
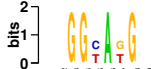

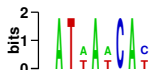




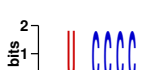
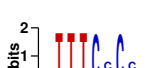




optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.016	79.5	10/10	Y	↔	0.99	AAAUAAA	-	-
	5'	0.006	29.3	10/10	-	↔	0.67	AGGCAGG	-	-
	5'	0.005	27.3	10/10	-	↔	0.73	ATAGTAA	-	-
	5'	0.004	17.0	10/10	-	→	0.45	ATAATCA	FKH-2_FKH_2, FKH_6	-
	5'	0.003	15.0	9/10	-	↔	0.80	TAGTATC	PIE_1, DMD_4, MED_1_MED_2	-
	5'	0.003	13.0	8/10	-	←	0.79	AACTTTG	PIE_1, NHR_64, NHR_69 ...	-
	5'	0.010	53.0	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH_38 ...	-
	5'	0.009	44.4	10/10	-	↔	1.00	ACGAAGA	-	-
	3'UTR	0.008	39.4	10/10	Y	↔	1.00	UUUCCCC	-	-
	5'	0.004	22.4	10/10	-	→	0.92	TTTCCCC	BLMP_1.2, EFL_3, PIE_1	-
	5'	0.003	14.6	9/10	-	↔	0.69	AATCGCG	DPY-27, DPY-27_DPY_27, PIE_1	-
	5'	0.002	9.1	6/10	-	←	0.84	CTGTTTC	SNPC_4.2, PIE_1	-