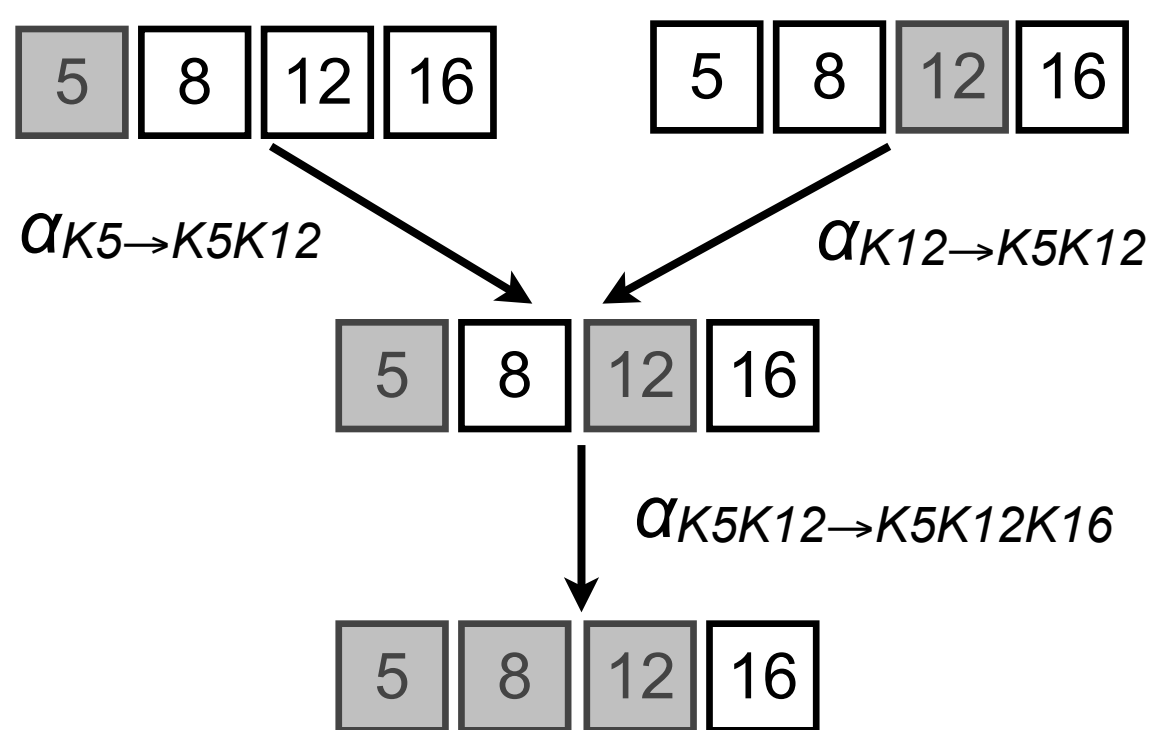


A

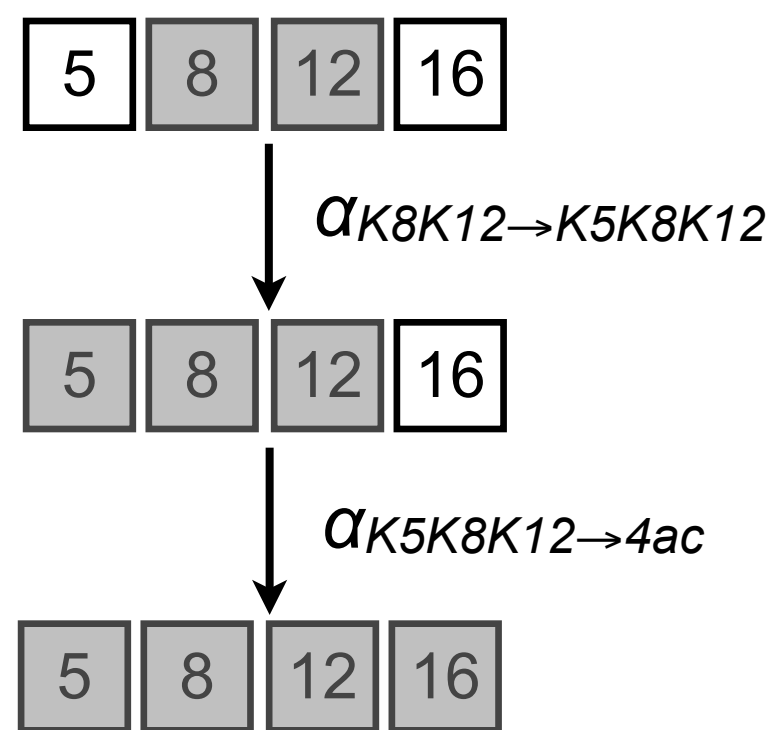
pathway 1

(45.8% models family 3)

