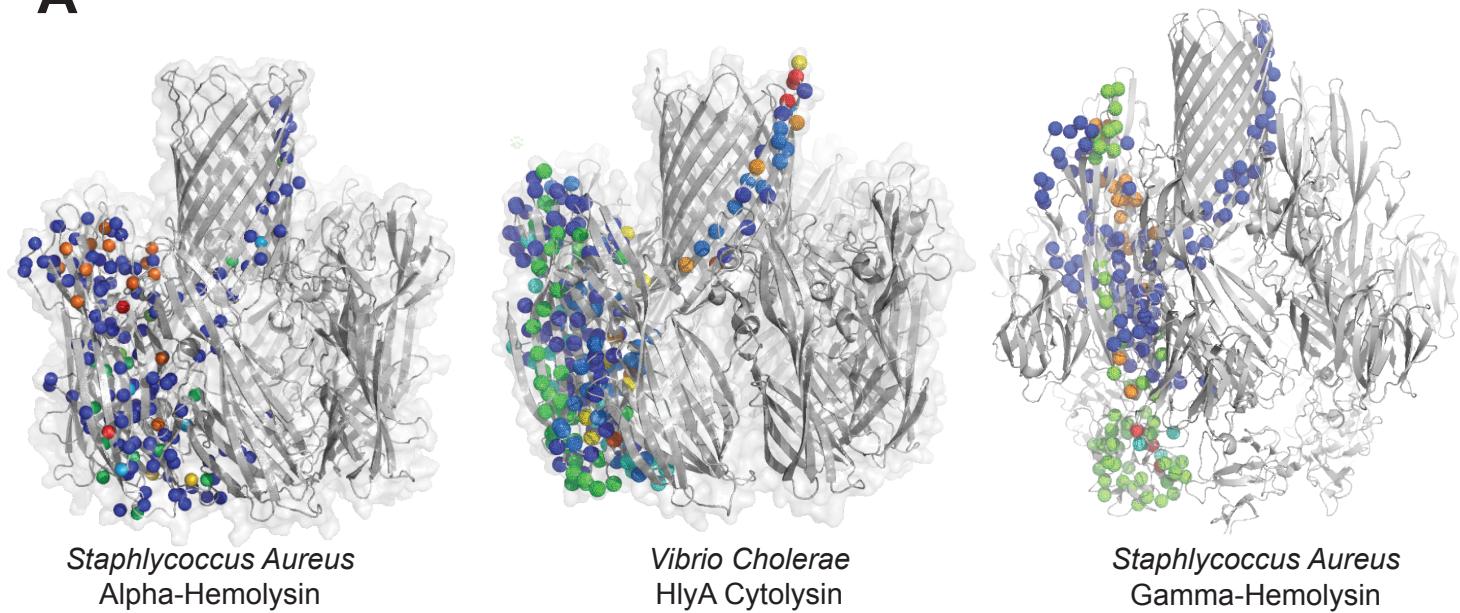
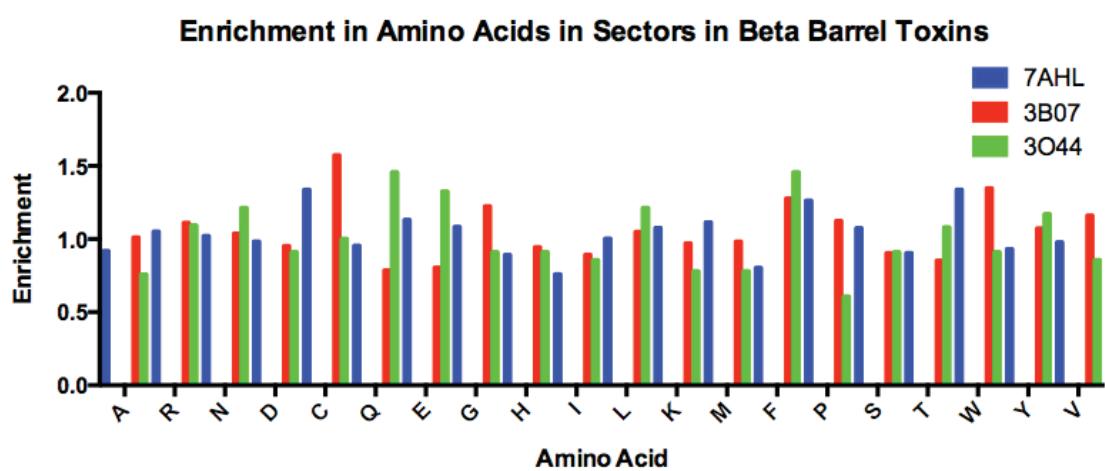
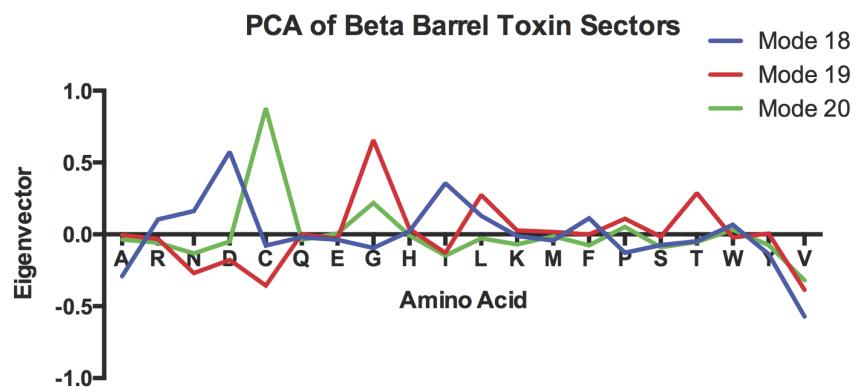


**A****B****C**

**Figure x. Sectors in ‘Beta-Barrel Pore Forming Toxins’ have similar structure.** **A** Mapped sectors co-evolving sectors on Beta-Barrel Pore Forming Toxins. Similarly colored spheres represent the spatial coordinates of the amino acids within a single sector. PDB IDs from left: 7HAL, 3B07, 3O44. **B** Amino acid enrichment of all sectors in beta barrel toxins. There is enrichment in differential residues in the different proteins. There is an increase in Phe in all of the sectors across these toxins. **C** Residue principle components analysis was performed on all beta barrel toxins in the membrane SDB. Mode 20 accounts for 19 percent of the variance, mode 19 accounts for 14.5 percent of the variance, and mode 18 accounts for 11.3 percent of the data.