



DREME

Discriminative Regular Expression Motif Elicitation

For further information on how to interpret these results or to get a copy of the MEME software please access <http://meme.nbcr.net>.

If you use DREME in your research please cite the following paper:

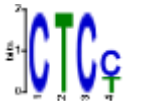





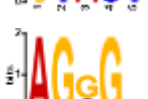

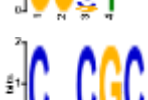

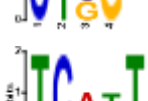
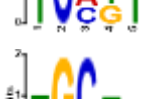

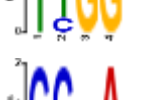
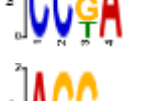

Timothy L. Bailey, "DREME: Motif discovery in transcription factor ChIP-seq data", *Bioinformatics*, 27(12):1653-1659, 2011. [\[full text\]](#)

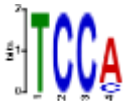

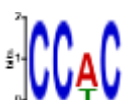

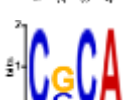
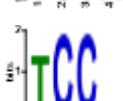
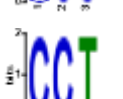
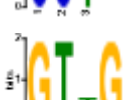
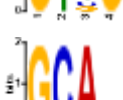
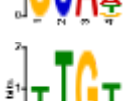
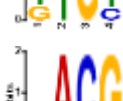
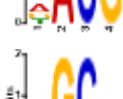
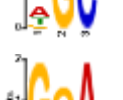
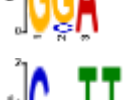
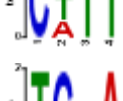
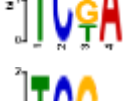
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DISCOVERED MOTIFS

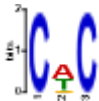

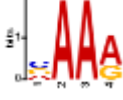
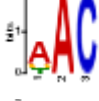
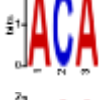
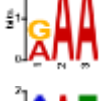
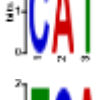
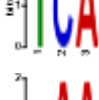
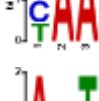
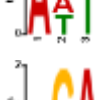
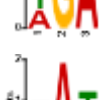
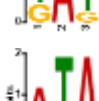

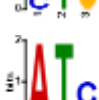
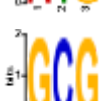

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	Motif	Logo	E-value	Unersased E-value	More	Submit/Download
1.	TCCSC		8.3e-076	8.3e-076	↓	→
2.	CCCTD		1.1e-069	2.4e-059	↓	→
3.	CCCVC		3.0e-071	8.7e-065	↓	→
4.	CTCST		1.4e-069	1.8e-070	↓	→
5.	VCGCC		2.3e-067	1.5e-064	↓	→
6.	CCHGT		3.4e-067	5.6e-066	↓	→
7.	TYTCC		8.7e-065	1.4e-069	↓	→
8.	BCTCT		4.5e-063	1.2e-056	↓	→
9.	CGRSC		4.3e-061	7.3e-057	↓	→
10.	CCTDG		8.7e-059	7.4e-066	↓	→
11.	CTGBC		6.4e-056	1.4e-062	↓	→

	Motif	Logo	E-value	Unersased E-value	More	Submit/Download
12.	CTCY		8.1e-054	1.6e-034	↓	...>
13.	CGWCK		1.6e-054	2.0e-050	↓	...>
14.	GCTDC		2.5e-053	6.7e-056	↓	...>
15.	TACCD		3.3e-049	7.9e-044	↓	...>
16.	CCCB		4.1e-049	1.2e-039	↓	...>
17.	GCASC		1.2e-049	3.1e-055	↓	...>
18.	AGSG		1.0e-048	9.1e-048	↓	...>
19.	GGBT		1.0e-050	5.1e-054	↓	...>
20.	CDCGC		5.3e-045	2.0e-057	↓	...>
21.	CTSG		1.1e-046	7.7e-034	↓	...>
22.	TCMKT		2.1e-043	2.8e-041	↓	...>
23.	YGCY		6.7e-048	5.3e-028	↓	...>
24.	TYGG		1.6e-041	6.1e-038	↓	...>
25.	CCKA		1.9e-040	2.5e-030	↓	...>
26.	AGG		4.4e-040	2.0e-033	↓	...>
27.	GGK		2.6e-040	1.5e-025	↓	...>

