

## Supplement Table for Prediction of RNA binding proteins comes of age from low resolution to high resolution

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Table S1 Method Performance based on published results

Author/Method Name [Ref.]	#RBPs	Sensitivity	Specificity	Accuracy	MCC	Validation
<b>Structure-based</b>						
Jeong et al. <sup>1</sup>	96	-	-	59.1	0.52	10-fold CV
KYG <sup>2</sup>	86	-	50	80	-	Jack-knife
Chen and Lim <sup>3</sup>	69	51	-	-	-	Independent test
Maetschke and Yuan <sup>4</sup>	144	58	85	-	0.38	5-fold CV
Struct-NB <sup>5</sup>	147	35.9	44.3	-	-	Sequence-based CV
Li et al. <sup>6</sup>	107	87.8	93.4	-	0.47	6-fold CV
OPRA <sup>7</sup>	12	-	-	-	-	Excluding homology by 70% sequence identity
Liu et al. <sup>8</sup>	205	-	-	84.5	-	5 fold CV
SPalign <sup>9*</sup>	257	40	91	73	0.34	Independent Test
SPOT-Struc <sup>10*</sup>	77	75	96	93	0.72	Excluding homology by 30% sequence identity
<b>Sequence-based</b>						
BindN <sup>11</sup>	25	66.3	69.8	69.3	0.27	5-fold CV
RNABindR <sup>12</sup>	147	37	90	85.5	-	Independent test
Pprint <sup>13</sup>	86	70.1	75.5	75.4	0.32	5-fold CV
RNAProB <sup>14</sup>	147	77.7	71.1	74.4	0.49	5-fold CV
BindN+ <sup>15</sup>	25	77.7	71.6	78.7	0.39	5-fold CV
NAPS <sup>16</sup>	109	75	77	76	0.52	10-fold CV
PBRpred <sup>17</sup>	48	-	-	-	0.51	5-fold CV
PiRaNhA <sup>18</sup>	81	56.3	92.8	87.2	0.499	Independent test
PRBR <sup>19</sup>	180	53.7	96.97	88.63	0.563	Independent test
SPOT-Seq <sup>20</sup>	116	53	93	85	0.47	Excluding homology by 30% sequence identity

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