



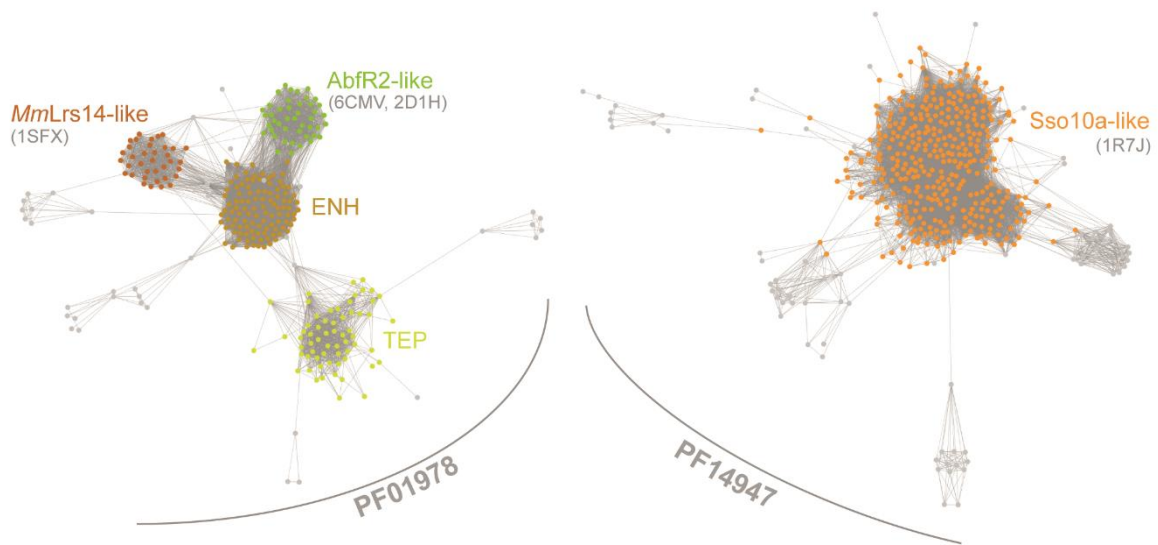
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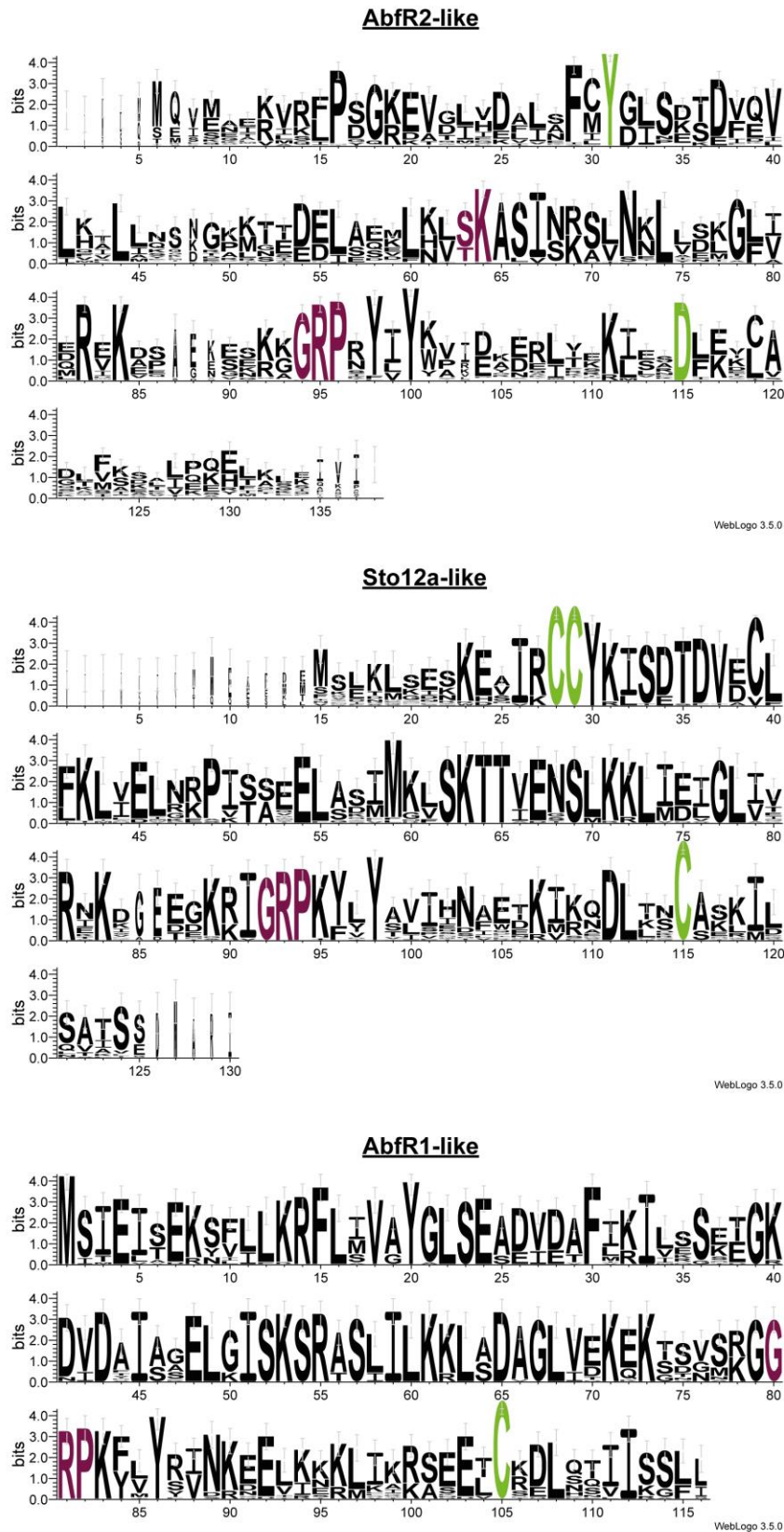
**Supporting information for article:**

