

**Table S1 The Performances of Different Features in 19**

Features	Sn(%)	Sp(%)	Acc(%)	F1	MCC
Binary Encoding	53.94	72.29	63.12	0.5939	0.2669
AA Composition	62.42	59.28	60.85	0.6146	0.2172
Grouping AA Composition	69.36	68.53	68.95	0.6908	0.3790
Physicochemical Properties	73.11	70.42	71.77	0.7214	0.4355
KNN Features	72.52	62.34	67.43	0.6901	0.3505
Secondary Tendency Structure	67.54	73.89	70.72	0.6976	0.4152
PSSM	68.78	75.88	72.33	0.7131	0.4478
BPB	70.39	75.00	72.70	0.7205	0.4544
Bi-gram	72.75	73.30	73.03	0.7295	0.4606
Tri-gram	74.86	74.76	74.81	0.7482	0.4962
Proposed Algorithm	78.65	76.78	77.72	0.7792	0.5544

**Table S2 The Performances of Different Methods in 19**

Method	Sn(%)	Sp(%)	Acc(%)	F1	MCC
DNABIND <sup>65</sup>	67.36	67.46	67.41	0.6740	0.3482
DNAbinder <sup>65</sup>	67.47	70.28	68.88	0.6843	0.3777
DBD-Threader <sup>66</sup>	55.37	91.20	73.29	0.6746	0.4989
DNA-Prot <sup>66</sup>	65.39	77.20	71.30	0.6950	0.4290
iDNA-Prot <sup>67</sup>	74.29	72.01	73.15	0.7345	0.4632
DBPPred <sup>68</sup>	76.95	71.31	74.13	0.7484	0.4834
PLMLA <sup>69</sup>	63.38	66.20	64.79	0.6429	0.2960
Phosida <sup>70</sup>	76.19	81.40	78.80	0.7823	0.5767
LysAcet <sup>71</sup>	75.08	71.63	73.36	0.7381	0.4674
EnsemblePail <sup>72</sup>	74.89	68.73	71.81	0.7265	0.4371
PSKAcePred <sup>73</sup>	68.78	66.36	67.57	0.6796	0.3516
BRABSB <sup>74</sup>	78.67	68.77	73.72	0.7496	0.4768
SSPKA <sup>75</sup>	73.39	76.06	74.73	0.7438	0.4947
Proposed Algorithm	78.65	76.78	77.72	0.7792	0.5544

**Table S3 The Performances of Different Features in 23**

Features	Sn(%)	Sp(%)	Acc(%)	F1	MCC
Binary Encoding	56.36	75.80	66.08	0.6243	0.3279
AA Composition	64.84	62.79	63.82	0.6418	0.2764
Grouping AA Composition	71.78	72.04	71.91	0.7187	0.4382
Physicochemical Properties	75.53	73.93	74.73	0.7493	0.4947

KNN Features	74.94	65.85	70.40	0.7168	0.4096
Secondary Tendency Structure	69.96	77.40	73.68	0.7266	0.4749
PSSM	71.20	79.39	75.30	0.7424	0.5076
BPB	72.81	78.51	75.66	0.7495	0.5140
Bi-gram	75.17	76.81	75.99	0.7579	0.5199
Tri-gram	77.28	78.27	77.78	0.7766	0.5555
Proposed Algorithm	81.07	80.29	80.68	0.8076	0.6136

