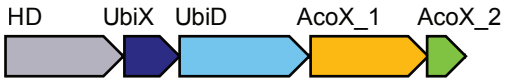
Methanonatronarchaeia, Euryarchaea

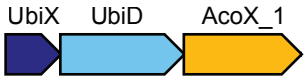
Methanonatronarchaeum thermophilum strain AMET1, MRZU01000003, 82704..78029

Candidatus Methanohalarchaeum thermophilum isolate HMET1, MSDW01000001 1612290..1607688

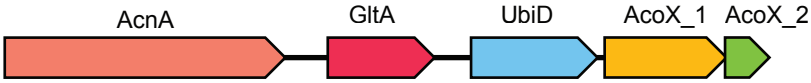


Euryarchaea

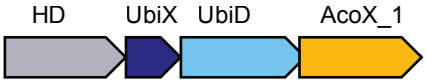
Methanoregula boonei 6A8, NC_009712, 110616..113576



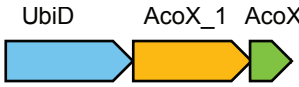
Methanosarcina barkeri Fusaro, NC_007355, 857778..865412



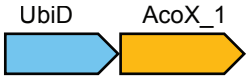
Methanoculleus bourgensis MS2, NC_018227, 1386054..1381888



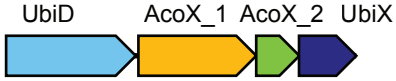
Methanosalsum zhilinae DSM 4017, NC_015676, 1658160..1655301



Archaeoglobus veneficus SNP6, NC_015320, 535436..533048

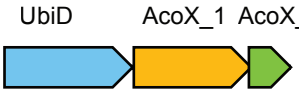


Halorhabdus tiamatea SARL4B, NC_021921, 366631..363130

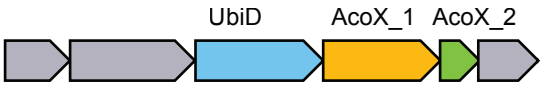


Crenarchaea

Ignisphaera aggregans DSM 17230, NC_014471, 1826877..1824014



Staphylothermus marinus F1, NC_009033, 635314..640645



Pyrobaculum aerophilum IM2 NC_003364 1318103..1320870

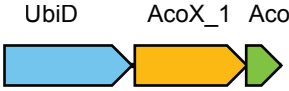


Figure S1: UbiD co-localization with predicted archaeal aconitase AcoX.

For each locus, species name, genome accession number and the respective nucleotide coordinates are indicated.
The genes are shown by arrows. The scale of an arrow is roughly proportional to gene length.
The arrow indicates direction of the respective gene. Homologous genes and domains are color-coded.
Abbreviations and gene names: UbiX and UbiD – decarboxylase system components;
AcoX_1 – predicted aconitase, enzymatic subunit; AcoX_2 – AcoX_1 associated swivelling domain;
AcoA – aconitase A; GltA – citrate synthase; HD – HD family hydrolase.