

ATTACHMENT 1  
GRANT OUTCOMES, PAYMENTS & REQUIREMENTS PLAN (#3300)

<b>OUTCOME TABLE</b>						
<b>Due Date</b>	<b>Act/ Ind</b>	<b>Description</b>	<b>Linked to Requirement</b>	<b>Contingent on Payment #</b>	<b>% Complete</b>	<b>Progress Report</b>
6/15/15		<b>OUTCOME 1: Predictive models of the global distributions of marine microbes at both the taxonomic level (e.g., genera and operational taxonomic units) and the functional level (e.g., protein families and their functions) are developed.</b>				
		<b>Output 1.1: Define protein families from sequenced genomes, catalog existing metagenomic data, and develop geographic distribution models.</b>				
6/15/13	<b>1.1.1</b>	Catalog protein families. Compare these with other protein family databases (e.g., Pfam).				
6/15/13	<b>1.1.2</b>	Develop models for protein family geographic distributions with statistical techniques such as niche modeling.				
6/15/13	<b>1.1.3</b>	Identify, process, and assess usefulness of current data sets (public or available through MMI collaborations) for making niche maps.				
		<b>Output 1.2: Develop methods to classify metagenomic data into protein families, to update families with new genome data, and to model the environmental niches of families.</b>				
6/15/14	<b>1.2.1</b>	Design and validate a novel, fully automated method to classify metagenomic sequence reads into protein families.				
6/15/14	<b>1.2.2</b>	Develop methods for updating protein families as new genomes are sequenced.				
6/15/14	<b>1.2.3</b>	Design methods to estimate taxon and protein family ranges in environmental niche space, defined by biogeochemical data.				
6/15/14	<b>1.2.4</b>	Evaluate what models (e.g., from Activities 1.1.2 and 1.2.3) are appropriate for existing data. Determine if sufficient metagenomic data exists for accurate modeling.				
		<b>Output 1.3: Phylogenetically and functionally annotate protein families, generate niche maps, and analyze maps to characterize global diversity.</b>				
6/15/15	<b>1.3.1</b>	Develop metrics to quantify protein distributions and diversity from metagenomic data.				
6/15/15	<b>1.3.2</b>	Design bioinformatics tools for mapping known protein functions onto classified metagenomic sequence reads.				
6/15/15	<b>1.3.3</b>	Implement algorithms for drawing environmental and geographic niche maps.				
6/15/15	<b>1.3.4</b>	Given sufficient metagenomic data, apply tools developed to characterize protein families and predict niches to publicly available marine microbial data. Else, apply tools for taxon niche modeling only.				
6/15/15	<b>1.3.5</b>	Given sufficient metagenomic data, compare functional and taxonomic diversity maps to elucidate patterns of selection and convergence; identify diversity hot spots; and propose testable hypotheses about the roles of microbial functions in marine ecosystems. Else, make recommendations about future sampling needed in order to perform niche modeling.				