Electronic Supplementary Information

S1. The training dataset and the testing dataset. The accession numbers of the proteins and the positions of the central lysine sites were given.

S2. The amino acid frequency around the carbamylated lysine sites.

S3. The training set with the 666 features.

S4. The testing dataset with the 666 features.

S5. The features ranked by the mRMR algorithm.

S6. The training set with the 280 optimal features.

S7. The testing set with the 280 optimal features.

S8. The datasets of acetylation, sumoylation and ubiquitination proteins. The accession numbers of the proteins and the positions of acetylation, sumoylation and ubiquitination sites were given.