

# Mixed Effects Model of Evolution results summary

INPUT DATA | spike.fas | 118 sequences | 1273 sites

Export

MEME found evidence of  
+ episodic positive/diversifying selection at 6 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



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

Showing entries 1 through 20 out of 1273.

Export Table to CSV

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Site	Partition	$\alpha$	$\beta^-$	$p^-$	$\beta^+$	$p^+$	LRT	p-value	# branches under selection	Total branch length	MEME LogL	FEL LogL
1	1	1.22	0.55	0.99	2557.85	0.01	9.76	0.00	1.00	0.00	-19.14	-14.26
470	1	4.21	1.65	0.99	10000.00	0.01	7.46	0.01	1.00	0.00	-24.32	-20.11
1243	1	0.00	0.00	0.98	608.47	0.02	8.85	0.01	2.00	0.00	-23.28	-19.43
452	1	0.00	0.00	0.01	14.48	0.99	8.77	0.01	5.00	0.00	-36.49	-36.49
501	1	0.00	0.00	0.92	328.53	0.08	5.02	0.04	5.00	0.00	-37.07	-36.20
157	1	0.00	0.00	0.01	7.32	0.99	3.71	0.07	4.00	0.00	-29.55	-29.55

```
hyphy meme --alignment spike.fas --tree spike.tree
```

# Interpreting dN/dS for intra-host and intra-species pathogen

- **dN/dS** can be estimated for all sorts of sequence data (e.g., it has been done for cancer SNP data)
- Traditional interpretation of dN/dS is based on the assumption that **substitution ~ fixation**
- Not the same for intra-species / intra-host pathogens
- Much of variation is due to polymorphism, or even dead-end mutations
- This is because selection has not had a chance to “filter” mutations (except for patently deleterious ones)
- This often manifests as differences in selective “regimes” between tips and internal branches