

URL: <https://www.datamonkey.org/meme/5e72c12cf2d22859c642ac8f>  
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# Mixed Effects Model of Evolution results summary

INPUT DATA | **5e72c12cf2d22859c642ac8f** | 39 sequences | 570 sites

 Export ▾

MEME **found evidence** of  
**⊕** episodic positive/diversifying selection at **6** sites  
with p-value threshold of .

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 570.

 Export Table to CSV

[⏪](#) [⏴](#) [⏵](#) [⏩](#)

Site ↕	Partition ↕	$\alpha$ ↕	$\beta^-$ ↕	$p^-$ ↕	$\beta^+$ ↕	$p^+$ ↕	LRT ↕	p-value ↕	# branches under selection ↕	Total branch length ↕	MEME LogL ↕	FEL LogL ↕
72	1	0.00	0.00	0.97	87.58	0.03	10.60	0.00	1.00	0.56	-16.11	-11.70
421	1	0.00	0.00	0.93	52.69	0.07	9.73	0.00	2.00	0.81	-21.33	-18.00
476	1	1.11	0.00	0.97	114.01	0.03	6.82	0.01	1.00	0.74	-19.48	-15.24
67	1	0.00	0.00	0.98	390.83	0.02	6.63	0.02	1.00	1.67	-17.11	-13.79
297	1	1.51	0.00	0.92	32.22	0.08	5.86	0.02	2.00	0.73	-27.28	-22.70
298	1	1.42	0.00	0.96	201.91	0.04	5.24	0.03	2.00	2.02	-23.98	-21.28
442	1	0.00	0.00	0.98	488.83	0.02	4.30	0.05	1.00	2.11	-13.86	-12.14
160	1	0.00	0.00	0.00	2.47	1.00	3.99	0.06	1.00	0.54	-20.56	-20.56
474	1	0.00	0.00	0.94	77.59	0.06	4.08	0.06	2.00	0.99	-17.23	-15.84
418	1	0.00	0.00	0.00	2.22	1.00	3.73	0.07	2.00	0.49	-19.17	-19.17
18	1	0.00	0.00	0.94	65.12	0.06	3.44	0.08	2.00	0.88	-17.84	-17.07
174	1	0.00	0.00	0.64	5.96	0.36	3.65	0.08	1.00	0.47	-21.43	-20.96
233	1	1.72	0.00	0.98	420.44	0.02	3.25	0.09	1.00	1.96	-17.68	-15.98
258	1	0.00	0.00	0.00	2.78	1.00	3.26	0.09	2.00	0.61	-25.74	-25.74
477	1	1.71	0.00	0.95	171.71	0.05	3.29	0.09	2.00	2.01	-23.50	-21.82
138	1	0.00	0.00	0.98	168.47	0.02	3.07	0.10	1.00	0.87	-11.81	-10.68
17	1	0.00	0.00	0.98	369.56	0.02	3.01	0.11	1.00	1.65	-12.67	-11.55