**C**

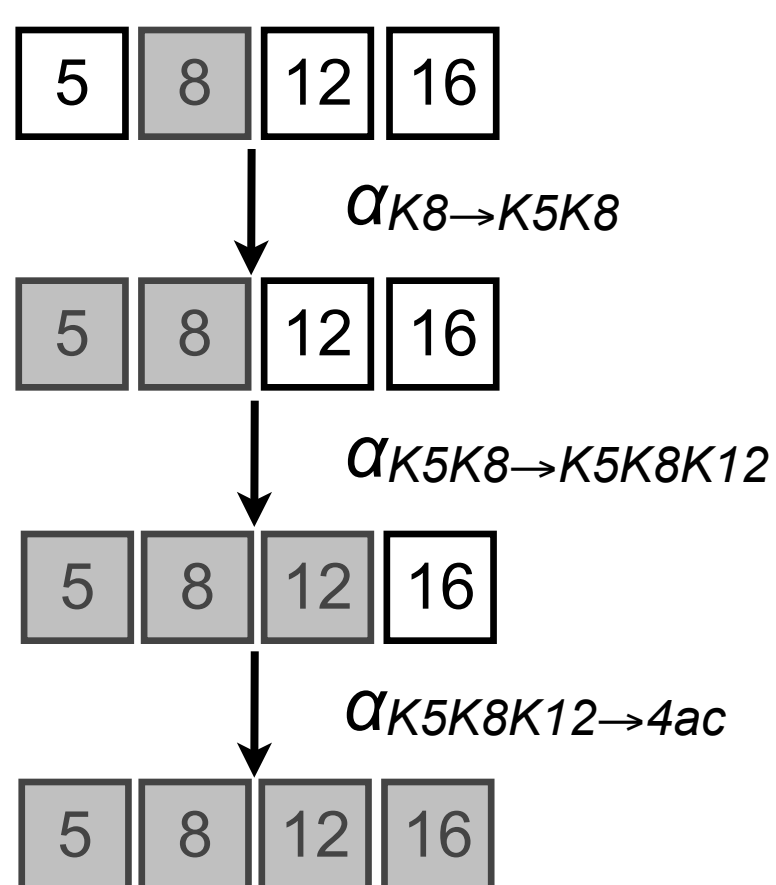
pathway 3

(42.3% models family 2)

**B**

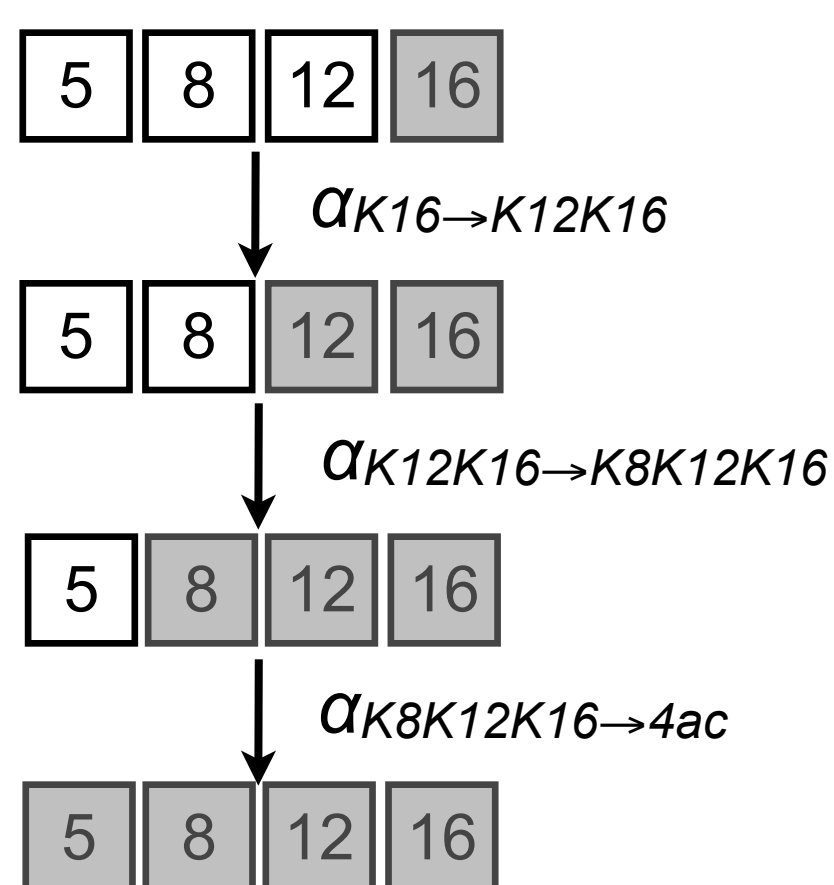
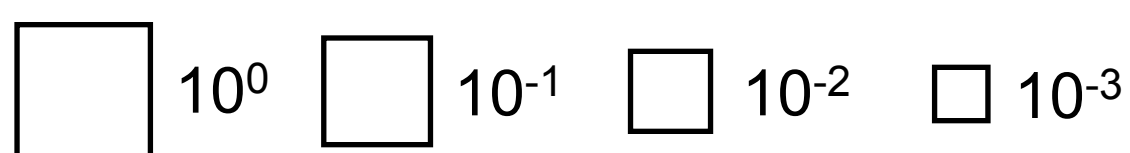
pathway 2

