Hydrophobic Moments - analysing the surface polarity of membrane-active amphiphilic peptides

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We define the hydrophobic moment of macromolecule, a vector that summarizes the surface distribution of hydrophilic and lipophilic regions. The concept extends the established 2D hydrophobic vector computed from helical wheel projections to three-dimensional molecules of arbitrary shape. Long all-atom MD simulations are used to calculate equilibrium hydrophobic moments for four different antimicrobial peptides: Gramicidin S, PGLa, Temporin A and BP100 .

We show that hydrophobic moment vectors reflect the distribution of polar and unpolar patches on the molecular surface and the calculated electrostatic surface potential. Comparing simulations in solution and DMPC membranes shows the internal rearrangement of the peptides in response to bilayer surface binding. Comparison to NMR experiment shows the hydrophobic moment vector can be used to predict the membrane binding geometry of peptides.