13

1

0.00

0.00

0.68

8.28

0.32

2.68

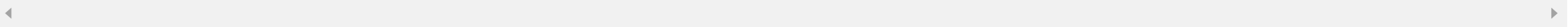
0.13

3.00

0.59

-26.39

-26.28



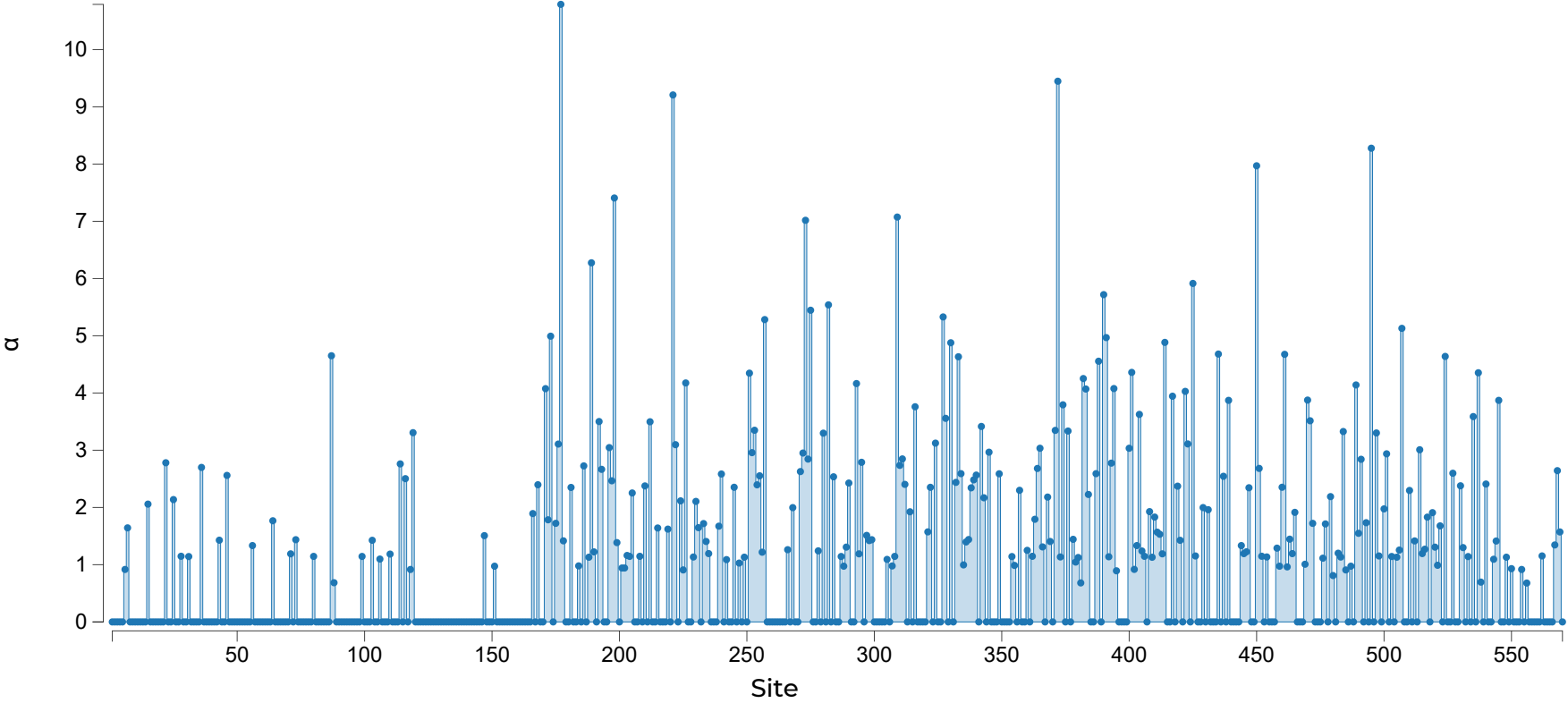
MEME Site Plot

Y-axis:

$\alpha$  ▾

[Export Chart to PNG](#)

[Export Chart to SVG](#)



