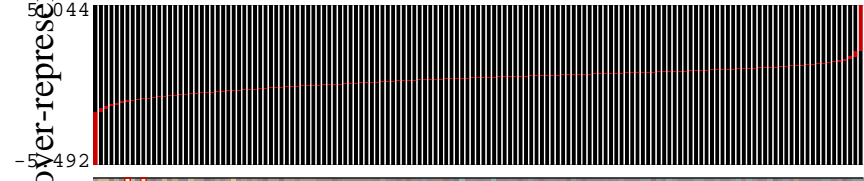


over-representation

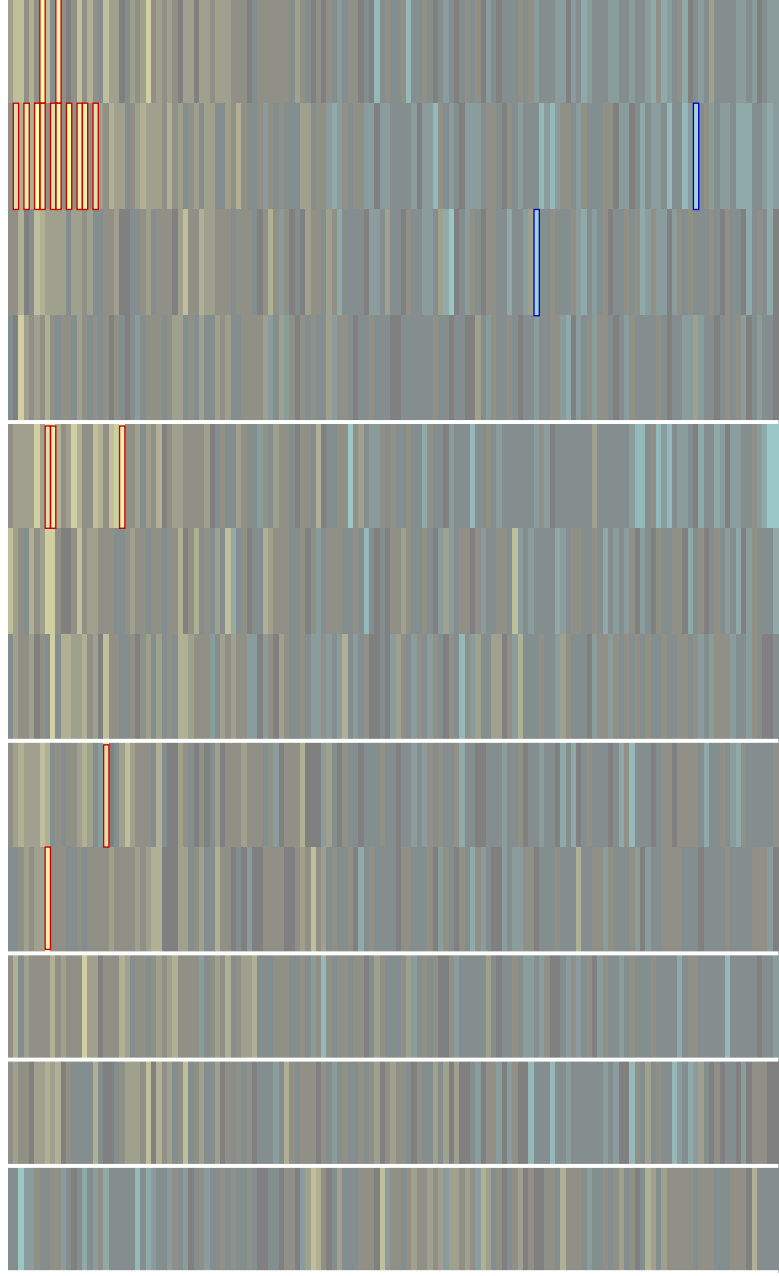
under-representation

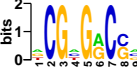
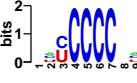



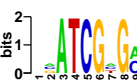
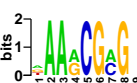
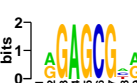

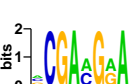


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structural protease activity, p=1e-09  
vacuole, p<0.01



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	5'	0.024	19.8	10/10	-	-	1.00	CGAGACC	-
	3'UTR	0.022	17.4	10/10	Y	→	1.00	UCCCCC	-
	5'	0.018	13.1	10/10	-	←	0.99	ATCGATA	-
	5'	0.014	8.2	8/10	-	←	0.96	GACGCGC	-
	3'UTR	0.017	12.0	10/10	-	→	0.99	UUCGUUU	-
	5'	0.017	11.1	10/10	Y	-	0.71	AATCGCG	-
	5'	0.015	9.7	10/10	-	←	0.92	AAACGAG	-
	5'	0.017	10.8	10/10	-	←	1.00	AGAGCGC	-
	5'	0.013	7.2	6/10	-	←	0.87	TCGTTGC	-
	5'	0.015	9.1	10/10	-	←	0.93	CGAAGAA	-
	5'	0.015	8.7	9/10	-	←	0.95	CCGTTCG	-
	5'	0.013	6.7	7/10	-	←	0.79	ATATGTA	-