**Table S4 The Performances of Different Methods in 23**

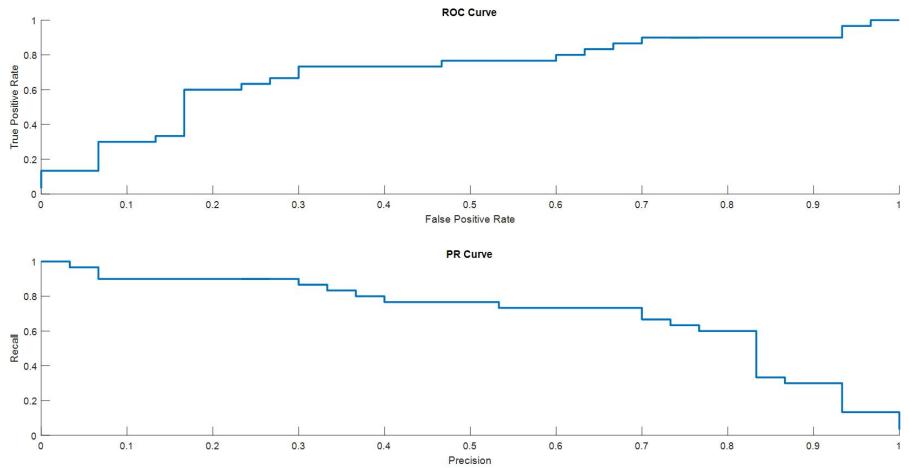
<i>Method</i>	<i>Sn(%)</i>	<i>Sp(%)</i>	<i>Acc(%)</i>	<i>F1</i>	<i>MCC</i>
DNABIND <sup>65</sup>	69.78	70.97	70.38	0.7020	0.4075
DNAbinder <sup>65</sup>	69.89	73.79	71.84	0.7128	0.4371
DBD-Threader <sup>66</sup>	57.79	94.71	76.25	0.7087	0.5649
DNA-Prot <sup>66</sup>	67.81	80.71	74.26	0.7249	0.4893
iDNA-Prot <sup>67</sup>	76.71	75.52	76.12	0.7626	0.5223
DBPPred <sup>68</sup>	79.37	74.82	77.10	0.7760	0.5425
PLMLA <sup>69</sup>	65.80	69.71	67.76	0.6711	0.3554
Phosida <sup>70</sup>	78.61	84.91	81.76	0.8117	0.6365
LysAcet <sup>71</sup>	77.50	75.14	76.32	0.7660	0.5265
EnsemblePail <sup>72</sup>	77.31	72.24	74.78	0.7540	0.4961
PSKAcePred <sup>73</sup>	71.20	69.87	70.54	0.7073	0.4107
BRABSB <sup>74</sup>	81.09	72.28	76.65	0.7762	0.5349
SSPKA <sup>75</sup>	75.81	79.57	77.69	0.7726	0.5542
Proposed Algorithm	81.07	80.29	80.68	0.8076	0.6136

**Table S5 The Performances of Different Features in 25**

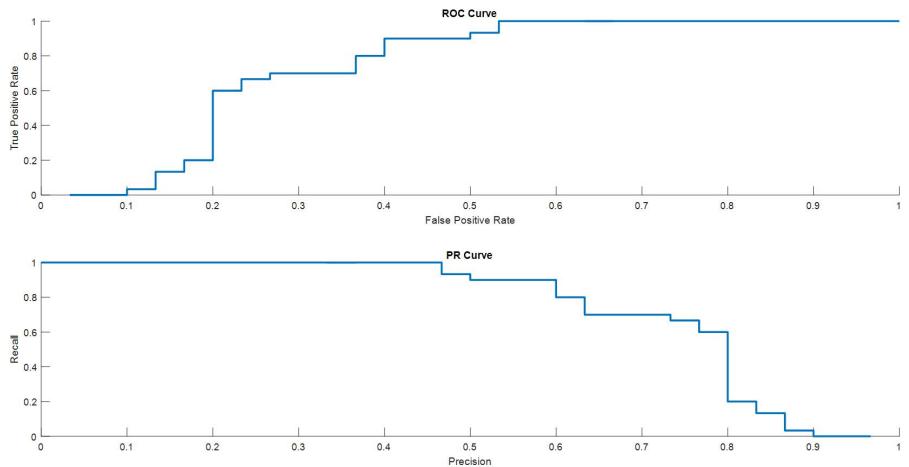
Features	Sn(%)	Sp(%)	Acc(%)	F1	MCC
Binary Encoding	56.16	74.09	65.13	0.6169	0.3075
AA Composition	64.64	61.08	62.86	0.6351	0.2574
Grouping AA Composition	71.58	70.33	70.96	0.7114	0.4192
Physicochemical Properties	75.33	72.22	73.78	0.7418	0.4758
KNN Features	74.74	64.14	69.44	0.7098	0.3910
Secondary Tendency Structure	69.76	75.69	72.73	0.7189	0.4553
PSSM	71.00	77.68	74.34	0.7345	0.4879
BPB	72.61	76.80	74.71	0.7416	0.4946
Bi-gram	74.97	75.10	75.04	0.7502	0.5007
Tri-gram	77.08	76.56	76.82	0.7688	0.5364
Proposed Algorithm	80.87	78.58	79.73	0.7996	0.5947

