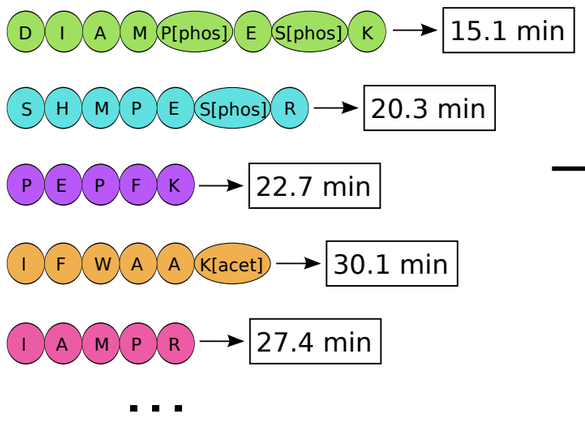
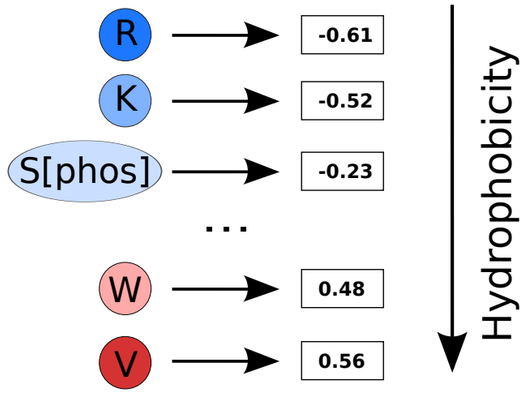
Training peptides



Support vector regression

Retention index

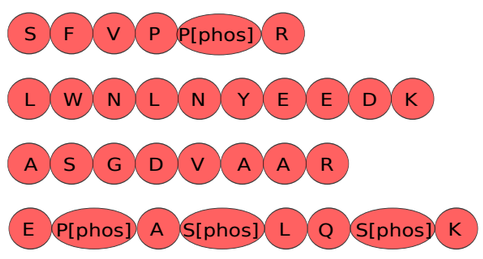


1	Sum of amino acids' retention coefficients
2	Average of amino acids' retention coefficients
3	*N*-terminal amino acid's retention coefficient
4	*C*-terminal amino acid's retention coefficient
5	Peptide's length
6	Sum of squared difference in retention coefficients between neighboring amino acids
7	Sum of retention coefficients of amino acids next to the 25% least hydrophobic amino acids
8-9	Sum of the retention coefficients of the 2 consecutive amino acids with most and least retention coefficient
10-11	Sum of the retention coefficients of the 5 consecutive amino acids with most and least retention coefficient
12-13	Number of occurences of the 25% least and most hydrophobic amino acids as indicated by the internal retention index
14-15	Number of consecutive occurences of the 25% least and most hydrophobic amino acids as indicated by the internal retention index
16-19	Highest and lowest values of the "hydrophobic moment" for alpha helices and beta sheets
20-21	Highest and lowest normalized alpha helical retention coefficient
22-41	Number of occurrences of each amino acid

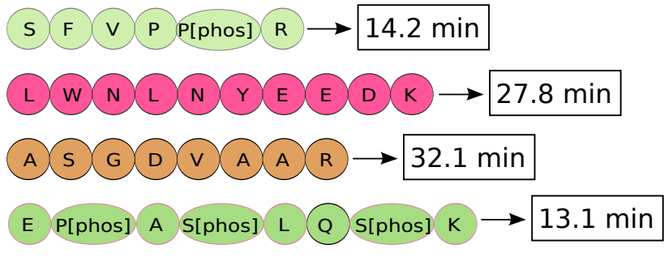
Peptide Features

Retention Model

Support vector regression



Peptides of interest



Retention time predictions