


Detecting Individual Sites Subject to Episodic Diversifying Selection

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- Best-in-class power
- Able to detect episodes of selection, not just selection on average at a site
- Embarrassingly parallel (farm out each site), so runs reasonably fast
- Sample size is ~sequences, site level rate estimates imprecise
- Cannot estimate which individual branches are subject to selection with any precision
- Does not scale especially well with the number of sequences

MEME **found evidence** of
+ episodic positive/diversifying selection at 9 sites
with p-value threshold of 0.1.

See [here](#) for more information about the MEME method.
Please cite [PMID 22807683](#) if you use this result in a publication, presentation, or other scientific work.

MEME Table i

Sites that yielded a statistically significant result are highlighted in green.

Showing entries 1 through 20 out of 288.

 **Export Table to CSV**

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Site ↕	Partition ↕	α ↕	β^- ↕	p^- ↕	β^+ ↕	p^+ ↕	LRT ↕	p-value ⌵	# branches under selection ↕	Total branch length ↕	MEME LogL ↕	FEL LogL ↕
161	1	0.00	0.00	0.82	114.39	0.18	7.58	0.01	0.00	0.00	-16.57	-14.14
19	1	0.00	0.00	0.95	2106.40	0.05	6.61	0.02	0.00	0.00	-14.85	-11.57
274	1	2.77	2.77	0.95	10000.00	0.05	4.98	0.04	1.00	0.00	-20.16	-17.67
165	1	0.00	0.00	0.78	52.90	0.22	4.25	0.06	0.00	0.00	-15.51	-14.44
225	1	0.00	0.00	0.74	43.93	0.26	3.71	0.07	2.00	0.00	-13.87	-13.06
264	1	0.00	0.00	0.90	176.76	0.10	3.64	0.08	0.00	0.00	-11.73	-10.17
282	1	0.00	0.00	0.00	8.19	1.00	3.65	0.08	0.00	0.00	-19.33	-19.32
272	1	0.00	0.00	0.85	38.49	0.15	3.33	0.09	1.00	0.00	-10.45	-9.37

```
hyphy meme --alignment HIV-sets.fas
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