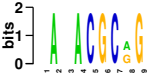
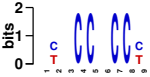
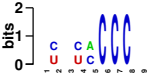
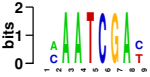



Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.004	20.3	10/10	-	←	1.00	AGACGCA	MADF_9	-
	5'	0.004	20.3	10/10	-	↔	1.00	CCCCGCC	-	-
	3'UTR	0.004	19.2	10/10	Y	→	1.00	UUUCCCC	-	-
	5'	0.003	15.4	8/10	Y	←	1.00	AAATCGA	CEH_28, CEH-28, PIE_1 ...	-
	3'UTR	0.002	11.1	8/10	-	→	0.30	AGCUAUG	-	-