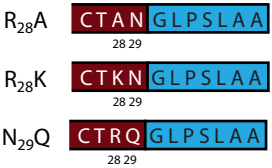
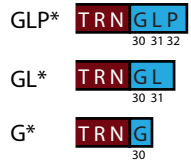
1. Ntr P2 P1

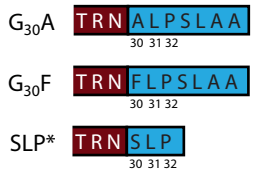
2. Cyclotide P2 P1



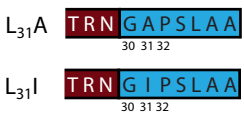
3. Ctr truncation



4. Ctr P1′ mutants

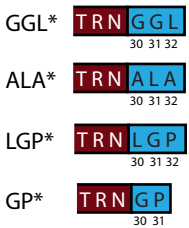


5. Ctr P2′ mutants

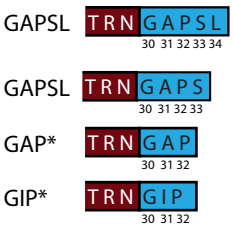


6. Ctr P3′ mutant

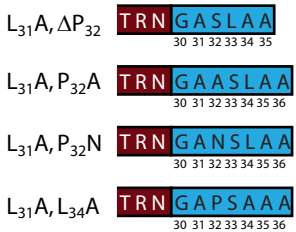
7. Ctr shuffling



8. L31 Ctr truncation



9. L31A mutants



Supp Fig 2: Oak1 mutants constructed for evaluation of the residues required for enzymatic cyclization. 1) mutants with changes in the Ntr. 2) mutants with changes within the cyclotide domain. 3) truncation mutants of the Ctr to determine the minimum number of amino acids for cyclization. 4) mutants of the P1′ position of the Ctr. 5) mutants of the P2′ position of the Ctr. 6) mutant of the P3′ position of the Ctr. 7) shuffling of the Ctr. 8) truncation mutants of the Ctr containing a substitution at position L31. 9) Double mutants containing the L31A substitution and additional substitutions within the Ctr