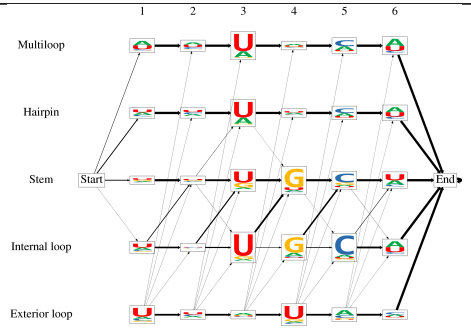
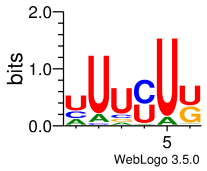
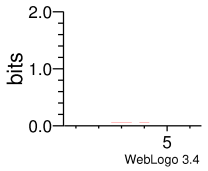
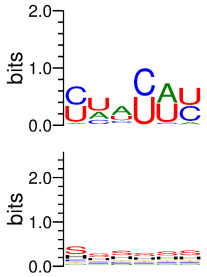
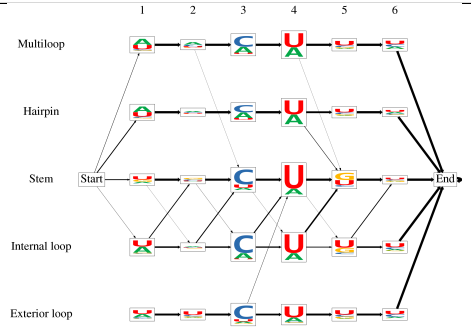
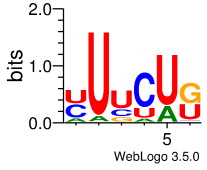
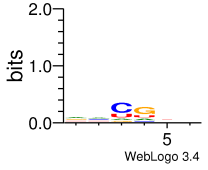
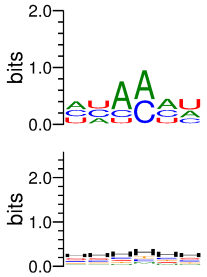
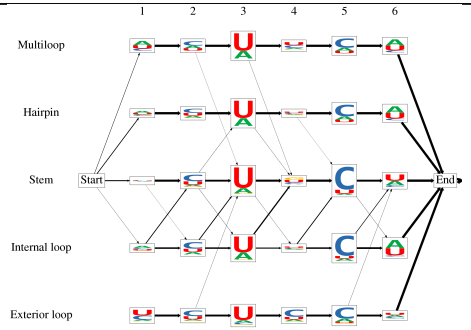
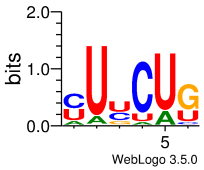
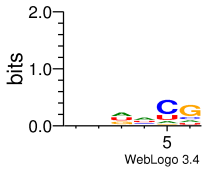
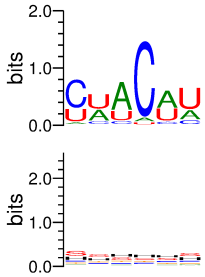
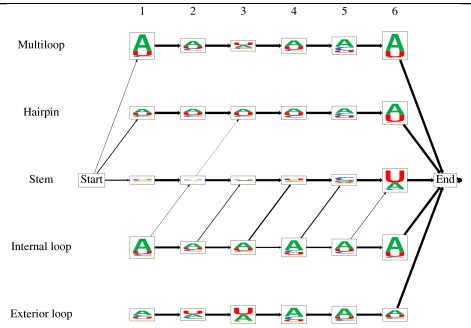
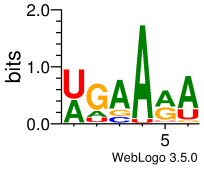
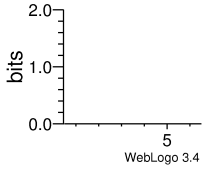
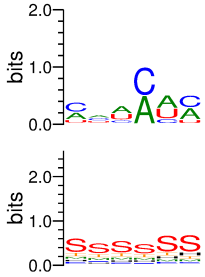
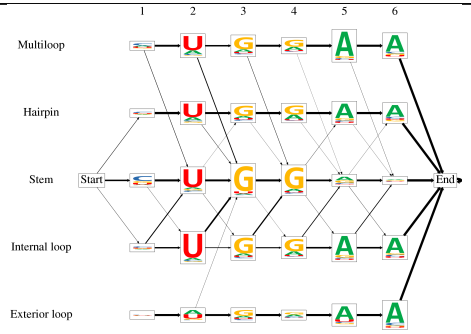
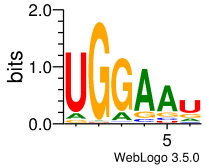
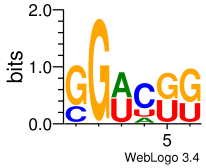
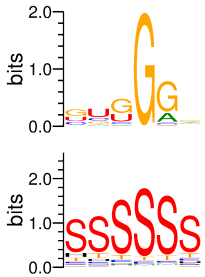
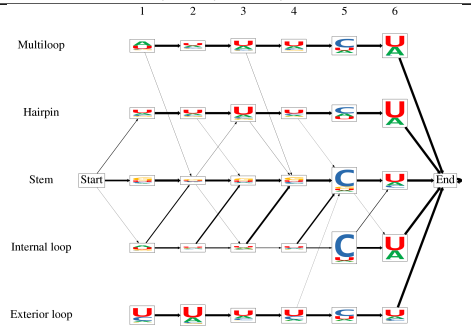
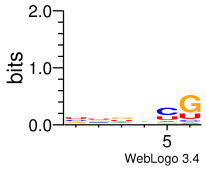
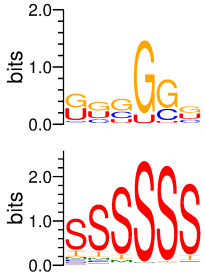
Additional File 2: Full CLIP-Seq results

