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Large serine integrases, a class of site-specific recombinases associated with some bacteriophage, are of great use in bacterial genetic engineering and synthetic biology; they stably and unidirectionally integrate genetic material into a bacterial genome without the requirement of accessory proteins. Of particular interest are serine integrases that allow for site-specific integration into Actinobacteria genomes. Tools like the cloning vector pSET152 (using the φC31 integrase) have revolutionized biotechnology in drug-producing actinomycetes and even found application in human cell lines. Additional phage recombinases are desirable, and to this end we bioinformatically mined the genomes of 17 newly sequenced *Streptomyces* bacteriophage from the Washington University Phage Hunters program, looking for the presence of novel large serine integrases. Three phage carrying large serine integrase genes of interest were identified, and two were selected for *int* and *attP* cloning from phage lysate. Recombinant plasmids carrying these genes were tested for integration ability on a range of *Streptomyces* hosts. Early results indicate that an *OzzyJ* phage integrase can integrate into a number of streptomycete genomes, allowing us to design a novel integration vector, pJMD9. Current experiments are determining the *attB* site in cognate hosts. We anticipate that pJMD9 will become another valuable tool for engineering *Streptomyces* genomes.