



Figure S4 Initial and final path models obtained with structural equation modeling. In the final model (E→A) the path is directed from enzyme activities to ARISA and in final model (A→E) the direction of the path is reversed. The tables show the significance value for the Chi-square test, assessing whether the model is significantly different from a correlation matrix of the data based on the RV coefficient. The goodness-of-fit index and Bentler CFI (Comparative Fit Index) indicate the goodness of fit of the model, the best fit would result in a value of 1. The BIC (Bayesian Information Criterion) is another measure of the goodness of fit and needs to be minimized. The coefficient of non-determination (ND = 1-R²) determines the fraction of the variance in bacterial community structure and enzyme activity that is not explained by the model.