**Table S6 The Performances of Different Methods in 25**

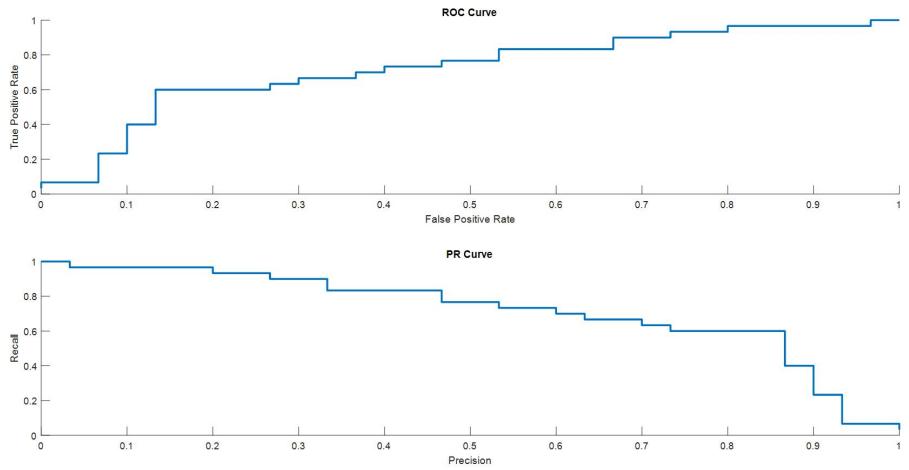
<i>Method</i>	<i>Sn(%)</i>	<i>Sp(%)</i>	<i>Acc(%)</i>	<i>F1</i>	<i>MCC</i>
DNABIND <sup>65</sup>	69.58	69.26	69.42	0.6947	0.3884
DNAbinder <sup>65</sup>	69.69	72.08	70.89	0.7053	0.4178
DBD-Threader <sup>66</sup>	57.59	93.00	75.30	0.6998	0.5410
DNA-Prot <sup>66</sup>	67.61	79.00	73.31	0.7169	0.4692
iDNA-Prot <sup>67</sup>	76.51	73.81	75.16	0.7549	0.5034
DBPPred <sup>68</sup>	79.17	73.11	76.14	0.7684	0.5238
PLMLA <sup>69</sup>	65.60	68.00	66.80	0.6640	0.3361
Phosida <sup>70</sup>	78.41	83.20	80.81	0.8034	0.6168
LysAcet <sup>71</sup>	77.30	73.43	75.37	0.7583	0.5077
EnsemblePail <sup>72</sup>	77.11	70.53	73.82	0.7465	0.4775
PSKAcePred <sup>73</sup>	71.00	68.16	69.58	0.7001	0.3918
BRABSB <sup>74</sup>	80.89	70.57	75.73	0.7692	0.5174
SSPKA <sup>75</sup>	75.61	77.86	76.74	0.7647	0.5349
Proposed Algorithm	80.87	78.58	79.73	0.7996	0.5947



