



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.006	32.6	10/10	-	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH-28 ...	-
	5'	0.004	18.5	10/10	-	↔	0.35	ATAGTAA	MEF_2	-
	5'	0.003	12.3	9/10	-	←	0.38	TGGTTGC	DAF_19, PIE_1	-