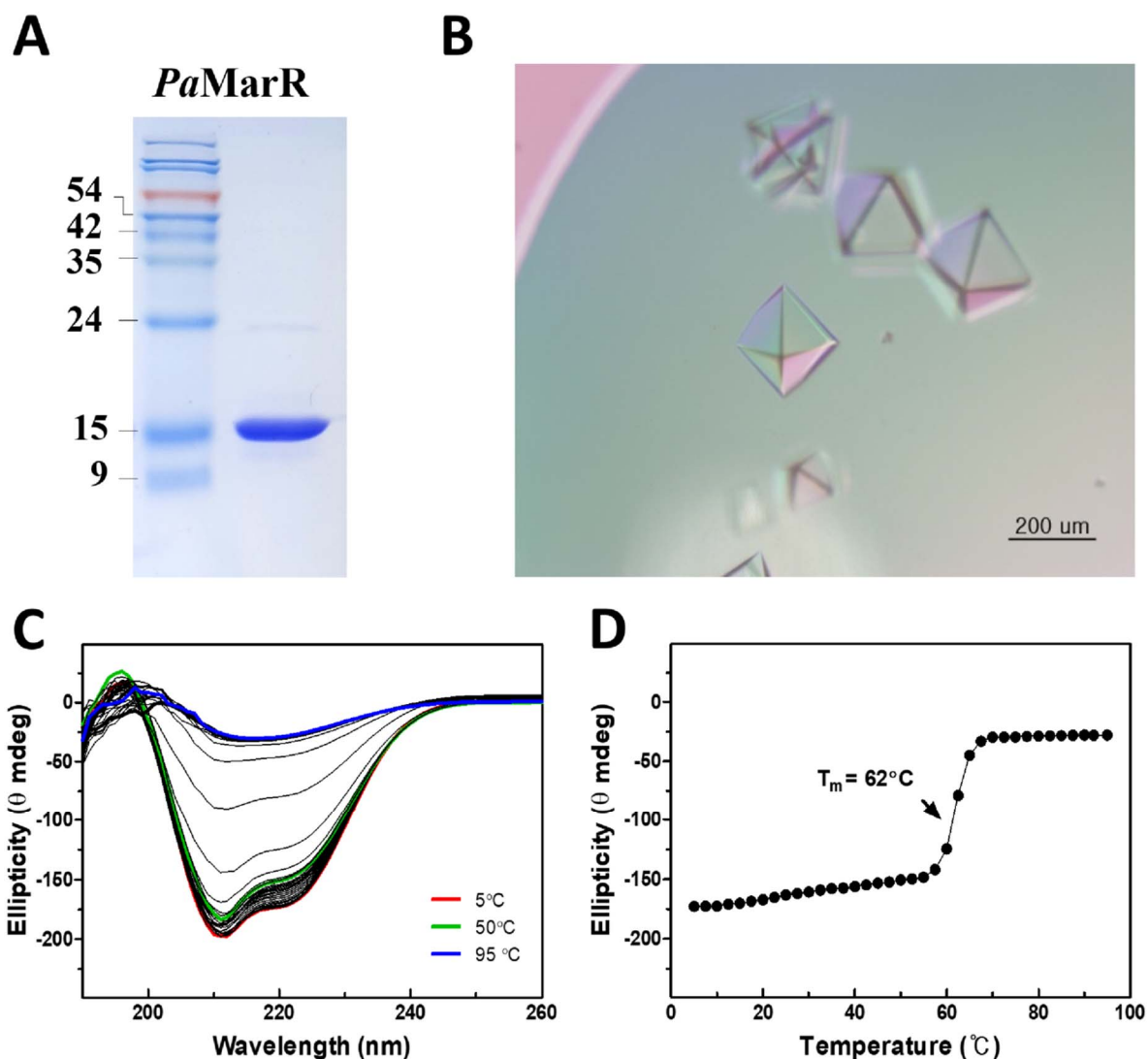
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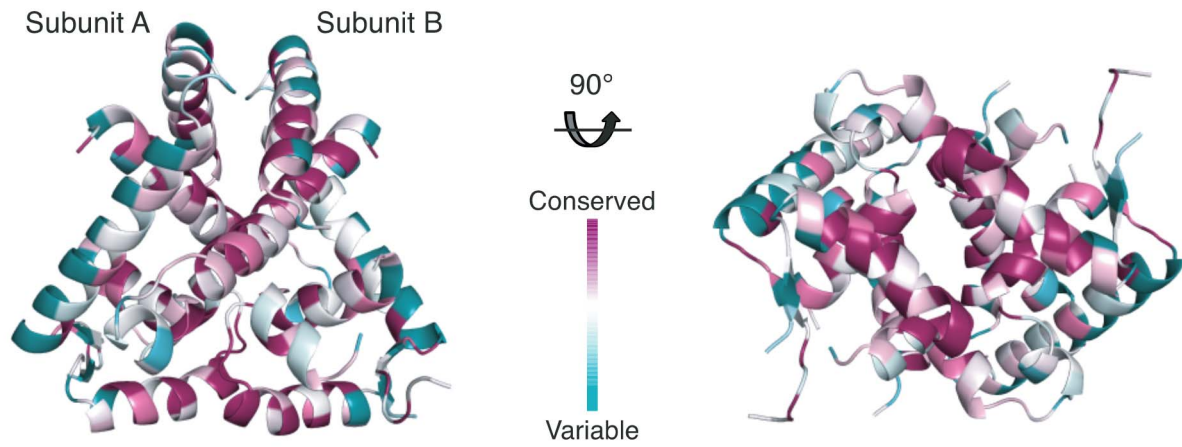
Supporting information for article:

