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Archaeal Diversity Sequencing Project: Preliminary Results

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Several orders of Archaea are not yet represented by genome sequences. The Department of Energy's Joint Genome Institute is sequencing six diverse Archaea in order to remedy this problem. Three are methanogens, two from the order Methanomicrobiales and one from Methanobacteriales, and one is a psychrotolerant halophile. Two are Crenarchaeotes, one from the order Thermoproteales and one from Desulfurococcales. Preliminary sequence data are available for *Thermofilum pendens*. The genome of approximately 1.85 Mbp is in 8 contigs and is currently in finishing. Preliminary analysis shows that this organism apparently lacks the ability to synthesize almost all of the standard amino acids. While *T. pendens* does grow on proteinaceous substrates, the lack of amino acid synthesis is surprising as it does not grow in nutrient-rich environments. *T. pendens* has a genome size similar to other Crenarchaeota suggesting that genome reduction is not a driving force in the loss of amino acid biosynthetic genes.