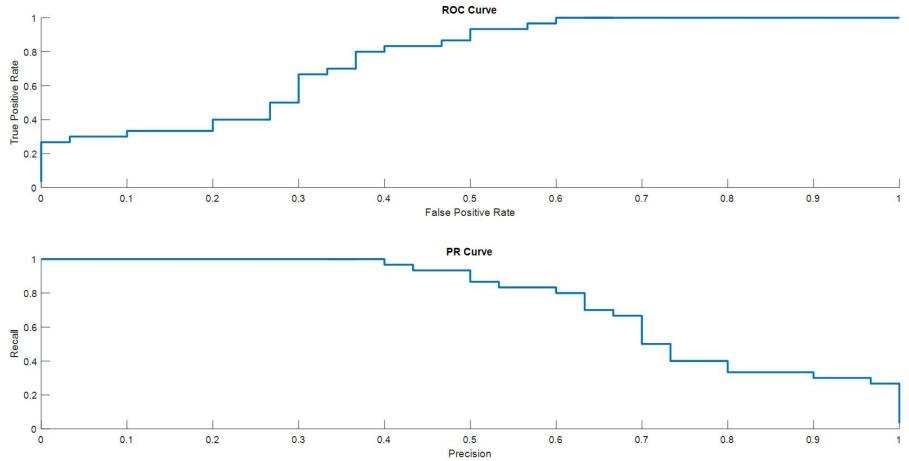
**Figure S1 The ROC and Recall Curves of Length=3**



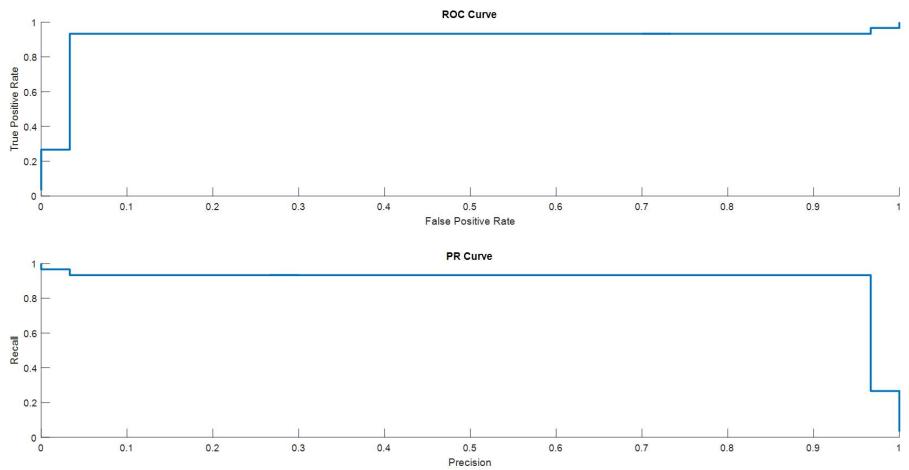
**Figure S2 The ROC and Recall Curves of Length=5**



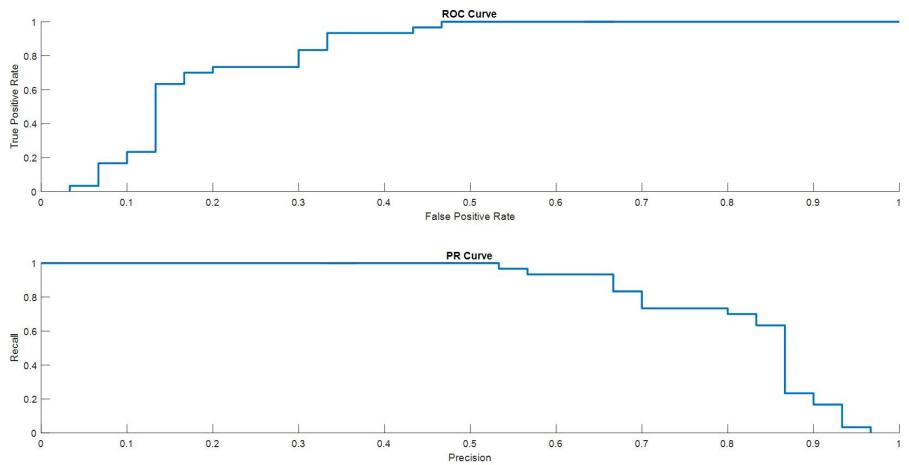
**Figure S3 The ROC and Recall Curves of Length=7**