(81.8% models family 1)

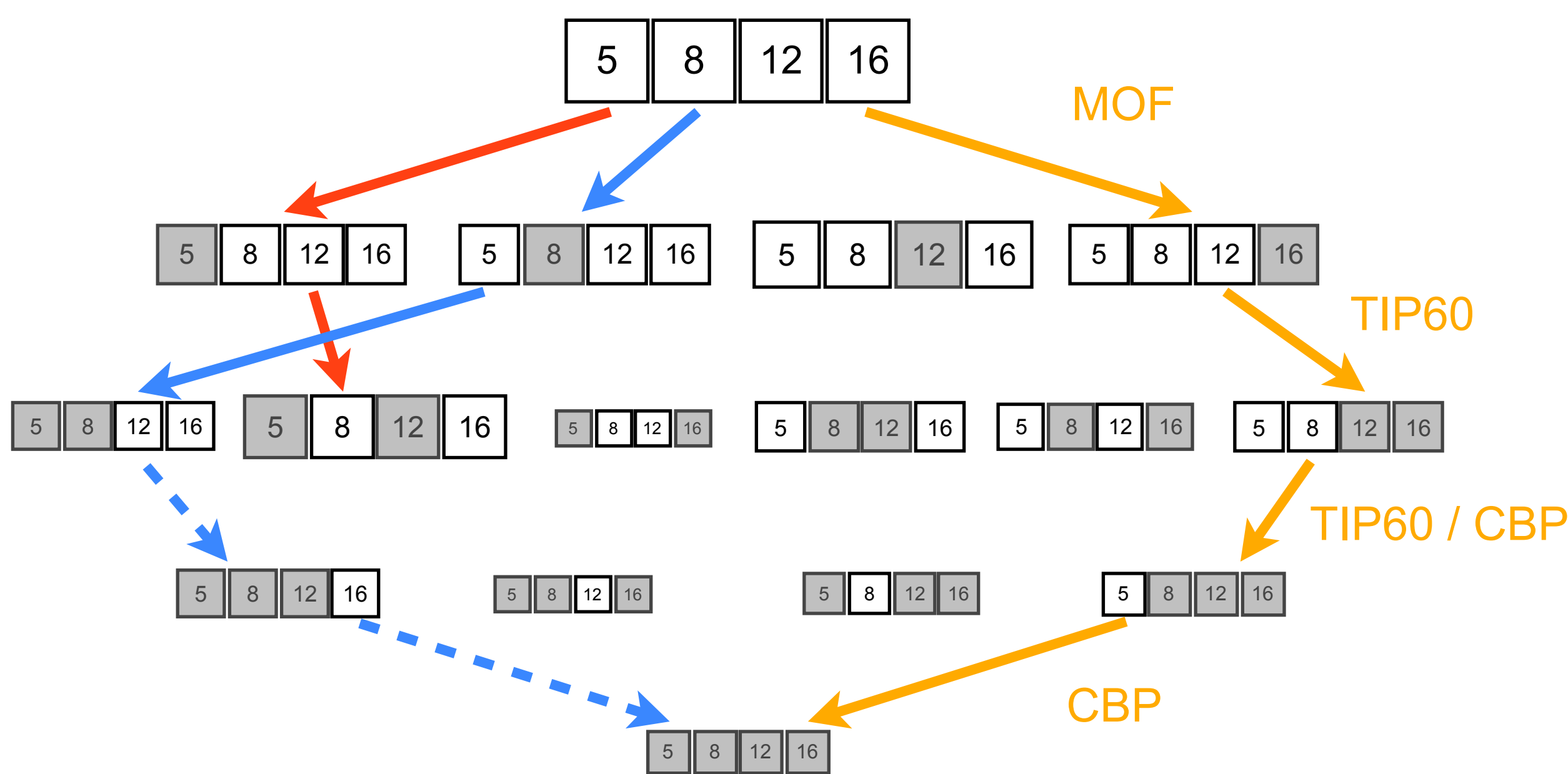
**D**

pathway 4

(84.8% models family 3)

**E**measured motif abundance x_m [a.u.]

proposed enzyme activity



pathway 1: K5K12 (HAT1)

pathway 2: inverse K5K8 zipper (CBP, NAA10, NAT10, MGEA5)

pathway 4: K16 zipper