

**P043** CRISPR in *Thermoproteus tenax*: functional analysis of *cas* genes

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Clustered regularly interspaced short palindromic repeats (CRISPR) are a novel class of direct repeats found in nearly all archaeal and some bacterial genomes. They consist of nearly-exact repeat sequences of 24 to 48 nt, separated by unique slightly longer spacers. These clusters are accompanied by a variety of *cas* (CRISPR-associated) genes, classified in more than 40 different gene families. The encoded Cas proteins are thought to be involved in propagation and function of CRISPR. It has been suggested, that CRISPR, together with the *cas* genes, provided resistance against phages, whereas the specificity is determined by sequence similarity between spacer and phage. The underlying molecular mechanisms remained unknown yet. To get a closer insight into the functional impact of CRISPR in Archaea the seven CRISPR clusters (TTX\_1-7) and the *cas* genes 1 to 4 of the hyperthermophilic Crenarchaeote *Thermoproteus tenax*, were subject to detailed analysis. Homologues of *cas* genes 1 to 4 are found in a variety of prokaryotes and are assumed to play an important role in the resistance mechanism. Homology searches account for the presence of e.g. RecB-family nuclease, DEAD-box helicase and regulator protein of DevR family. The relevant genes located between CRISPR TTX\_5 and 6 (ORF TTX1245-1254) were heterologously expressed in *E. coli*, purified and the function of the encoded proteins analysed.