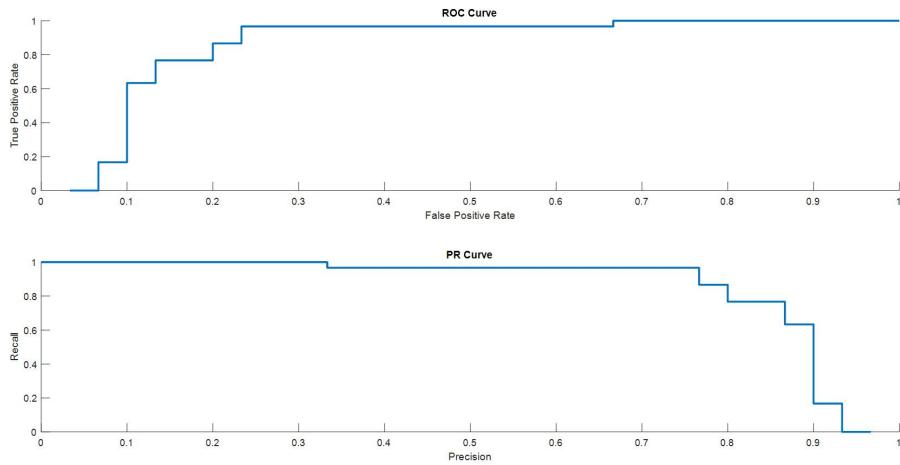
**Figure S4 The ROC and Recall Curves of Length=9**



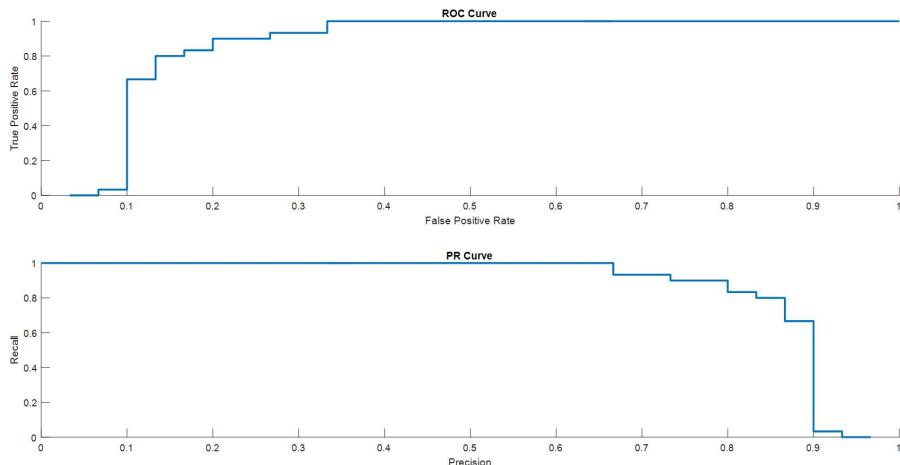
**Figure S5 The ROC and Recall Curves of Length=11**



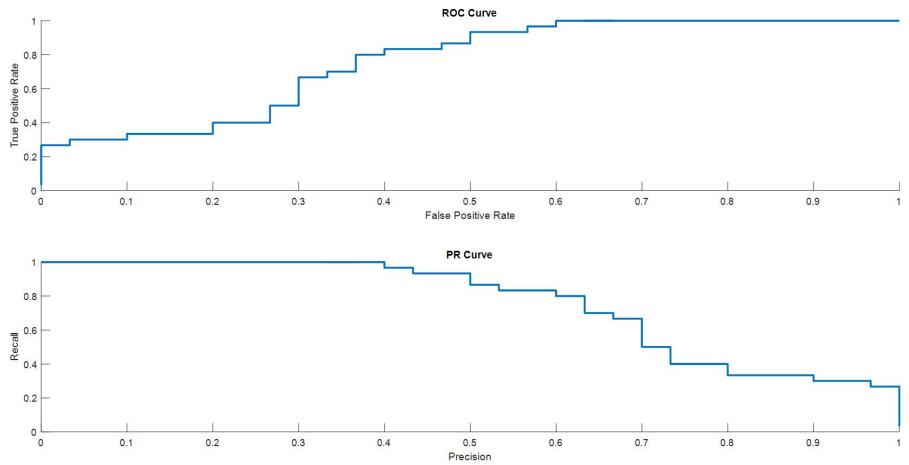
**Figure S6 The ROC and Recall Curves of Length=13**



