Mycotoxins are ubiquitous fungal secondary metabolites that contaminant certain cereal crops and fruits. Of concern are deoxynivalenol (DON) produced by F. graminearum and patulin (PAT) produced by P. expansum. Mycotoxin carry-over to finished food products compromises food safety as consumption of tainted goods results in gastrointestinal disorders. Current decontamination strategies come with an inevitable trade-off to the nutritional content and quality of the finished food product. Enzymatic detoxification presents an alternative approach to address this issue. Indeed, the screening of several metagenomes has unearthed novel enzymes with the potential for detoxification. However, structure-function studies on these enzymes are scarce and yet a vital step for industrial applications. Such is the case for the enzymes DepA and DepB, two oxidoreductases that epimerize DON to its less toxic isomer, 3-epi-DON. The first enzyme DepA (PQQ-dependent ADH) requires the cofactor PQQ while its partner, DepB is an NADPH dependent aldo-keto reductase. To address the apparent costs associated with this expensive co-factor, I will engineer DepB to utilize the cheaper co-factor, NADH. I have solved a preliminary crystal structure of the DepB apo-enzyme (2.1Å) and will employ bioinformatics methods along with site directed mutagenesis to design mutants that use NADH instead. I will screen potential candidates using binding affinity assays and follow up with steady-state kinetics assays to derive the Michaelis Menton parameters. To date, a PAT degrading enzyme has not been isolated. Therefore, I will screen microbial candidates for patulin biotransformation activity with microbial growth assays followed by protein purification techniques and LC-MS/MS.