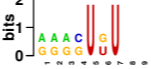
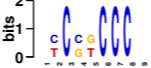




Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.006	33.6	10/10	Y	↔	0.87	AACUUUU	-	-
	5'	0.004	21.0	10/10	Y	→	1.00	TCCTCCC	DPY-27_DPY_27, DPY-27, SPTF_3	-
	5'	0.003	15.9	9/10	-	→	0.97	AATCGAT	PIE_1	-
	5'	0.002	11.5	8/10	-	←	0.76	CATTGTA	NHR_5	-