Crystal structure of a MarR family protein from the psychrophilic bacterium *Paenisporosarcina* sp. TG-14 in complex with a lipid-like molecule

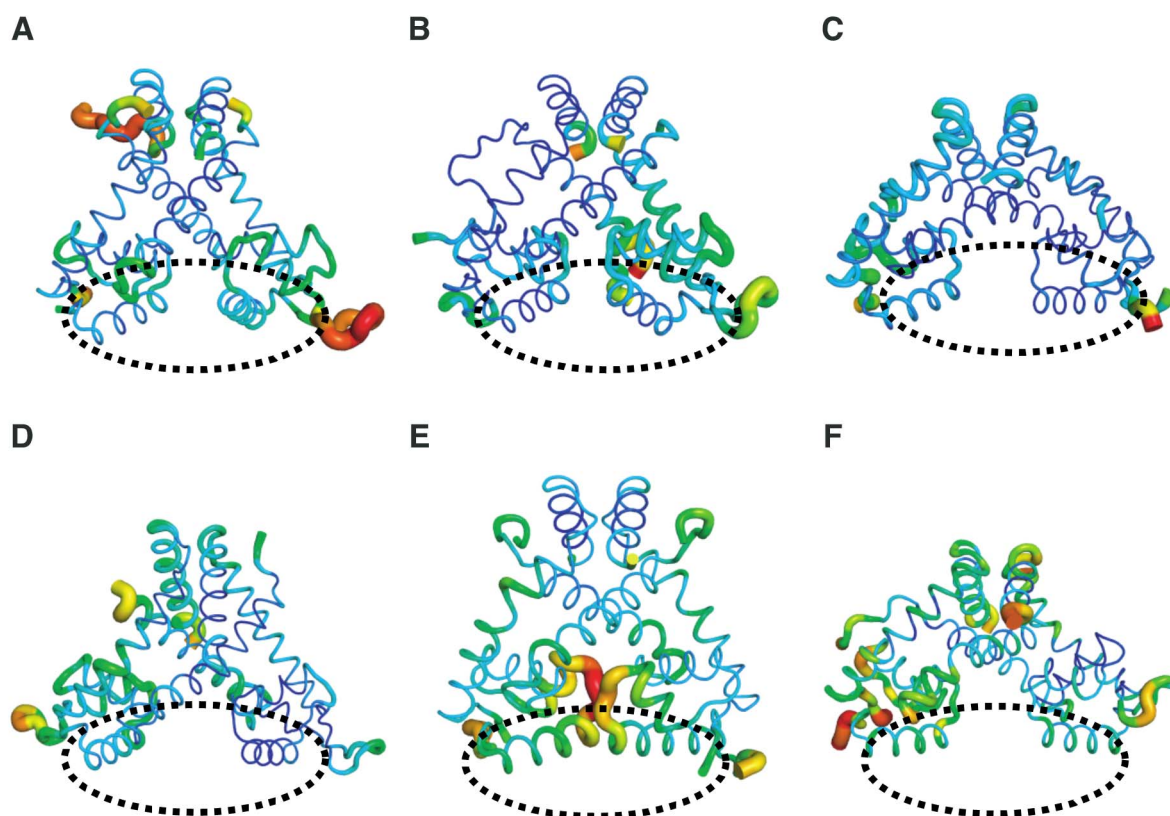
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**Figure S1** Recombinant *PaMarR* protein purification, crystallization, and CD analysis. (A) Purified *PaMarR* protein was loaded and visualized using 12% SDS-PAGE (B) Octahedron shaped crystals of *PaMarR* used for X-ray diffraction data collection. (C) CD spectrum of *PaMarR*, as analysed in the 190~260 nm UV range. The structural denaturation profile of *PaMarR* was monitored at 5, 50, and 95 $^{\circ}\text{C}$ . (D) Thermal denaturation curve of *PaMarR*, as measured at 220 nm. The  $T_m$  value is identified as 62 $^{\circ}\text{C}$ .



**Figure S2** Evolutionary conservation in the structure of *PaMarR*. The dimeric structure is coloured by the degree of sequence conservation, and viewed in two different orientations.



**Figure S3** *B*-factor analysis of MarR family proteins from mesophiles. Six proteins shown in Table 2 are depicted in putty representation; MexR from *Pseudomonas aeruginosa* (A), MexR R21W derepressor mutant from *Pseudomonas aeruginosa* (B), CouR from *Rhodopseudomonas palustris* (C), FabT from *Streptococcus pneumoniae* (D), MarR from *Escherichia coli* K-12 (E), NadR from *Neisseria meningitidis* (F). The dashed ellipses indicate the DNA-binding domain.

**Table S1** DNA sequences of the double-stranded probes used for EMSA.

Palindrome probe
TTTTAATAGTTCACCCCCTAAACTAACGTTATTGGTTTAGGGGGTGAAC TATTATGCCCCCATA ATAGTTCACCCCCTAAACCAATAACGTTAGTTTAGGGGGTGAAC TATTA AAA
Non-specific palindrome probe
TGTCACTAATGCACTCCATAGACGACCATCAGTAGTCTAGTAGATTAGATAGTCTACCCCCTAG ACTATCTAATCTACTAGACTACTGATGGTCGTCTATGGAGTGCATTAGTGACA