

Table S2. (Putative) binding motifs in the sequences bound by Ss-LrpB *in vivo* and *in vitro*. Predictions of recognized binding motifs were performed using the binding energy based position weight matrix (Peeters *et al.* 2007) (indicated by “binding energy”), MEME (indicated by “MEME”) or were confirmed by experimental observations (indicated by “footprinting”) (Fig. 4). In case of different predictions by the binding energy based position weight matrix and MEME, multiple fragments were tested for binding to avoid missing a binding motif. Binding affinities (expressed as K_D) are theoretical and predicted using the binding energy based position weight matrix.

Target name	Binding motif sequence	Prediction/identification of binding motif	K_D (μ M)
<i>Sso118</i>	5'-CAGTAATTATTATAA-3'	binding energy	290
<i>Sso1027</i>	5'-TTTCAAAATGTTAAA-3'	MEME	43538
<i>Sso1135</i>	5'-TTGTCACCTATTCCTT-3'	MEME	585
<i>Sso1272</i>	5'-TTGCCAGAAATGCAA-3'	binding energy	6
<i>Sso1371</i>	5'-ATGGAAAGCTTACAT-3'	binding energy	237
<i>Sso1389</i>	5'-TTGTAATTAATTTAA-3'	footprinting	137
<i>Sso1433</i>	5'-TTGCATATAATTCCG-3'	binding energy	56
<i>CRISPR4</i>	5'-TTGTAATTAATTTAA-3'	footprinting	137
<i>Sso2133</i>	5'-TCGCCCATTTTACAA-3'	binding energy	40
<i>Sso2233</i>	5'-ATGATGAAATTTCTA-3'	MEME	884
<i>Sso2801</i>	5'-TAGCAAATGTTCCAA-3'	binding energy	3
<i>Sso3072</i>	5'-TTGCCATTTTCCAA-3'	binding energy	5

Reference

Peeters E, Wartel C, Maes D, Charlier D: **Analysis of the DNA-binding sequence specificity of the archaeal transcriptional regulator Ss-LrpB from *Sulfolobus solfataricus* by systematic mutagenesis and high resolution contact probing.** *Nucleic Acids Res* 2007, **35**:623–633.