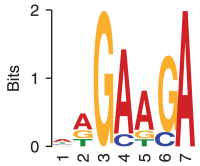
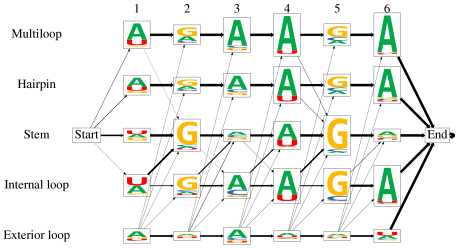
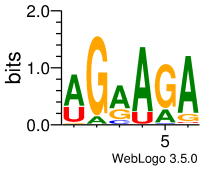
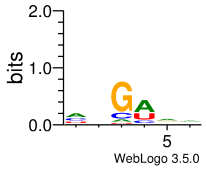
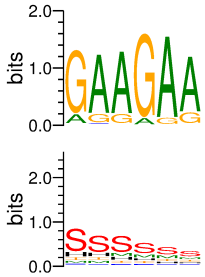
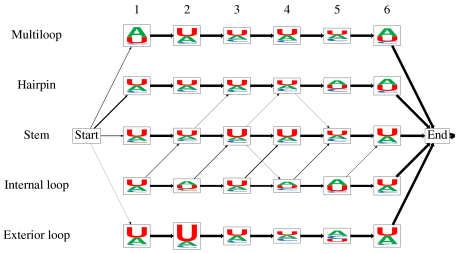
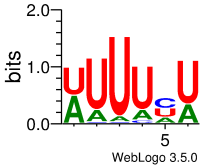
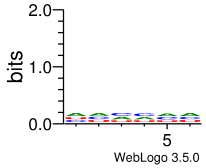
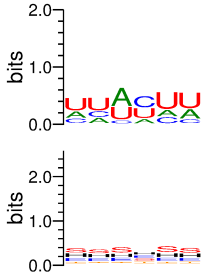
On the following pages, the motifs that were recovered by *MEMERIS*, *RNAcontext*, *GraphProt*, and ssHMM from each of the 25 CLIP-Seq datasets are shown. The table has the following six columns:

