The numbers and percentages of proteins from the Huang dataset and PPDBv4 for which iJET\textsuperscript{2} consensus predictions (8 iterations over 10) have positive predictive values of 100, at least 80 or at least 60 were computed for each step of JET\textsuperscript{2} clustering procedure. The different structural or functional classes of the two datasets were considered. Homo: Homodimers; Hetero: Heterodimers; Transients: Transient proteins; All: all proteins from the Huang dataset. EI: enzyme-inhibitor; A: antibody-antigen; AB: bound antibody-antigen; O: proteins with other function; All: all proteins from PPDBv4.