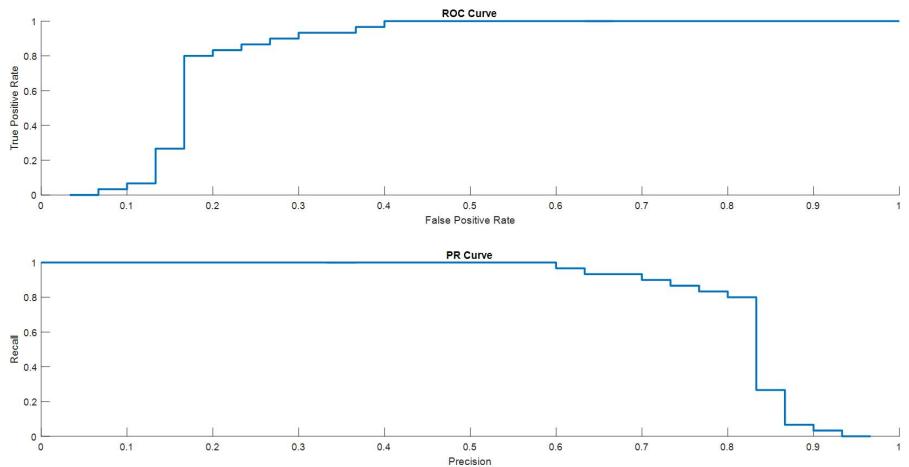
**Figure S7 The ROC and Recall Curves of Length=15**



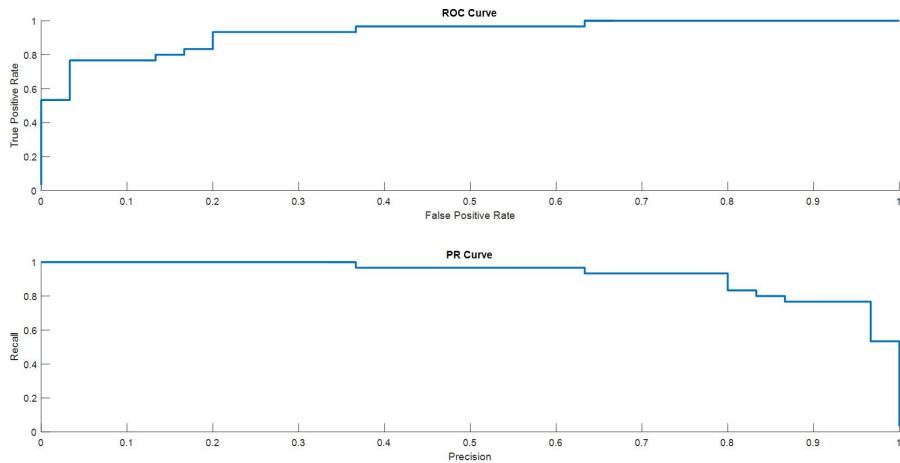
**Figure S8 The ROC and Recall Curves of Length=17**



