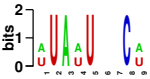

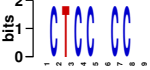


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.005	27.8	10/10	Y	→	0.87	UAUUUUC	-	-
	5'	0.003	17.8	10/10	-	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH-38 ...	-
	5'	0.003	17.6	9/10	-	→	1.00	CTCCGCC	PIE_1	-