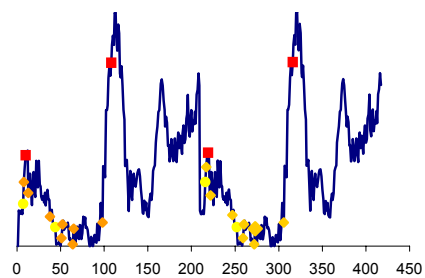
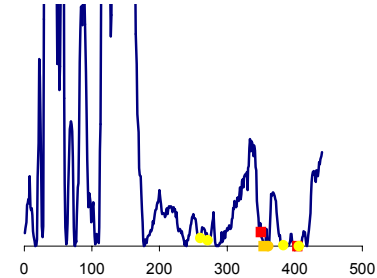


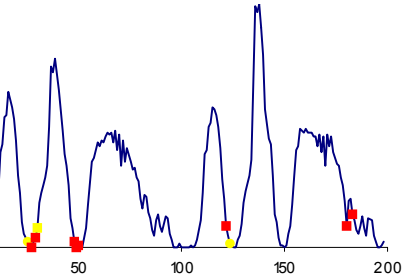
(a) 10GS



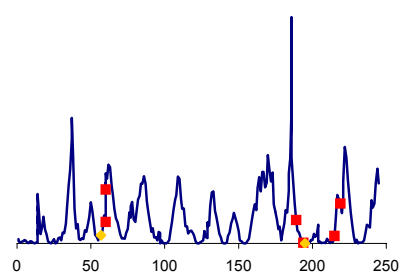
(b) 1A16



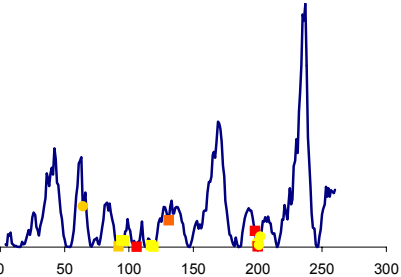
(c) 1A30



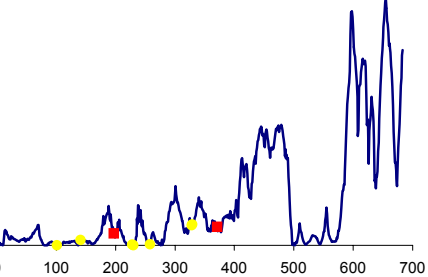
(d) 1A3B



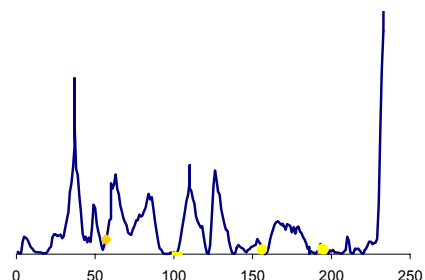
(e) 1A42



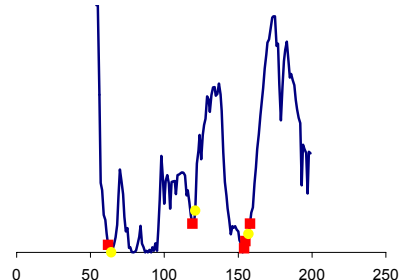
(f) 1A47



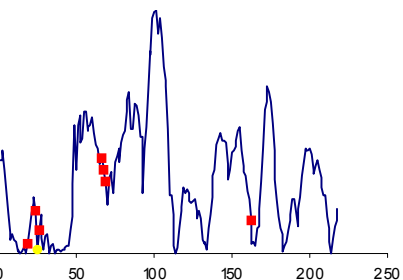
(g) 1A5I



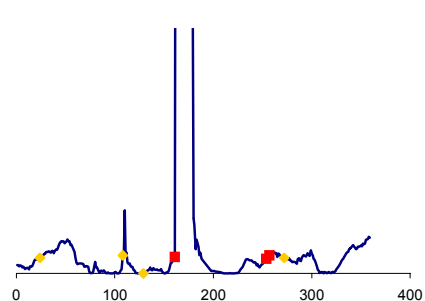
(h) 1A5V



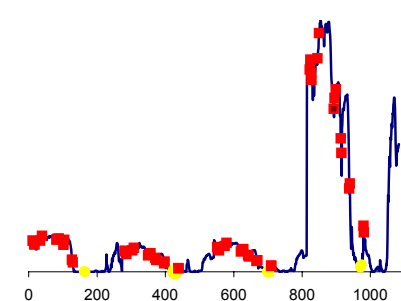
(i) 1AEC



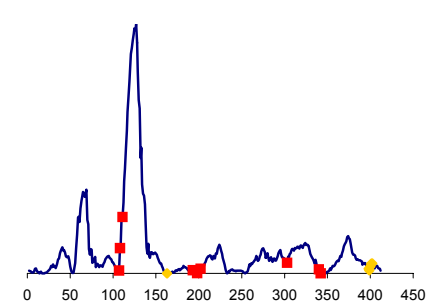
(j) 1AL8



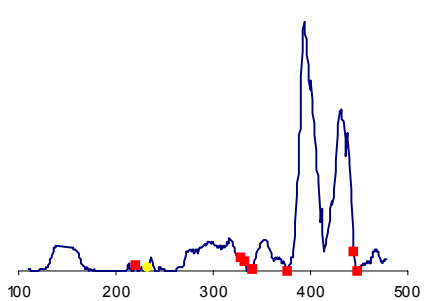
(k) 1ARZ



