optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5′	0.014	80.6	10/10	Y	↔	1.00	CAGGTGA	SNAI_1, HLH_1.4	-
	5′	0.004	22.4	10/10	-	↔	0.55	ATCAAAT	PIE_1	-
	5′	0.003	14.8	8/10	-	←	0.22	AAGGTAG	PIE_1, NSY_7	-
	5′	0.007	37.5	10/10	-	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH-28 ...	-
	5′	0.006	32.2	10/10	Y	↔	0.98	CTCTCTC	KLU_2	-