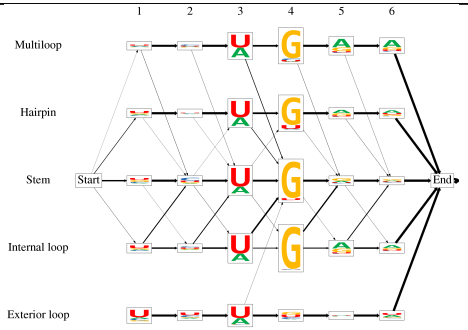
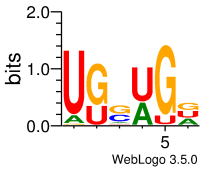
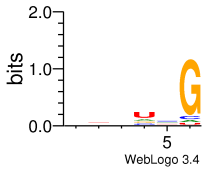
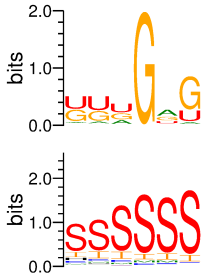
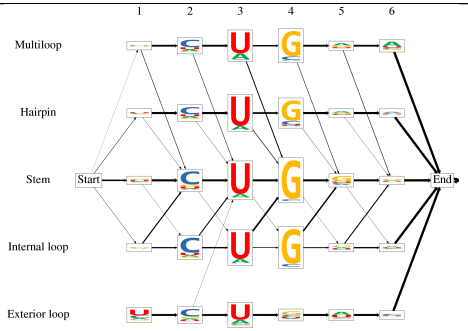
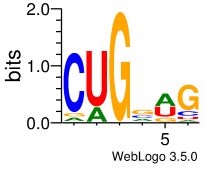
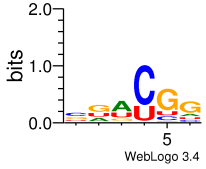
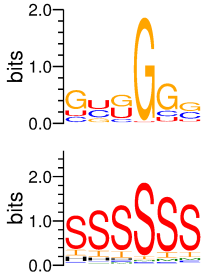
1. Protein - Name of the RBP (with protocol in parentheses if multiple CLIP-Seq datasets exist for the protein)
2. Literature motif - Motifs published by other studies (if present)
3. ssHMM - Visualization of the ssHMM trained on the CLIP-Seq dataset. Below the visualization, four numbers are printed: the sequence, structure, and combined information content for comparison with *GraphProt* (in red) and the sequence information content for comparison with *MEMERIS* and *RNAcontext* (in blue)
4. MEMERIS - Sequence motif by *MEMERIS*. Below, the information content of the sequence logo is printed.
5. RNAcontext - Sequence motif by *RNAcontext*. Below, the information content of the sequence logo is printed.
6. GraphProt - Sequence and structure motif by *GraphProt*. Below, the sequence, structure, and combined information content of the logos is printed.

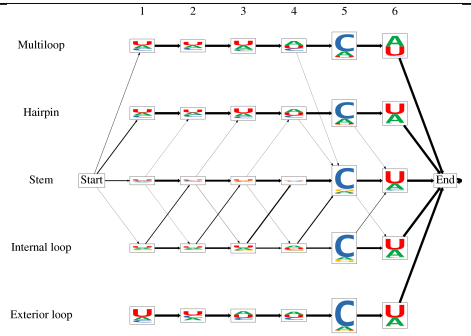
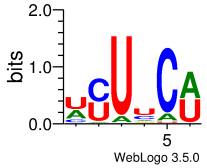
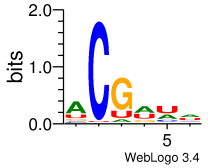
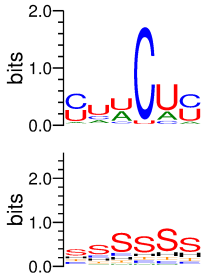
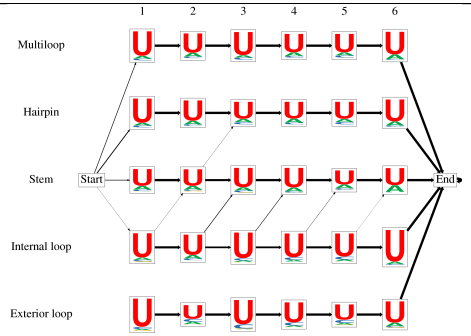
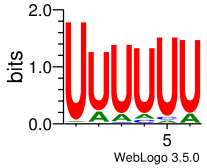
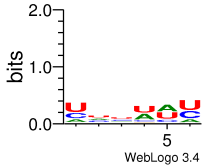
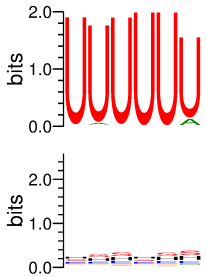
Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
Ago1234					
		0.69/0.86/1.82/0.34	0.91	0.04	0.64/0.34/0.95
Ago2 (HITSCLIP)					
		0.67/0.85/1.76/0.42	0.91	0.15	0.56/0.31/0.84

