Biofilm infections on indwelling biomedical devices are the leading cause of hospital infections around the world. The most common are catheter-associated infections caused by *Escherichia coli* and *Staphylococcus aureus*. Prevention and treatment of these infections typically rely on broad-spectrum antibiotics, yet these strategies often promote antibiotic resistance and are not fully effective. Elucidating the genetic elements responsible for biofilm formation on biomaterials and antibiotic resistance of such biofilms could be used for the rational design of targeted antibiofouling and antimicrobial agents that prevent and treat infections on biomedical device surfaces. In this work, we aim to systematically map the genomes of *E. coli* and *S. aureus* to identify genes associated with biofilm formation and antibiotic resistance and quantify their fitness using a multiplexed, high-throughput approach. In this approach, we design comprehensive genome-wide CRISPR interference (CRISPRi) gene repression libraries for *E. coli* and *S. aureus* and apply pooled selections on a platform of biomaterials (PEG and PDMS gels) that systematically vary in their physicochemical properties to uncover gene expression associated with bacterial attachment to various surfaces and increased antibiotic resistance of attached bacteria. We have developed and characterized CRISPRi tools in *E. coli* MG1655 using three CRISPRi systems to determine their design rules and appropriate expression levels of each component to limit cellular toxicity. Repression of native genes, including genes associated with biofilm formation, was also tested and quantified using fluorescent protein fusions. Using the determined design rules and custom Python scripts, we have designed genome-wide CRISPRi libraries (>40,000 designs each) for each CRISPRi system to target nearly every annotated gene in the *E. coli* genome (95.9%–99.1%). For *S. aureus*, very few synthetic DNA parts have been characterized and reported in the literature. Here, we created and report what we believe to be the first characterized genetic part toolbox for *S. aureus*, including promoters, ribosome binding sites, terminators, and plasmid origins of replication. We then used the genetic toolbox to rationally design CRISPRi tools for *S. aureus*. These genome-wide CRISPRi tools can be applied to study relationships between observed behavior and gene expression under different conditions and can be developed for any organism with an annotated genome that can be genetically manipulated.
The sustainable production of numerous chemicals from biomass resources provides a renewable and alternative to existing production routes from fossil fuels. Although new biomass upgrading technologies have been developed, the inherently higher water content of biomass remains a technical challenge that needs to be addressed, particularly when designing catalytic upgrading strategies. Reactions like dehydration, aldol condensation, and pyrolysis that are typically involved in biomass upgrading, involve water as a product, which further exacerbate the technological challenges brought by the presence of water. Moreover, many biomass-derived components are highly non-volatile, requiring the use of a solvent, where water is intuitively used given its abundance in biomass derived feeds. Therefore, it is crucial to develop a fundamental understanding of solvation on biomass upgrading, particularly in the context of commonly employed heterogeneous catalysts that facilitate the chemical upgrading.

Central to many proposed biomass catalytic upgrading strategies is the use of solid acids that catalyze dehydration and carbon-carbon coupling reactions. While it is well recognized that water significantly affects catalytic kinetics over solid acids, the source of such solvation effects on an atomistic scale remains debated. The challenge with elucidating the role of solvents in heterogeneously catalyzed cycles usually arises from the highly non-ideal thermodynamics of the aqueous phase, further complicated by reactions that already involve water as a reactant or product. We therefore present a kinetic investigation of the vapor phase Hofmann elimination of tert-butylamine (TBA) over an aluminosilicate zeolite catalyst (H-ZSM-5) as a model reaction for deciphering the effect of water on solid acid catalysis. The Hofmann elimination offers a purely Brønsted acid catalyzed and water-free chemistry, allowing us to systematically study the effect of a solvent like water in the more thermodynamically ideal vapor phase. Kinetic measurements in the absence of water reveal an E1-like elimination mechanism with tert-butylammonium adsorbate as reaction intermediate. Under controlled water partial pressures, the rate of Hofmann elimination was significantly reduced, the extent of which was unaffected by Al content, and such loss in catalytic activity was found to be reversible upon removal of water. A combination of kinetic measurements, in-situ spectroscopy, and kinetic modeling reveal that water reduces the rate of Hofmann elimination, without competing for adsorption on the catalytically active Brønsted acid sites. Reaction order studies in water implicate only one water molecule per active site for the observed loss in activity, despite the ability of water clusters to form under investigated reaction conditions. Based on the results, we proposed that the formation of a water-TBA cooperative adsorption complex inhibits the catalytic cycle of Hofmann elimination, which was quantitatively examined through microkinetic modeling.