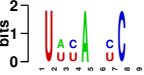
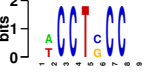
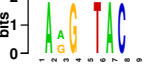
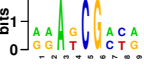


Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.007	33.9	10/10	Y	↔	0.98	UUUAUUC	-	-
	5'	0.003	17.3	10/10	-	↔	0.94	ACCTGCC	DPY-27_DPY_27, DPY-27	-
	5'	0.003	12.3	9/10	-	-	0.69	AGGTTAC	DMD_4	-
	5'	0.003	16.0	8/10	-	←	1.00	AATCGAT	PIE_1	-