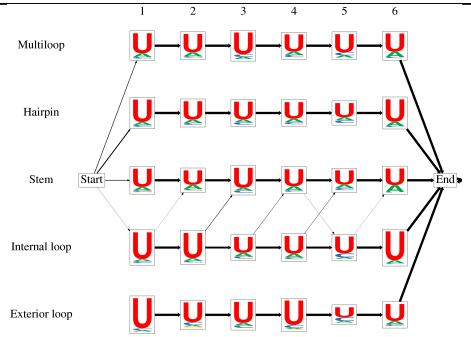
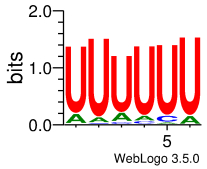
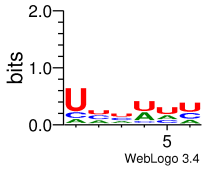
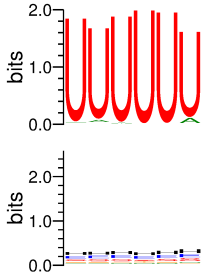
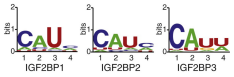
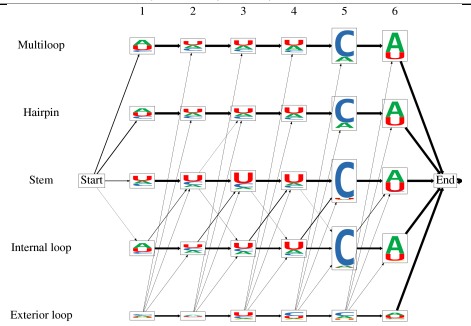
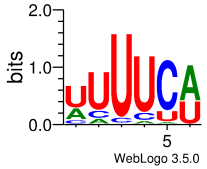
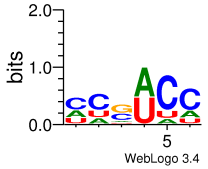
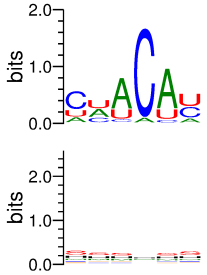
Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
Ago2 (PARCLIP)					
		0.88/0.9/1.87/0.52	0.92	0.21	0.8/0.28/1.04
CAPRIN1					
		0.7/0.84/1.82/0.24	0.93	0.01	0.47/0.57/1.03

