
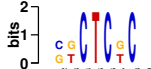




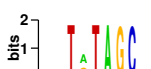


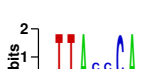
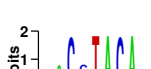



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.010	50.8	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH_38 ...	-
	5'	0.007	34.0	10/10	Y	↔	0.99	CTCTCTC	PIE_1	-
	5'	0.003	15.0	10/10	-	↔	0.99	CTCCACG	PIE_1	-
	5'	0.006	31.0	10/10	-	↔	0.90	TACCAAA	TBX_40	-
	5'	0.006	28.1	10/10	Y	↔	0.98	CAGGTGA	SNAI_1, UNC-62	-
	5'	0.006	28.5	10/10	-	↔	0.73	CATATAA	-	-
	5'	0.004	20.9	10/10	-	↔	0.51	TTATAGC	HAM_2	-
	5'	0.004	17.8	10/10	-	↔	0.44	ATAGTAA	MEF_2, DAF_19	-
	5'	0.003	16.3	9/10	-	→	0.92	TTGTGAC	NHR_102_NHR_142_NHR_170_NHR_213_NHR_218_NHR_54, NHR_84, NHR_134_N	-
	5'	0.003	15.1	10/10	-	←	0.75	TTACTCA	JUN_1, PIE_1	-
	5'	0.003	14.9	10/10	-	→	0.59	ACTTACA	NHR_2_NHR_85	-
	5'	0.003	11.7	6/10	-	→	0.93	CCGCGGA	MADF_9, PIE_1	-