Table S1. The performance of the permease-specific models on different feature sets using training set and 5-fold cross validation.

Method	Sensitivity (%)	Specificity (%)	Accuracy (%)	MCC
AAC[a]	64.34	88.76	85.03	0.5527
CTD[b]	57.44	87.78	83.87	0.5032
AAI[c]	56.15	87.56	82.88	0.4500
PSSM[d]	76.38	91.94	89.59	0.7078
AAC+CTD	57.17	87.58	83.87	0.4647
AAC+AAI	59.57	88.17	84.56	0.4970
AAC+PSSM	68.86	90.95	88.18	0.6169
CTD+AAI	59.89	87.96	84.06	0.5081
CTD+PSSM	58.45	88.09	84.32	0.5100
AAI+PSSM	74.95	91.77	89.40	0.6926
AAC+CTD+AAI	56.19	87.52	83.13	0.4596
AAC+CTD+PSSM	55.93	87.13	82.63	0.4629
AAC+AAI+PSSM	72.91	91.06	88.39	0.6531
CTD+AAI+PSSM	70.00	90.98	88.40	0.6486
AAC+CTD+AAI+PSSM	54.59	87.24	83.31	0.4546

[a] AAC: amino acid composition; [b]CTD: composition transition and distribution; [c]AAI: biochemical properties (AAindex); [d] PSSM: position-specificscoring matrix.

Table S2. The performance of the ATP binding protein-specific models on different feature sets using training set and 5-fold cross validation.

Method	Sensitivity (%)	Specificity (%)	Accuracy (%)	MCC
AAC[a]	44.78	80.78	72.76	0.2615
CTD[b]	56.25	84.27	75.30	0.4353
AAI[c]	43.47	79.71	70.31	0.2263
PSSM[b]	57.28	85.33	79.26	0.4348
AAC+CTD	56.25	84.27	75.30	0.4353
AAC+AAI	44.92	80.93	72.79	0.2388
AAC+PSSM	44.78	80.78	72.76	0.2615
CTD+AAI	55.68	84.44	77.19	0.4429
CTD+PSSM	50.75	83.10	76.74	0.3488
AAI+PSSM	64.81	86.61	80.36	0.5050
AAC+CTD+AAI	50.23	82.88	74.86	0.3684
AAC+CTD+PSSM	53.53	82.52	75.29	0.3632
AAC+AAI+PSSM	58.62	85.99	79.71	0.4648
CTD+AAI+PSSM	57.26	83.96	76.74	0.4233
AAC+CTD+AAI+PSSM	52.62	83.25	74.79	0.3738

[a] AAC: amino acid composition; [b] CTD: composition transition and distribution; [c] AAI: biochemical properties (AAindex); [d] PSSM: position-specific scoring matrix.

Table S3. The performance of the substrate binding protein-specific models on different feature sets using training set and 5-fold cross validation.

Method	Sensitivity (%)	Specificity (%)	Accuracy (%)	MCC
AAC[a]	34.79	73.44	62.16	0.0803
CTD[b]	49.56	75.28	67.23	0.2483
AAI[c]	41.21	76.22	65.21	0.1783
PSSM[d]	80.94	87.71	86.12	0.6784
AAC+CTD	50.95	74.73	68.53	0.2856
AAC+AAI	43.22	72.74	63.74	0.1487
AAC+PSSM	79.49	85.47	83.08	0.6278
CTD+AAI	61.21	76.29	71.86	0.3699
CTD+PSSM	65.78	79.02	74.51	0.4293
AAI+PSSM	67.54	81.22	78.64	0.4954
AAC+CTD+AAI	52.05	76.34	70.33	0.3078
AAC+CTD+PSSM	56.29	77.54	72.82	0.3482
AAC+AAI+PSSM	69.41	82.82	77.25	0.5029
CTD+AAI+PSSM	68.86	80.04	75.75	0.4747
AAC+CTD+AAI+PSSM	70.59	79.38	76.85	0.4846

[a]AAC: amino acid composition; [b]CTD: composition transition and distribution; [c]AAI: biochemical properties (AAindex); [d]PSSM: position-specific scoring matrix.

Table S4. The performance of the uniform models with different feature sets on the training set of all proteins and 5-fold cross validation.

Method	Sensitivity (%)	Specificity (%)	Accuracy (%)	MCC
AAC[a]	44.27	82.97	75.74	0.2727
CTD[b]	51.91	84.92	78.57	0.3896
AAI[c]	47.95	83.66	76.23	0.3167
PSSM[d]	64.53	88.07	83.29	0.5503
AAC+CTD	52.95	84.32	77.45	0.3841
AAC+AAI	45.58	82.98	75.61	0.2953
AAC+PSSM	58.86	86.49	80.74	0.5005
CTD+AAI	56.63	85.08	78.76	0.4278
CTD+PSSM	49.65	83.40	76.26	0.3551
AAI+PSSM	66.47	88.64	84.22	0.5821
AAC+CTD+AAI	61.26	88.10	83.03	0.5356
AAC+CTD+PSSM	57.33	85.68	79.96	0.4493
AAC+AAI+PSSM	68.82	89.47	85.02	0.5881
CTD+AAI+PSSM	48.50	83.15	76.38	0.3430
AAC+CTD+AAI+PSSM	53.88	85.01	78.64	0.4074

[a] AAC: amino acid composition; [b]CTD: composition transition and distribution; [c]AAI: biochemical properties (AAindex); [d]PSSM: position-specific scoring matrix.

Table S5. The performance of BLAST on test data set.

Transporter class	Sensitivity (%)	Specificity (%)	Accuracy (%)	MCC	Total unclassified(%)
Sugar	66.67	95.31	90.79	0.6424	
Ion	81.25	98.33	94.74	0.8369	20.83
Amino acid/protein	72.73	88.89	84.21	0.6162	
Others	73.08	80.00	77.63	0.5184	

Transporter class	Sensitivity (%)	Specificity (%)	Accuracy (%)	MCC	Total unclassified(%)
	66.67	95.31	90.79	0.6424	
					20.83