Supplementary Table 1. Important mathematical equations have been included for the implemented descriptors.

Descriptor name	**Formula**
Charge Density	$CD = C/D$, C = Charge, D = Density
Isoelectric point	pI = ½(pK_{a1} + pKa2)
Instabiliity Index	$II = \frac{10}{L} \times \sum DIWV(x[i] \times [i+1])$ DIWV-Di-peptide weight value L length of sequence. I Position
GetAAComp	$f(t) = \frac{N(t)}{N}, \quad t \in \{A, C, D, ..Y\}$ N is number of Amino Acids, t is type $A, C, D, ..Y$
GetDPComp	$D(r,s) = \frac{Nrs}{N-1}, \quad r,s \in \{A, C, D, ..Y\}$ *Nrs* is dipeptides represented by amino acid types *r* and *s*.
GetTPComp	$D(r,s,t) = \frac{Nrst}{N-2}, \quad r,s,t \in \{A, C, D, ..Y\}$ *Nrst* tripeptides represented by amino acid types *r, s and t.*
GetMoranAuto	$AC(d) = \sum_{i=1}^{N-d} P_i \times P_{i+d} , \quad d = 1, 2, ..., nlag$ *d* is the lag of the autocorrelation, *nlag* is the maximum value of the lag *Pi* and *Pi+d* are the properties of the amino acids at positions *i* and *i* + *d*, respectively.
GetMoreauBrotoAuto	$ATS(d) = \frac{AC(d)}{N-d}, \quad d = 1, 2, ..., nlag$ *D N and nlag* have the same definitions as described above
GetGearAuto	$C(d) = \frac{\frac{1}{2(N-d)} \sum_{i=1}^{N-d} (P_i - P_{i+d})^2}{\frac{1}{N-1} \sum_{i=1}^{N} (P_i - \bar{P}')^2}, \quad d = 1, 2, ..., nlag$

	d, P, Pi, $Pi+d$ and $nlag$ same as above.
GetCTD	$C(r)=\frac{N(r)}{N}, \quad r\in\{polar, neutral, hydrophobic\}$ $N(r)$ is the number of amino acid. r is the type and N is the length of the sequence.
GetPAAC	$H_1(i)=\frac{H_1^o(i)-\frac{1}{20}\sum_{i=1}^{20}H_1^o(i)}{\sqrt{\frac{\sum_{i=1}^{20}[H_1^o(i)-\frac{1}{20}\sum_{i=1}^{20}H_1^o(i)]^2}{20}}}$ $H_1^0(1)$, $H_2^0(1)$ and $M^o(i)$ are original hydrophobicity values for i = 1,2,3,4…20 amino Acids.
GetSOCN	$\tau_d=\sum_{i=1}^{N-d}(d_{i,i+d})^2, \quad d=1,2,3,...,nlag$ $di, i+d$ distance between the two amino acids at position i and $i+d$. $nlag$ denotes the maximum value of the lag, N is the length of a protein or peptide sequence.
GetQSO	$X_r=\frac{f_r}{\sum_{r=1}^{20}f_r+w\sum_{d=1}^{nlag}\tau_d}, \quad r=1,2,...,20$ fr is the normalized occurrence of amino acid, r *is the type,* w *is* weighting factor ($w = 0.1$), $nlag$ and τ_d same as described above.
GetTriad	$d_i=\frac{f_i-\min\{f_1,f_2,...,f_{343}\}}{\max\{f_1,f_2,...,f_{343}\}}$ fi, the value of the i-th dimension of number vectors correspond to the vector space of a sequence features and each feature.
Calculate AutoCor	Standardization of amino acid

	$P_r = \frac{P_r - \bar{P}}{\sigma}$ Auto correlation $\bar{P} = \frac{\sum_{r=1}^{20} P_r}{20}$ and $\sigma = \sqrt{\frac{1}{2}\sum_{r=1}^{20}(P_r - \bar{P})^2}$ P is the property and P¯ is the average of the property of the 20 amino acids