Project thoughts:

-Main goal is to use a fast-growing methanogen with developed genetic tools, *M. maripaludis S2*, as a host for an engineered pathway to produce methanol from methane through anaerobic biosynthesis.

-*M. maripaludis S2* is a hydrogenotrophic methanogen that must necessarily produce methane to achieve growth.

Short and sweet version:

*Methanococcus maripaludis S2* is a methanogenic archaeon notable for its fast doubling time and well-developed set of genetic tools. We have constructed a genome-scale metabolic reconstruction and computable model of *M. maripaludis S2*

We also care more about the overall project goal…what is that?

\*\*We want to create a process to efficiently biosynthesize methanol, a liquid fuel, from methane, a potent greenhouse gas. We already know of archaea that anaerobically oxidize methane, but these methanotrophic archaea are poorly understood, slow-growing, and do not have a well-developed set of genetic tools. By contrast, *Methanoccocus maripaludis S2*  is a model methanogenic archaeon notable for its fast doubling time and well-developed set of genetic tools.

Motivation: We want to develop a sustainable, efficient process to convert methane, a potent greenhouse gas, into methanol, a liquid fuel source.

Problem statement: For this conversion, we will metabolically engineer *Methanococcus maripaludis S2,* a methanogenic archaea than ordinarily produces methane to achieve growth, to function in reverse by inserting novel reaction pathways from methanotrophic organisms. To ensure that enzymes in the engineered strain operate at high efficiency, we have constructed a genome scale metabolic model of *M. maripaludis S2* that allows us to predict experimental outcomes of our engineering efforts. This model accounts for 477 of the 1722 protein-coding genes (%) in the *M. maripaludis* genome and is the first metabolic model to accurately depict the Wolfe cycle, the central catabolic pathway in hydrogenotrophic methanogens.

First sentence: we want to make methanol from methane

Second sentence: we will use THIS organism that naturally makes methane by turning its metabolism in reverse

Third: to aid in our engineering, we have built a model to help us make predictions

Fourth: the model consists of X genes and X reactions, covering X % of the ORFs and is the first model of this organism that contains an accurate depiction of the Wolfe cycle, the central catabolic pathway for producing methane.

Fifth: first model that explicitly uses the likelihood-based gapfilling algorithm in conjunction with the reconstruction tools on Kbase.

Last: Using flux balance analysis, we’ll generate quantitative and qualitative hypotheses for how to engineer in pathways for sulfate reduction that can couple to methanol production to make the process energetically viable

Other considerations:

\*\*\*\*Also need relevant activities

In the box below, please indicate your particular activities which justify favorable consideration of you as a participant and contributor to this meeting.   
This information is important, as it allows the Scientific Organizers to make a thorough assessment when reviewing and selecting participants (max. 1700 characters).

Blah blah blah

What actually goes here?

Science communication and outreach in addition to the main stuff. And the ProbAnno morphing also, that’s important.