

Table S2: Cross Validation Results of Ion-ligand ipHMMs

Domain	SMART Abr.	Sens ¹	Spec ²	Acc ³
Alkaline phosphatase homologues	alkPPc	0.63	0.49	0.49
Zinc finger	ZnFC2H2	0.33	0.52	0.50
Insulin / insulin-like growth factor / relaxin family.	IIGF	0.00	0.67	0.66
Trypsin-like serine protease	TrypSPc	0.00	0.76	0.75
Alpha-lactalbumin / lysozyme C	LYZ1	0.33	0.68	0.67
EF-hand, calcium binding motif	EFh	1.00	0.83	0.86
DNA polymerase A domain	POLAc	1.00	0.64	0.64
Zinc-dependent metalloprotease	ZnMc	0.00	0.71	0.68
ATPases associated with a variety of cellular activities	AAA	1.00	0.95	0.95
Immunoglobulin V-Type	IGv	0.00	0.85	0.83
Eukaryotic homologues of bacterial periplasmic substrate binding proteins.	PBPc	1.00	0.57	0.57
Alpha-amylase domain	Aamy	0.00	0.81	0.80
C-type lectin (CTL) or carbohydrate-recognition domain (CRD)	CLECT	0.25	0.82	0.81
Gelsolin homology domain	GEL	0.50	0.70	0.69
Bacterial periplasmic substrate-binding proteins	PBPb	0.17	0.44	0.43
Summary		0.41	0.70	0.69

¹Sensitivity

²Specificity

³Accuracy = $\frac{TP+TN}{P+N}$