SpaMo
Spaced Motif Analysis Tool

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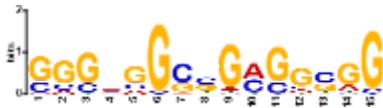To get a copy of the MEME software please access https://meme-suite.org.

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

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Database	Name	Preview	Significant Secondaries	List
meme.xml	GGGHGGCSGMGGSGG (MEME-2)		8	GCTGGGATTACAGGC (MEME-3), 3- TAATCCCAGCA (STREME-3), 5-

Alphabet

Background source: the file './background'

Name	Bg.			Bg.	Name
Adenine	0.2666	A	~ T	0.2666	Thymine
Cytosine	0.2334	C	~ G	0.2334	Guanine

SEQUENCE DATABASE

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Name	Last Modified	Contained	Too Short	Too Masked	No Primary	Too Similar	Used
Galaxy8-hyperacetylation_fasta	Thu Mar 2 08:04:26 2023	958	0	0	65	290	603

SECONDARY MOTIF DATABASES

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Name	Last Modified	Number of Motifs	Motifs Significant	Motifs Redundant
meme.xml	Thu Mar 2 13:34:08 2023	3	3	0
streme.xml	Thu Mar 2 13:34:29 2023	5	3	2

SETTINGS

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Match Score Threshold	7 (bits)	
Margin size	150	
Show Advanced Settings		

SPACING ANALYSIS FOR GGGHGGCSGMGGSGG (MEME-2)

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Secondary Motif:	GCTGGGATTACAGGC (MEME-3)	**Cluster:**	GCTGGGATTACAGGC (MEME-3)	**E-value:**	4.08e-236	**Best Gap:**	5	**Best Orientation:**	upstream / opposite 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
5	up-	5.10e-237
5	up+/up-	4.14e-203
5	up-/dn+	4.14e-203
5	all	7.45e-184
101	dn-	2.37e-12
99	dn-	5.98e-11
100	dn-	1.36e-9
101	up+/dn-	3.26e-9
101	dn+/dn-	3.26e-9
98	dn-	2.79e-8
102	dn-	2.79e-8
99	up+/dn-	4.12e-8
99	dn+/dn-	4.12e-8
98	up+/dn-	4.71e-7
100	up+/dn-	4.71e-7
100	dn+/dn-	4.71e-7
5	dn-	5.06e-7

Highlight: ☑ Selected ☑ All

Overview Graph

Number of Occurrences (total = 248)

Distance from Primary to Secondary Motif (gap)

[Download as EPS](#)

Selected Orientation Graph

Number of Occurrences

Distance from Primary to Secondary Motif (gap)

[Download as EPS](#)

Contributing Sequence IDs (113)

```
10020::chr4:156415650-15641839!
10097::chr4:169685400-16969259!
10103::chr4:169771180-16977319!
1019::chr1:39551200-39554149
10200::chr4:185665950-18566949!
1028::chr1:39656450-39663179
1029::chr1:39668980-39672849
10511::chr5:36689100-36693599
10543::chr5:39420680-39425729
10583::chr5:43063630-43068879
10641::chr5:54827750-54832679
10645::chr5:54886300-54890379
10833::chr5:72920350-72923599
10944::chr5:81642550-81646229
11548::chr5:142521680-14252387!
11550::chr5:142531550-14253704!
11596::chr5:147846830-14785517!
11733::chr5:151096950-15109894!
11807::chr5:156997500-15699962!
```
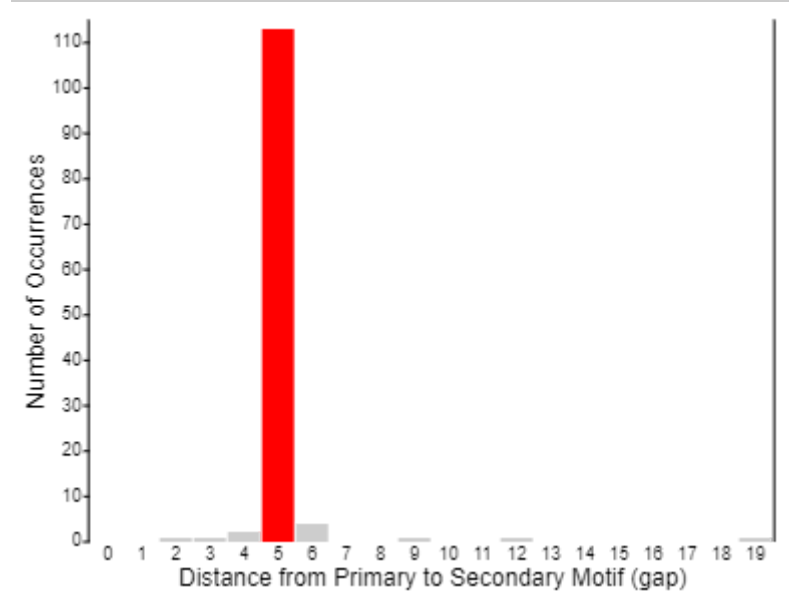
Plain Format ▾ [Download](#)
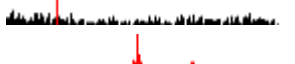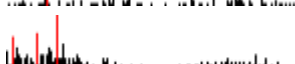
Secondaries

Filter

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

Sort

Sort by [E-value ▼]

[Update]

Lock	ID	Name	Cluster	E-value	Best Gap	Best Orientation	Spacings
☐	GCTGGGATTACAGGC	MEME-3	GCTGGGATTACAGGC	4.08e-236	5	upstream / opposite strand	
☐	3-TAATCCCAGCA	STREME-3	GCTGGGATTACAGGC	7.51e-219	4	upstream / same strand	
☐	5-GATGTCAG	STREME-5	5-GATGTCAG	2.57e-42	11	downstream / same strand	
☐	4-AAATGCAAAA	STREME-4	4-AAATGCAAAA	1.43e-33	67	downstream / same strand	
☐	GGGHGGCSGMGGSGG	MEME-2	GGGHGGCSGMGGSGG	2.37e-32	25	upstream / same strand	
☐	TTTTTTKTTTTTTTT	MEME-1	TTTTTTKTTTTTTTT	8.63e-29	65	downstream / opposite strand	
☐	2-ACTTTG	STREME-2	2-ACTTTG	1.12e-23	20	downstream / same strand	
☐	1-CCACCCCCACCTCC	STREME-1	GGGHGGCSGMGGSGG	2.09e-9	25	upstream / opposite strand	

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

Reference

Tom Whitington, 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_3 -bgfile ./background -keepprimary -primary GGGHGGCSGMGGSGG ./Galaxy8-hyperacetylation_fasta.fasta
```

Result calculation took 2 seconds