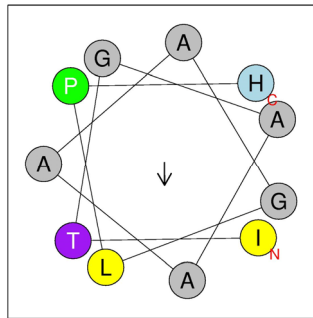
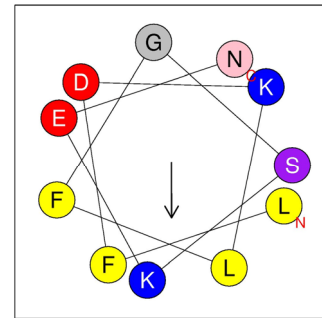


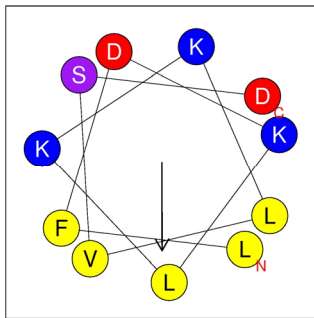
Borrelia burgdorferi
₁GFLDFFKKTAT₁₁
 μH 0.468



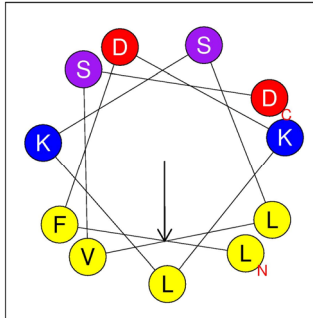
Streptomyces ScaeMP-e83
₂ITGAAAAGLPH₁₂
 μH 0.195



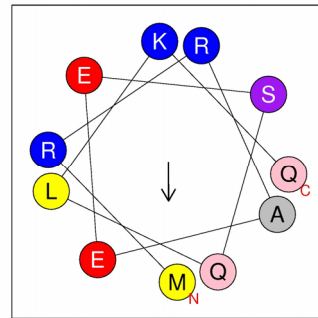
Streptococcus pneumoniae
₃LFDKLFSGKEN₁₃
 μH 0.465



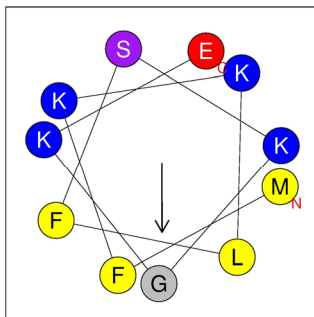
Vibrio cholerae
₃LFDKLLKLVSD₁₃
 μH 0.737



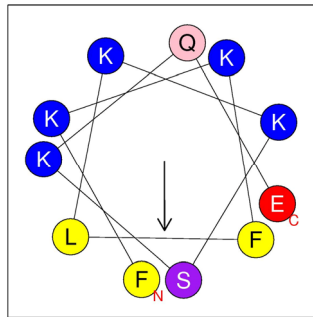
Escherichia coli
₃LFDKLLKLVSD₁₃
 μH 0.655



Burkholderia pseudomallei
₁RRAEESQLKQQ₁₁
 μH 0.195



Staphylococcus aureus
₃MFKKLFSGKGE₁₃
 μH 0.576



Listeria monocytogenes
₁FKKFLKKSQKE₁₁
 μH 0.578

Fig S5: In spite of poor N-terminal amino acid sequence conservation, the EIIA^{Glc} proteins of unrelated bacteria have a predicted N-terminal amphipathic helix. Heliquest software was used to identify amphipathic helices in the poorly conserved N-termini of EIIA^{Glc} proteins from the indicated organisms. In each case except that of the distantly related *Streptomyces* and *Burkholderia* species, an 11-amino acid amphipathic helix whose sequence is listed below the bacterial name, was found at the very beginning of the protein. The hydrophobic moment μH for each helix is given below.