Analysis and prediction of activity of parathyroid hormone using SVM

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Parathyroid hormone (PTH) is the major regulator of calcium and phosphate homeostasis. Moreover, when PTH is presented in an intermittent fashion, it stimulates a net increase in bone mass. Therefore, developing a successful PTH analogue is viewed with considerable interest for the treatment of osteoporosis. PTH is composed of 84 amino acids, but its full biological effects are limited to its N-terminus region, PTH (1-34). However, this 34-amino acid peptide has a low compliance problem, because the parenteral injections, nasal sprays and pulmonary inhalers are of limited effectiveness. To resolve this problem, many efforts to minimize the peptide size have been conducted. As the results, the PTH14 was found a good candidate for a drug design. In this study, 150 analogues of PTH14 with varying activity were analyzed to explore to find optimal sequence combination. The each amino acid from P1 to P14 positions in varying activity was examined. The method for predicting key regions and their property for the activation of PTH14 were derived using the site-directed mutagenesis data. We developed a support vector machine (SVM) method to model the activity of PTH.