optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3’UTR	0.006	28.6	10/10	Y	↔	0.97	AAAAAAU	-	-
	5’	0.003	17.5	10/10	-	↔	0.99	AATCGAT	PIE_1, CEH_28, CEH-28 ...	-
	5’	0.003	12.8	10/10	-	←	0.91	ATGTACA	DAF-16, PHA_4.3, FKH_8	-
	5’	0.002	10.3	8/10	-	←	0.99	AAGGTCA	NHR_91, SEX_1, NHR_84 ...	-