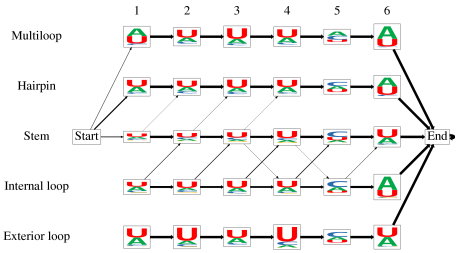
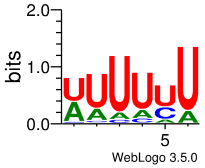
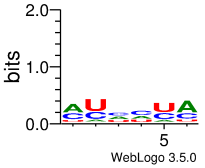
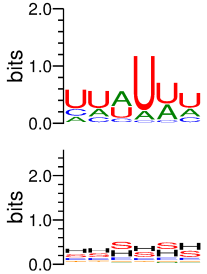
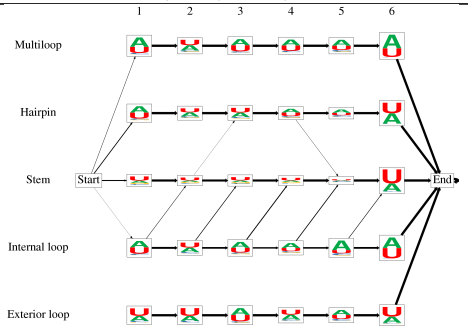
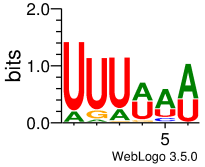
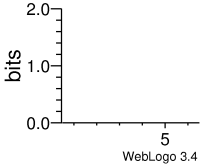
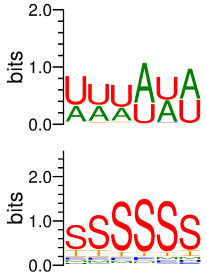
Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
DGCR8					
		1.4/1.2/2.71/0.66	1.04	1.06	0.76/1.49/2.2
DICER			runtime exceeded 7 days		
		0.91/1.62/2.8/0.31		0.21	0.65/1.75/2.38

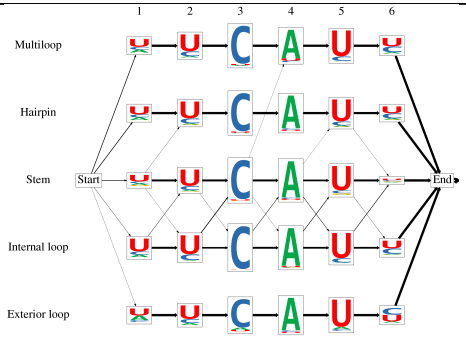
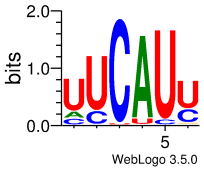
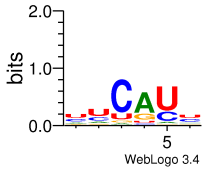
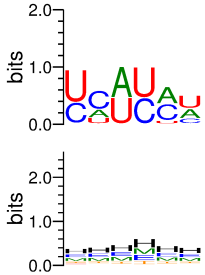
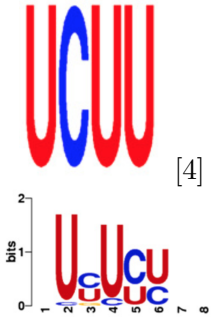
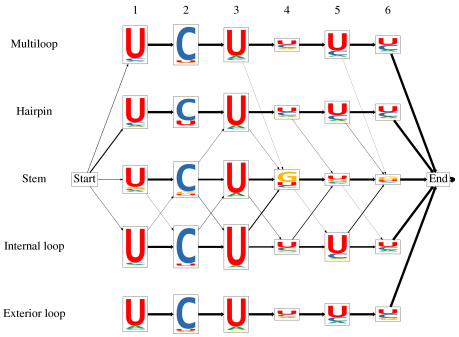
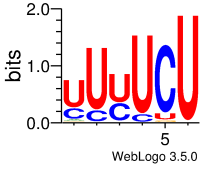
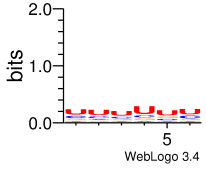
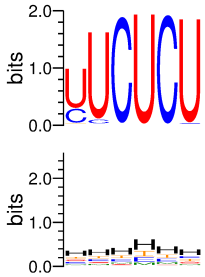
Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
EIF4A3					
		1.45/0.99/2.56/0.74	1.12	0.27	1.35/0.58/1.89
EWSR1	AU-rich stem-loops [7]				
		1.07/1.11/2.25/0.49	1.03	0.18	0.52/0.37/0.91