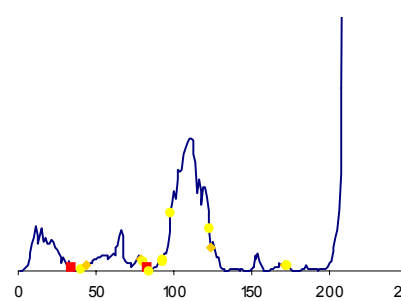
(l) 1B3N



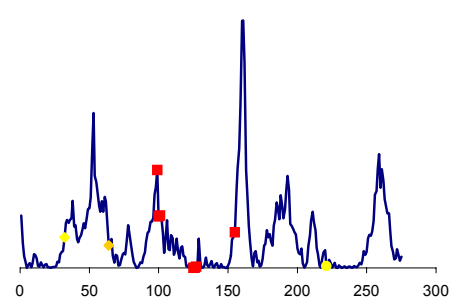
(m) 1B6A



(n) 1BGQ



(o) 1BH6



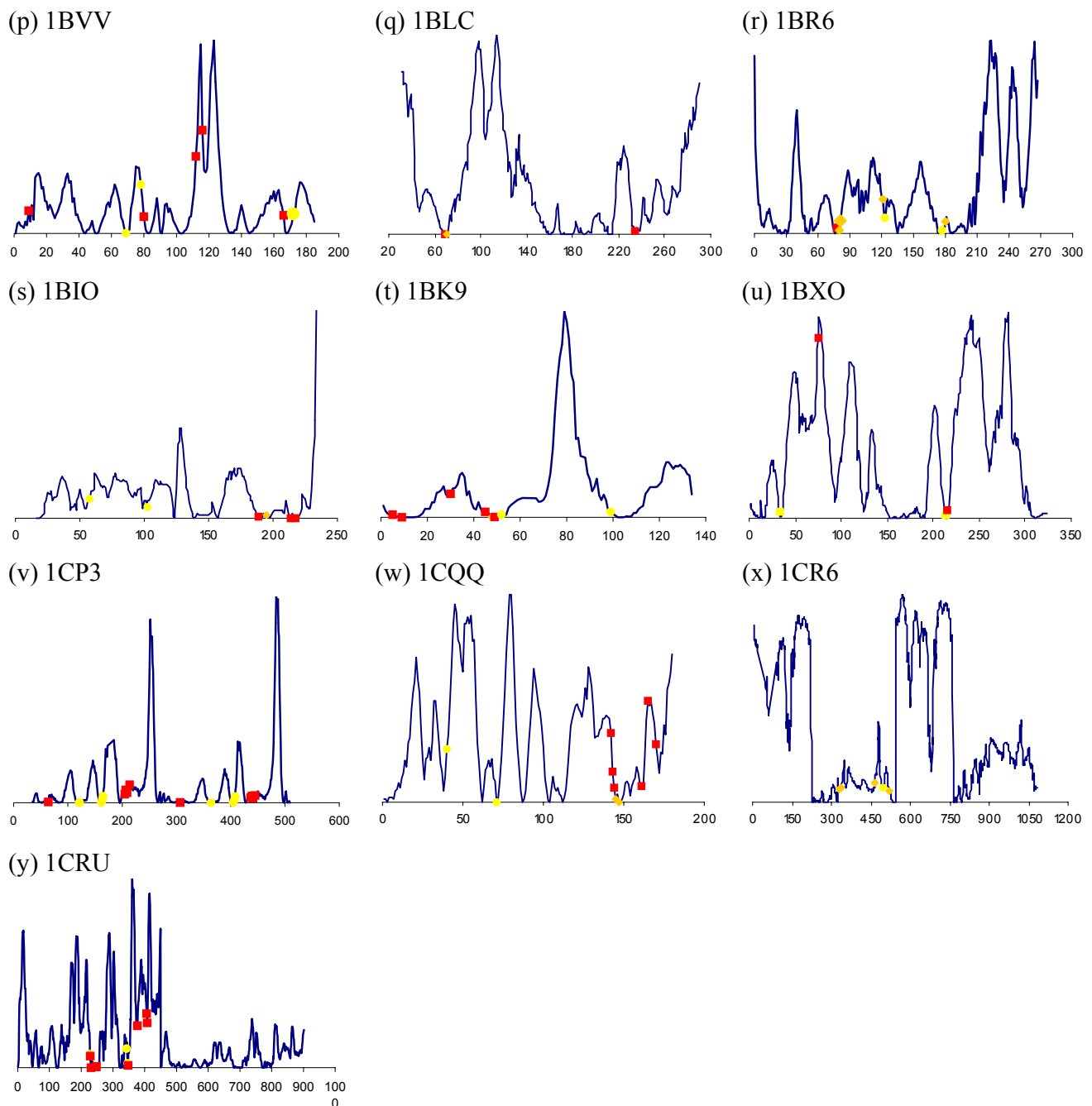


Fig. 1. Active and inhibitor binding residues located on the hinge region of representative modes of protein motion. Proteins dynamics were shown in global slowest mode (slow mode 1) except proteins (b)(k)(v)(y), which are shown in global second slowest mode (slow mode 2). Residues directly involved in catalytic function at active sites are marked in yellow circle (●), inhibitors binding residues are in red square (■) and residues served both catalytic and inhibitor binding functions are marked in orange rhomboid (◆).