



**FIGURE 4.** Kohn's symbols for describing protein–protein interactions (a) and alternative binding modes (b). For a global map of cell-cycle regulation, Kohn suggested symbols for representation of protein–protein interactions (shown in a) as well as a library of many additional symbols (not shown) representing enzymatic catalysis and stoichiometric conversion (e.g., of metabolite A into B); covalent modification of proteins (e.g., phosphorylation); degradation and cleavage of covalent bonds (e.g., dephosphorylation by a phosphatase or proteolytic cleavage); transport (e.g., from cytosol to nucleus); and transcriptional activation and inhibition. Panel b shows an example Kohn annotation of heterodimer formation between Cyclins E/A/B and Cdks 1/2. Nodes a, c, e, and g each represent a unique heterodimer, whereas b, d, and f represent the possibility of different dimer combinations. This notation simplifies the representation of multiple alternative interactions. A formal rule, required to avoid ambiguity, is that links representing alternative interactions must join at an acute angle. (Adapted, with permission, from Kohn 1999 [©The American Society for Cell Biology].)