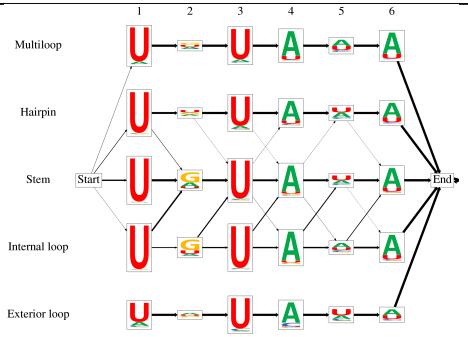
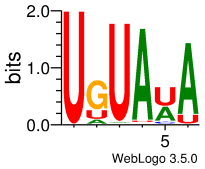
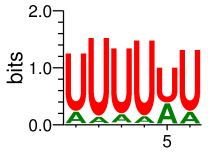
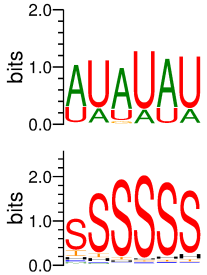
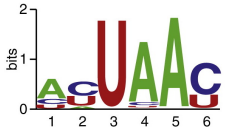
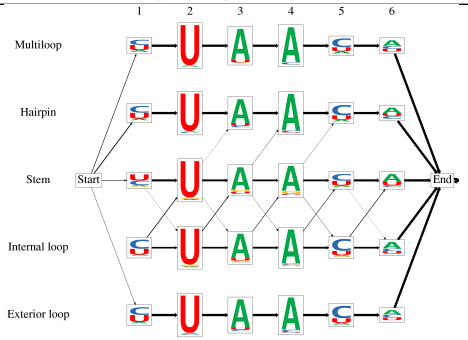
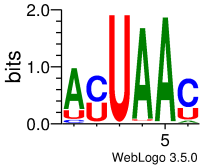
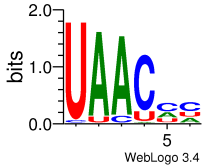
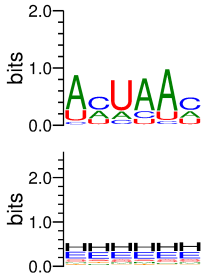
Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
EZH2					
		0.84/1.66/2.55/0.55	0.93	0.27	0.74/1.37/2.05
FMRP					
		0.98/1.83/2.84/0.67	0.97	0.47	0.8/1.53/2.32

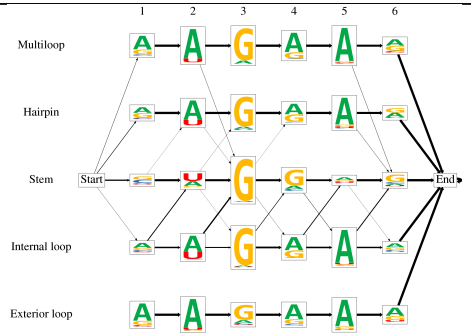
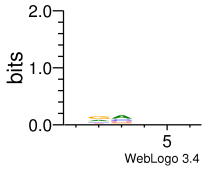
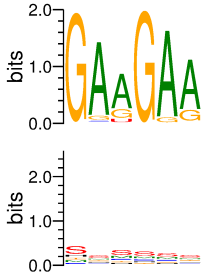
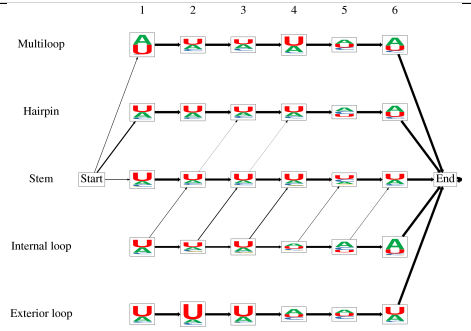
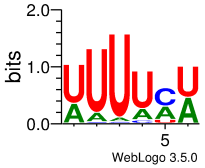
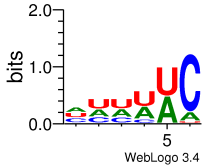
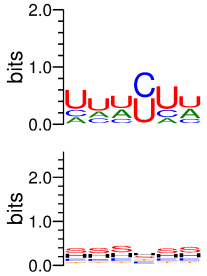
Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
FXR2					
		0.88/1.48/2.42/0.4	0.88	0.63	0.71/0.62/1.29
HuR (HITSCLIP)	AU-rich regions [1]				
		2/1.33/3.32/1.05	1.45	0.28	1.74/0.77/2.41

