



For further information on how to interpret these results please access <https://meme-suite.org/meme/doc/spamo-output-format.html>.
To get a copy of the MEME software please access <https://meme-suite.org>.


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

Tom Whittington, Martin C. Frith, James Johnson and Timothy L. Bailey "Inferring transcription factor complexes from ChIP-seq data", *Nucleic Acids Res.* **39**(15):e98, 2011. [\[full text\]](#)

[PRIMARY MOTIFS](#) | [SEQUENCE DATABASE](#) | [SECONDARY MOTIF DATABASES](#) | [SPACING ANALYSIS](#) | [INPUTS AND SETTINGS](#) | [PROGRAM INFORMATION](#) | [RESULTS IN TSV FORMAT](#) | CONTRIBUTING SEQUENCE IDS [\[DOWNLOAD PLAIN\]](#) [\[DOWNLOAD BED\]](#)

PRIMARY MOTIFS

[Next Top](#)

Database	Name	Preview	Significant Secondaries	List																		
meme.xml	CCTYRGCTCCCRAR (MEME-3)		7	GCTGGGATTACAGGC (MEME-2), 3-ACAGGCRTGAGCCAC (STREME-3), 1-																		
<div>Alphabet</div> <div>Background source: the file './background'</div> <table><thead><tr><th>Name</th><th>Bg.</th><th></th><th></th><th>Bg.</th><th>Name</th></tr></thead><tbody><tr><td>Adenine</td><td>0.2278</td><td>A</td><td>~</td><td>T</td><td>Thymine</td></tr><tr><td>Cytosine</td><td>0.2722</td><td>C</td><td>~</td><td>G</td><td>Guanine</td></tr></tbody></table>					Name	Bg.			Bg.	Name	Adenine	0.2278	A	~	T	Thymine	Cytosine	0.2722	C	~	G	Guanine
Name	Bg.			Bg.	Name																	
Adenine	0.2278	A	~	T	Thymine																	
Cytosine	0.2722	C	~	G	Guanine																	

SEQUENCE DATABASE

[Next Previous Top](#)

Name	Last Modified	Contained	Too Short	Too Masked	No Primary	Too Similar	Used
Galaxy7-hypoacetylation_fasta	Thu Mar 2 08:11:33 2023	1148	0	0	74	470	604

SECONDARY MOTIF DATABASES

[Next Previous Top](#)

SETTINGS

[Next](#) [Previous](#) [Top](#)

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[Next](#) [Previous](#) [Top](#)

Best downstream / same
Orientation: strand

Primary Motif Logo



Secondary Motif Logo



Inferred Secondary Motif Logo

[Download as EPS](#)

Alignment Logo

Up+

Up-

Dn+

Dn-

[Download as EPS](#)

Spacings

Gap	Orientation	p-value
2	dn+	0.00e+0
2	up-/dn+	0.00e+0
2	dn+/dn-	0.00e+0
2	all	0.00e+0
102	up+	2.89e-15
102	up+/up-	4.89e-11
102	up+/dn-	4.89e-11
101	up+	3.75e-10
103	up+	3.75e-10
104	up+	5.79e-9
103	up+/dn-	4.73e-8
101	up+/up-	4.01e-7
103	up+/up-	4.01e-7
101	up+/dn-	4.01e-7
102	all	4.29e-7
34	dn+	1.02e-6
104	up+/up-	3.11e-6

Highlight: ☒ Selected ☒ All

Contributing Sequence IDs (213)

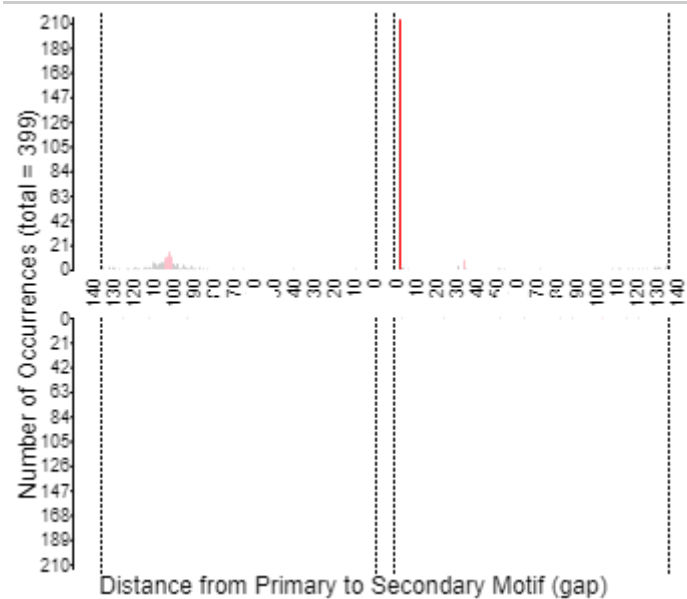
10174::chr4:184794050-184799749
 10176::chr4:184905150-184911799
 10183::chr4:185263550-185271629
 10185::chr4:185302650-185313499
 10254::chr4:186756200-186765249
 10256::chr4:186781430-186791099
 10258::chr4:186933700-186939029
 10283::chr5:269850-272399
 10298::chr5:1116580-1129679
 10667::chr5:56501430-56506299
 10792::chr5:68512880-68516199
 11264::chr5:133770180-133776179
 11272::chr5:133882480-133892179
 11274::chr5:133902550-133913399
 11401::chr5:139386650-139392579
 1140::chr1:43670600-43674649
 11514::chr5:142180550-142188049
 1160::chr1:44410650-44415499
 11650::chr5:149054880-149057479