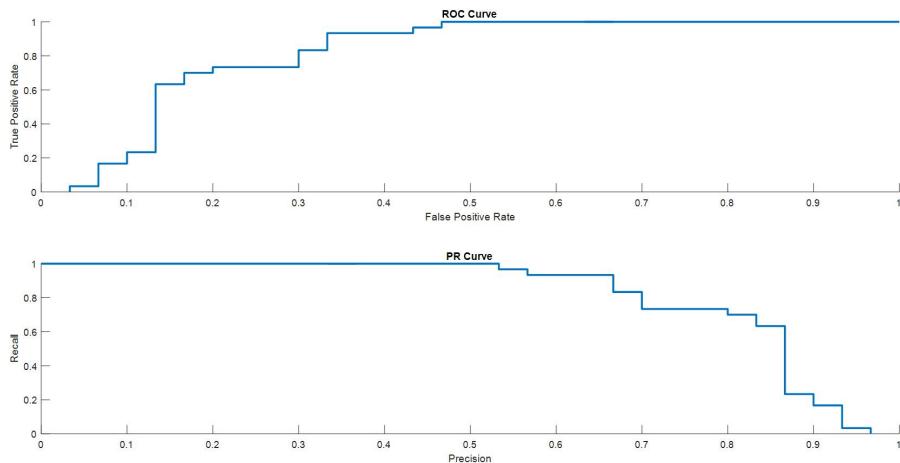
**Figure S9 The ROC and Recall Curves of Length=19**



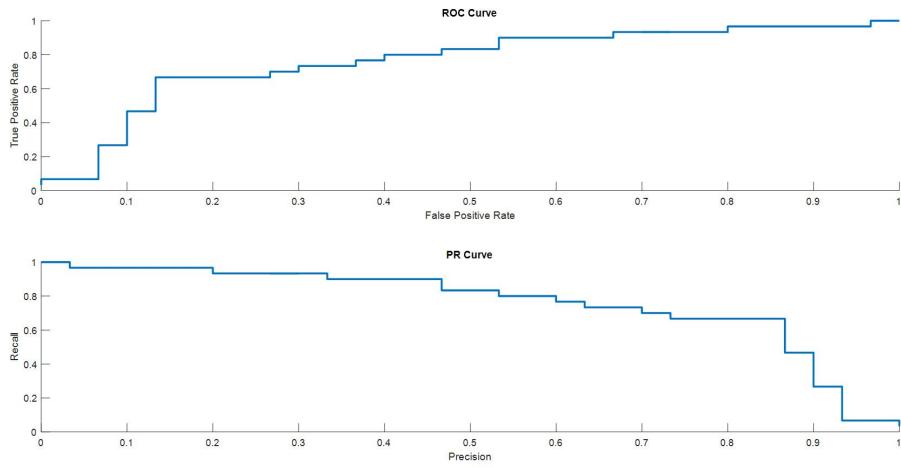
**Figure S10 The ROC and Recall Curves of Length=21**



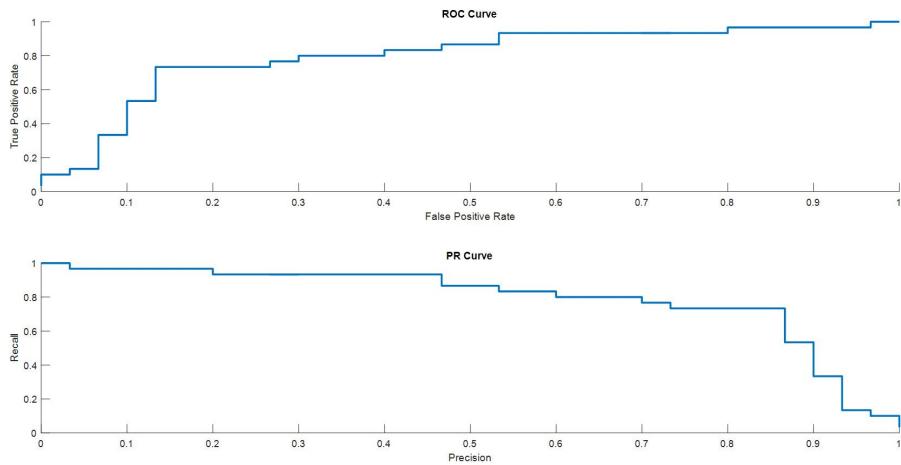
**Figure S11 The ROC and Recall Curves of Length=23**



**Figure S12 The ROC and Recall Curves of Length=25**



**Figure S13 The ROC and Recall Curves of Length=27**



**Figure S14 The ROC and Recall Curves of Length=29**