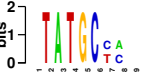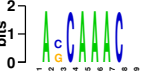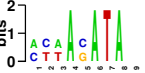| optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
ATCGAT (logo)	5'	0.004	21.8	10/10	–	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH_38 ...	–
CTCTGC (logo)	5'	0.003	12.4	8/10	Y	→	0.90	CTCTTCC	EOR_1.2, EOR-1, PIE_1	–
TATGC (logo)	5'	0.003	13.7	9/10	–	←	0.70	TATGCTA	–	–
ACCAAAC (logo)	5'	0.002	10.8	8/10	–	–	0.68	ACCAAAC	PIE_1	–
ACAACATA (logo)	5'	0.003	14.1	10/10	–	↔	0.83	TAAGATA	–	–
AGATCA (logo)	5'	0.003	12.3	8/10	–	←	0.94	ATGATCA	NHR_1_NHR_10_NHR_101_NHR_17_NHR_40_NHR_47_NHR_68, NHR_119_NHR_31_	–