

**P018** Global targets search for the DNA-binding protein gp08 from the hyperthermophilic archaeal virus SIRV1  
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Study of viral coded transcriptional regulator could help to better understand virus/host interaction. In the case of the archaeal viruses, structural approaches together with *in silico* predictions could be an attractive way to identify new viral regulators. We focused on protein gp08 from the rod-shaped hyperthermophilic archaeal virus SIRV1, infecting *Sulfolobus islandicus* that thrives in hot acidic springs (85°C, pH 1-2). *In silico* data (Prangishvili *et al*, *Virus Res.* 117; 2006) suggested that gp08 is involved in transcription regulation. We have now reinforced this hypothesis by the NMR structure and the DNA induced conformational changes presented here. To detect all gp08 DNA binding sites present in the 32,3 kb SIRV1 genome, we design a global screening system based on a simplified EMSA protocol. In these assays, the SIRV1 genome was represented by 25 small PCR amplified DNA fragments and their mobility was analysed in the presence of gp08 in a standard agarose gel. Four targets that include the promoter regions of gp02/gp44, gp08 and gp30 genes were recognized by the protein. The strongest binding was seen with the gp30 gene (a virion structural protein) promoter.