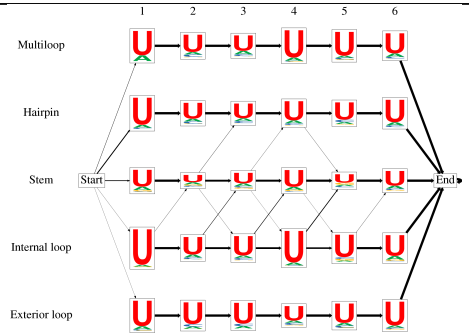
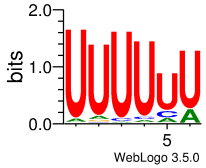
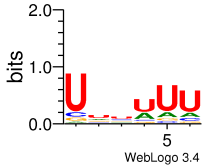
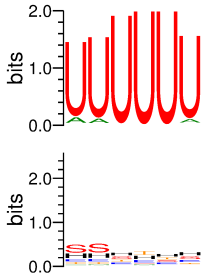
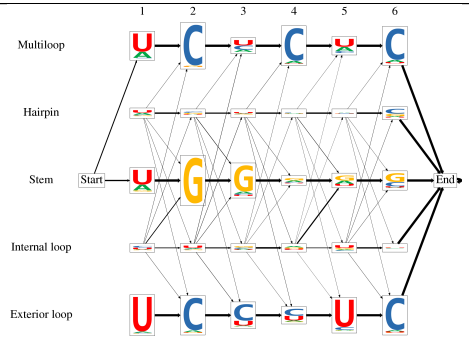
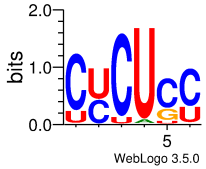
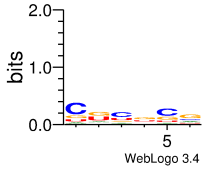
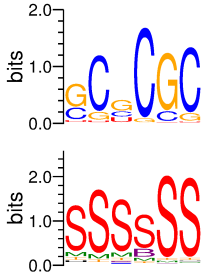
Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
HuR (PARCLIP)	AU-rich regions [1]	 2/0.91/2.9/1.01	 1.39	 0.37	 1.79/0.36/2.06
IGF2BP1/2/3	 [2]	 1.14/0.85/2.08/0.7	 1.08	 0.64	 0.87/0.32/1.19

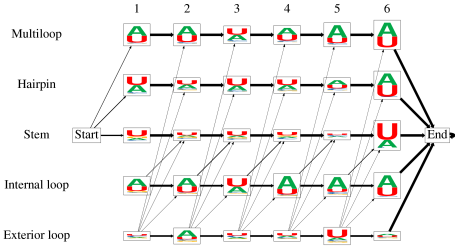
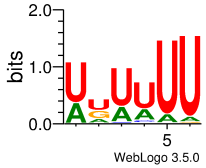
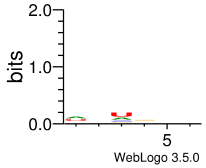
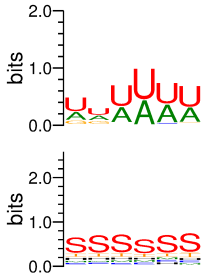
Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
LIN28B					
		1.03/1.3/2.37/0.49	0.96	0.33	0.68/0.42/1.09
MOV10					
		1.03/0.77/2.17/0.42	1.00	0.01	0.86/1.33/2.14

Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
Nova	UCAUY [3]	 1.7/1.04/2.75/1.05	 1.31	 0.46	 0.77/0.44/1.14
PTBP1	 [4] [5]	 1.54/1.44/2.99/0.82	 1.28	 0.24	 1.69/0.43/2.02

Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
PUM2	[2]	 1.54/1.26/2.89/1.07	 1.38	 1.31	 1.11/1.68/2.7
QKI	 [2]	 1.56/1.17/2.6/1.02	 1.34	 1.14	 0.73/0.52/1.22

Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
SRSF1/SF2	[6]	 1.44/1.59/3.42/0.74	runtime exceeded 7 days	 0.07	 1.48/0.29/1.79
TAF2N	AU-rich stem-loops [7]	 1.12/1.59/2.76/0.5	 1.07	 0.65	 0.59/0.38/0.99

Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
TIA1	U-rich region [8]	 1.92/0.68/2.61/0.94	 1.38	 0.47	 1.72/0.37/2
YY1		 0.84/1.33/2.84/0.52	 1.21	 0.23	 1.09/1.6/2.61

Protein	Literature motif	ssHMM	MEMERIS	RNAcontext	GraphProt
ZC3H7B					
		0.93/0.78/1.97/0.41	1.03	0.33	0.64/0.68/1.28

Bibliography

[1] Peng, S.S.-Y., Chen, C.-Y.A., Xu, N., Shyu, A.-B.: Rna stabilization by the au-rich element binding protein, hur, an elav protein. The EMBO journal **17**(12), 3461–3470 (1998)

[2] Hafner, M., Landthaler, M., Burger, L., Khorshid, M., Hausser, J., Berninger, P., Rothballer, A., Ascano, M., Jungkamp, A.-C., Munschauer, M., Ulrich, A., Wardle, G.S., Dewell, S., Zavolan, M., Tuschl, T.: Transcriptome-wide Identification of RNA-Binding Protein and MicroRNA Target Sites by PAR-CLIP. Cell **141**(1), 129–141 (2010)

[3] Jensen, K.B., Dredge, B.K., Stefani, G., Zhong, R., Buckanovich, R.J., Okano, H.J., Yang, Y.Y.L., Darnell, R.B.: Nova-1 regulates neuron-specific alternative splicing and is essential for neuronal viability. Neuron **25**(2), 359–371 (2000)

[4] I, P., Ch, L., Jg, M., Jg, P.: Mutation of PTB binding sites causes misregulation of alternative 3' splice site selection in vivo., Mutation of PTB binding sites causes misregulation of alternative 3' splice site selection in vivo. RNA **3 3**(7, 7), 764–764778 (1997)

[5] Xue, Y., Zhou, Y., Wu, T., Zhu, T., Ji, X., Kwon, Y.-S., Zhang, C., Yeo, G., Black, D.L., Sun, H., Fu, X.-D., Zhang, Y.: Genome-wide Analysis of PTB-RNA Interactions Reveals a Strategy Used by the General Splicing Repressor to Modulate Exon Inclusion or Skipping. Molecular Cell **36**(6), 996–1006 (2009)

[6] Sanford, J.R., Wang, X., Mort, M., VanDuyn, N., Cooper, D.N., Mooney, S.D., Edenberg, H.J., Liu, Y.: Splicing factor SFRS1 recognizes a functionally diverse landscape of RNA transcripts. Genome Research **19**(3), 381–394 (2009)

[7] Hoell, J.I., Larsson, E., Runge, S., Nusbaum, J.D., Duggimpudi, S., Farazi, T.A., Hafner, M., Borkhardt, A., Sander, C., Tuschl, T.: RNA targets of wild-type and mutant FET family proteins. Nature Structural & Molecular Biology **18**(12), 1428–1431 (2011)

[8] Dember, L.M., Kim, N.D., Liu, K.-Q., Anderson, P.: Individual RNA Recognition Motifs of TIA-1 and TIAR Have Different RNA Binding Specificities. Journal of Biological Chemistry **271**(5), 2783–2788 (1996)