



Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.007	38.7	10/10	Y	→	0.97	AAAACAA	-	-
	5'	0.004	23.4	10/10	-	↔	1.00	ATCGATA	CEH_28, CEH-28, CEH_38 ...	-
	5'	0.004	21.5	10/10	Y	↔	1.00	CTCCGCC	EGRH_3	-
	5'	0.002	11.1	7/10	-	→	0.56	ACCTGCC	-	-