Plain Format ▾

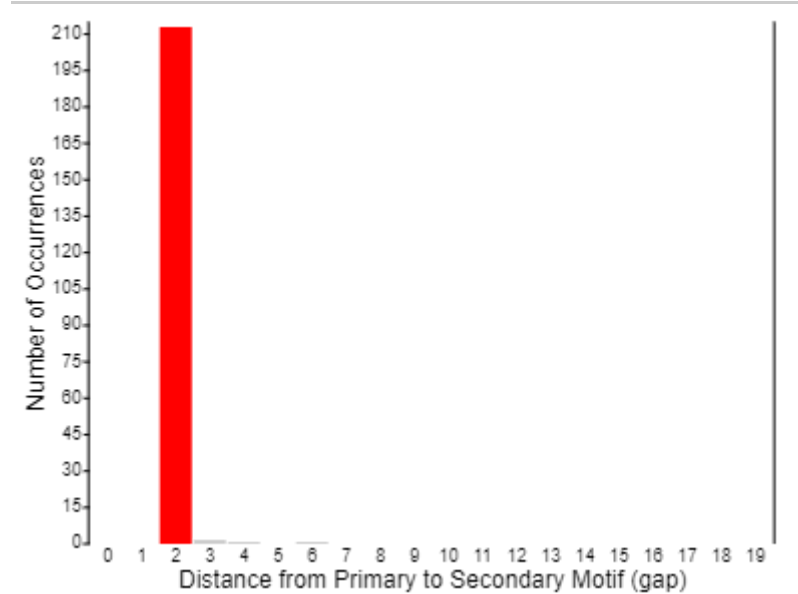
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Secondaries

Overview Graph

[Download as EPS](#)

Selected Orientation Graph

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Filter

- ☐ Top 10
- ☐ ID matches .*
- ☐ Name matches .*
- ☐ Cluster matches .*
- ☐ E-value \leq 1
- ☐ Gaps (ranges allowed) 0-10

Sort

Sort by E-value ▼

Update

Lock	ID	Name	Cluster	E-value	Best Gap	Best Orientation	Spacings
<input type="checkbox"/>	GCTGGGATTACAGGC	MEME-2	GCTGGGATTACAGGC	0.00e+0	2	downstream / same strand	
<input type="checkbox"/>	3-ACAGGCRTGAGCCAC	STREME-3	3-ACAGGCRTGAGCCAC	0.00e+0	11	downstream / same strand	
<input type="checkbox"/>	1-CTGGGAY	STREME-1	1-CTGGGAY	8.00e-312	3	downstream / same strand	
<input type="checkbox"/>	4-CCAGGCTGGWST	STREME-4	4-CCAGGCTGGWST	7.71e-165	29	upstream / same strand	
<input type="checkbox"/>	AAWAAAAAWAAAAAA	MEME-1	AAWAAAAAWAAAAAA	1.43e-53	65	upstream / opposite strand	
<input type="checkbox"/>	CCTYRGCCTCCCRAR	MEME-3	CCTYRGCCTCCCRAR	8.58e-29	17	upstream / same strand	
<input type="checkbox"/>	2-GCCTCRGCCTCCCAA	STREME-2	CCTYRGCCTCCCRAR	4.28e-17	18	upstream / same strand	

[Previous](#) [Top](#)**SpaMo version**

5.5.1 (Release date: Sun Jan 29 10:33:12 2023 -0800)

ReferenceTom Whittington, Martin C. Frith, James Johnson and Timothy L. Bailey "Inferring transcription factor complexes from ChIP-seq data", *Nucleic Acids Res.* **39**(15):e98, 2011. [\[full text\]](#)

Command line

```
spamo -verbosity 1 -oc spamo_out_2 -bgfile ./background -keepprimary -primary CCTYRGCTCCCRAR ./Galaxy7-hypoacetylation_fasta.fasta
```

Result calculation took 2 seconds