**Crystal structure of an Lrs14-like archaeal biofilm regulator from  
*Sulfolobus acidocaldarius***

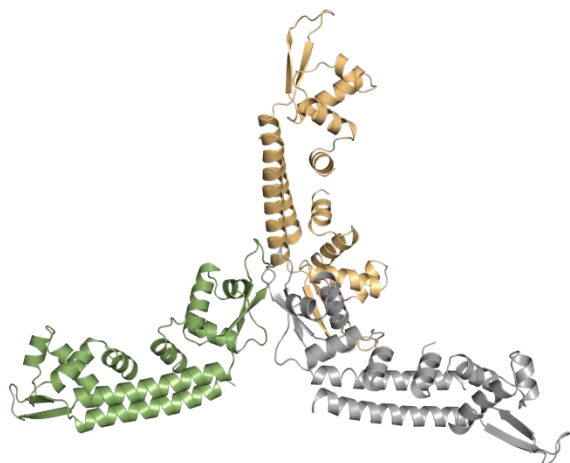
**Marian S. Vogt, Simon L. Völpel, Sonja-Verena Albers, Lars-Oliver Essen and  
Ankan Banerjee**



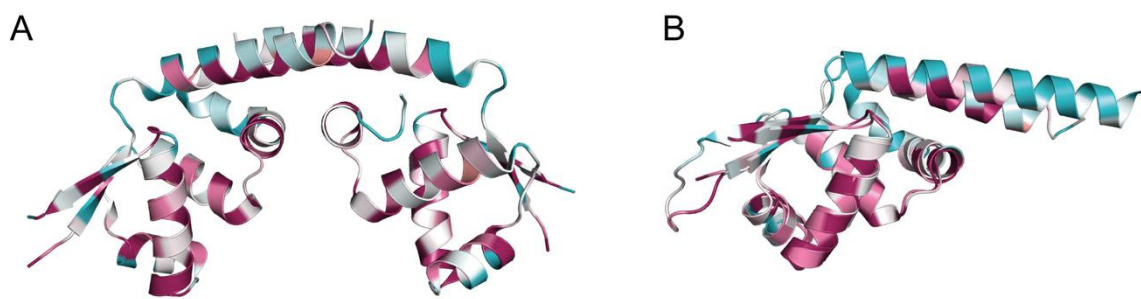
**Figure S1** Sequence similarity network of TrmB (PF01978) and related Lrp protein Sso10a-like (PF14947) proteins analyzed using EFI-EST (Gerlt *et al.*, 2015) and represented using Cytoscape (Cline *et al.*, 2007). Although these protein families shared structural similarities, they formed separate clusters with no evolutionary connections in the network analysis.



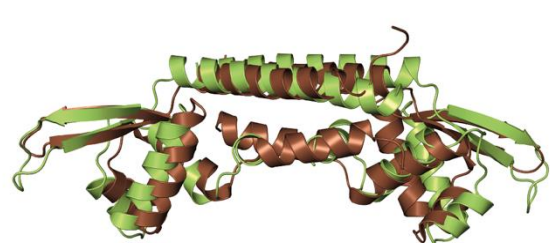
**Figure S2** Conserved residues in AbfR1, AbfR2 and Sto12a-like protein clusters obtained from EFI-EST sequence similarity network, represented using WEBLOGO.



**Figure S3** Three independent AbfR2 dimers were identified per asymmetric unit (ASU).



**Figure S4** (A) CONSURF analysis of Sto12a (2D1H). (B) Alignment of Sto12a and AbfR2 monomer in consurf generated colour scheme. The conservation scheme for both of the protein are comparable, where the H4 helix is the least conserved and DNA binding H3 helix is the most conserved.



**Figure S5** Superposition of AbfR2 (green) and structurally related Lrs14-like protein from *A. fulgidus* (1SFX, brown).