FIGURE 13: How many native structures does a given sequence have? This histogram derives from a 2D lattice model of self-avoiding flexible chains (of length = 24 monomers) subject only to hydrophobic interactions (Lau & Dill, 1990). Exhaustive search permits determination of the structure(s) of global minimum in free energy among the compact ensemble. These native structures are then found for many different sequences. The inset shows finer detail. This decreasing function implies that more sequences have only one native structure than have two, three, etc. Thus for a typical sequence, there are very few configurations that have the maximum possible number of nonpolar contacts.