	Motif	Logo	E-value	Unersased E-value	More	Submit/Download
28.	TCCM		2.2e-039	2.2e-020	↓	...>
29.	GCC		2.3e-037	1.0e-017	↓	...>
30.	CCWC		7.5e-039	3.9e-019	↓	...>
31.	CAGY		5.1e-037	1.8e-034	↓	...>
32.	CSCA		7.4e-038	3.3e-028	↓	...>
33.	YCC		9.3e-040	7.2e-005	↓	...>
34.	CCT		6.0e-039	2.4e-015	↓	...>
35.	GTBG		8.0e-038	9.2e-036	↓	...>
36.	GCAD		3.5e-038	1.8e-023	↓	...>
37.	KTGY		2.4e-037	9.7e-029	↓	...>
38.	DACG		3.1e-036	2.0e-026	↓	...>
39.	DGC		1.1e-035	1.9e-006	↓	...>
40.	GSA		5.4e-035	1.0e-008	↓	...>
41.	CWTT		8.6e-035	5.9e-018	↓	...>
42.	TCKA		8.8e-035	2.0e-025	↓	...>
43.	TCG		5.1e-038	5.5e-021	↓	...>

	Motif	Logo	E-value	Unersased E-value	More	Submit/Download
44.	TTTK		1.3e-033	6.7e-029	↓	...>
45.	AAMAA		4.2e-032	6.2e-028	↓	...>
46.	CVG		5.6e-032	1.0e-005	↓	...>
47.	TTT		2.7e-031	4.6e-013	↓	...>
48.	MGAS		2.7e-031	1.9e-016	↓	...>
49.	GTS		7.7e-031	3.6e-013	↓	...>
50.	MGT		9.4e-032	5.0e-012	↓	...>
51.	TTC		2.4e-031	8.3e-009	↓	...>
52.	WYACA		2.5e-030	2.1e-018	↓	...>
53.	BACM		1.8e-030	4.4e-002	↓	...>
54.	ACS		9.4e-033	2.7e-005	↓	...>
55.	CSA		7.8e-030	3.5e-002	↓	...>
56.	BACT		6.0e-029	4.4e-014	↓	...>
57.	STT		2.3e-031	1.5e-005	↓	...>
58.	YTA		2.1e-031	1.7e-010	↓	...>
59.	TST		1.0e-028	2.1e-005	↓	...>

	Motif	Logo	E-value	Unersased E-value	More	Submit/Download
60.	CDC		4.1e-029	1.0e-001	↓	...>
61.	RCT		8.5e-026	2.5e-007	↓	...>
62.	VAAR		2.1e-025	2.1e-013	↓	...>
63.	DAC		1.5e-027	8.4e-002	↓	...>
64.	ACA		4.1e-027	1.3e-008	↓	...>
65.	RAA		5.4e-026	7.9e-012	↓	...>
66.	CAT		2.7e-024	9.3e-009	↓	...>
67.	TCA		1.8e-024	9.1e-008	↓	...>
68.	YAA		7.1e-025	7.5e-006	↓	...>
69.	AWT		1.8e-025	6.7e-012	↓	...>
70.	WGA		9.5e-025	1.7e-008	↓	...>
71.	KAK		3.9e-026	2.7e-007	↓	...>
72.	RTA		1.6e-024	5.8e-014	↓	...>
73.	YTG		4.1e-023	1.5e-012	↓	...>
74.	ATS		3.7e-019	2.0e-008	↓	...>
75.	GCG		3.8e-011	2.1e-028	↓	...>

	Motif	Logo	E-value	Unersased E-value	More	Submit/Download
76.	AAG		1.9e-009	5.7e-019	↓	...>
77.	TGG		2.4e-007	8.2e-032	↓	...>

INPUTS & SETTINGS

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Sequences

Source	Alphabet	Sequence Count
untreated.5utr.fa	DNA	1184

Control Sequences

Source	Sequence Count
notenriched.5utr.fa	5293

Background

Name	Bg.			Bg.	Name
Adenine	0.246	A	~	T	Thymine
Cytosine	0.305	C	~	G	Guanine

Other Settings

Strand Handling	Only the given strand is processed
# REs to Generalize	100
Shuffle Seed	1
E-value Threshold	0.05
Max Motif Count	No maximum motif count.
Max Run Time	No maximum running time.

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DREME version

4.12.0 (Release date: Tue Jun 27 16:22:50 2017 -0700)

Reference

Timothy L. Bailey, "DREME: Motif discovery in transcription factor ChIP-seq data", *Bioinformatics*, 27(12):1653-1659, 2011. [\[full text\]](#)

Command line

```
dreme -dna -p untreated.5utr.fa -n notenriched.5utr.fa -norc -oc untreated_5utr
```