Supplementary Description S2. Usage of Pse-in-One

Listed here are a series of publications in which the key approach is in using the pseudo k-tuple nucleotide composition or pseudo amino acid composition, as reflected by the fact that the titles of all these papers explicitly contain the terms "PseKNC", "pseudo nucleotide composition", "PseAAC", or "pseudo amino acid composition" (1-194).

For these ongoing studies or topics in computational biology, it would be much more efficient by using **Pse-in-One.** Particularly, many of these topics are vitally important for both basic research and drug development, such as identification of recombination spots (22,155), identification of nucleosome positioning (1,195), prediction of promoters (2,173), identification of translation initiation sites (174), prediction of methylation status and sites (134,194,196), detecting splicing sites (175), identifying DNase I hypersensitive sites (177), identifying microRNA precursors (192,193), predicting posttranslational modification (PTM) sites in proteins (16,17,23-25,179,185,197), detecting protein remote homology (166), predicting antifreeze proteins (182), predicting protein structural class (180,187), predicting anticancer peptides (178), identifying bacterial virulent proteins (147), predicting protein subcellular location in various organisms and levels (10,21,26,28,75,82,93,102,188), predicting membrane protein types (19,156), discriminating outer membrane proteins (7,73), predicting beta-lactamase (191), discrimination of acidic and alkaline enzyme (190), analyzing genetic sequence (159), identifying cyclin proteins (104), predicting GABA(A) receptor proteins (124), identifying antibacterial peptides (164), identifying allergenic proteins (167), predicting metalloproteinase family (125), identifying GPCRs and their types (154), identifying protein quaternary structural attributes (12), identifying risk type of human papillomaviruses (98), and predicting drug-target interaction in cellular networking (14,198-202).

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