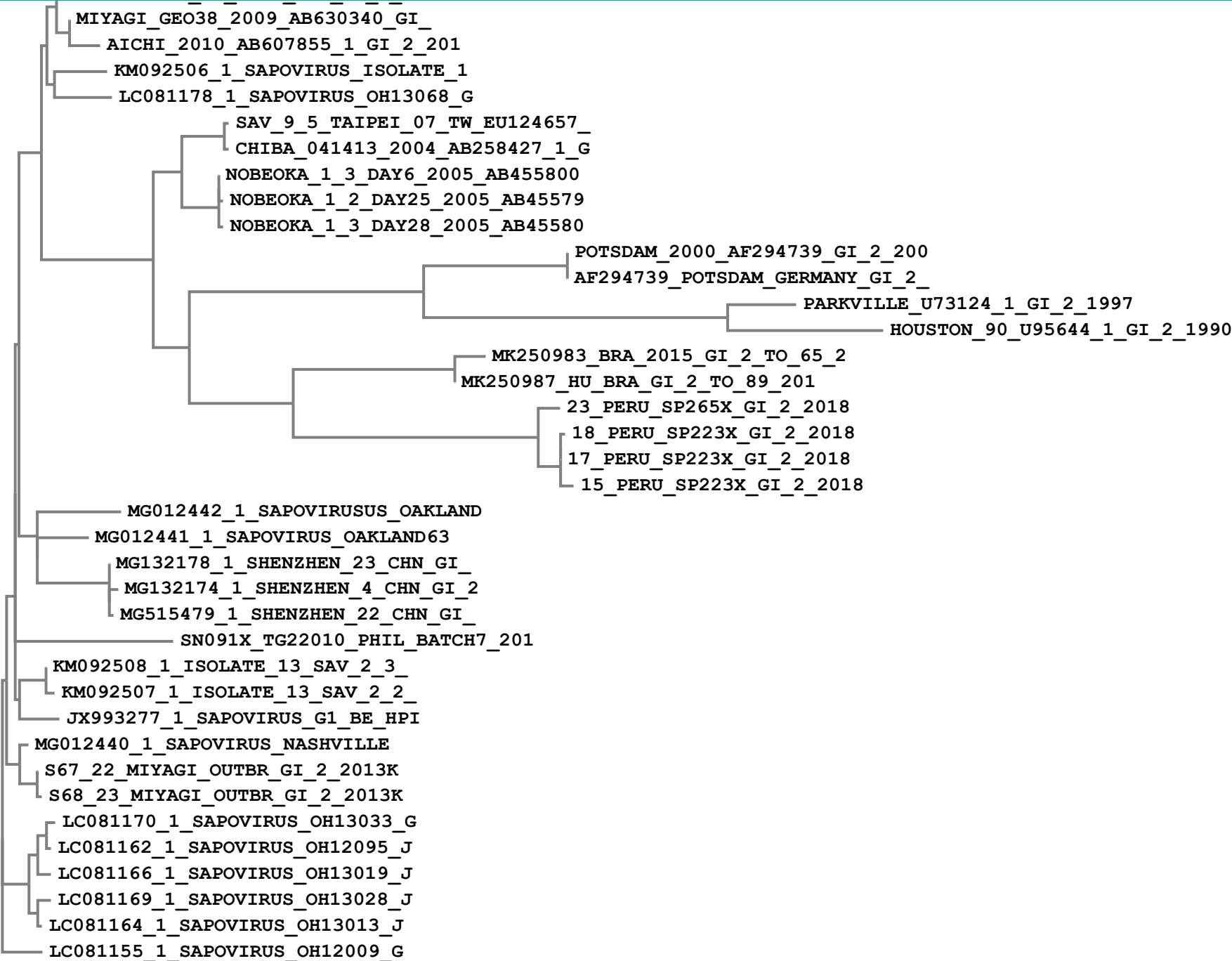
Fitted tree



Options ▾



Export ▾



MEME Branch EBF Table



Showing entries 1 through 10 out of 22950.

Export Table to CSV

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>>

Site ↕	Partition ↕	Branch	EBF ↕
103	0	15_PERU_SP223X_GI_2_2018	1
106	0	15_PERU_SP223X_GI_2_2018	1
110	0	15_PERU_SP223X_GI_2_2018	1
114	0	15_PERU_SP223X_GI_2_2018	1
116	0	15_PERU_SP223X_GI_2_2018	1
118	0	15_PERU_SP223X_GI_2_2018	1
119	0	15_PERU_SP223X_GI_2_2018	1
13	0	15_PERU_SP223X_GI_2_2018	0.92
135	0	15_PERU_SP223X_GI_2_2018	1
138	0	15_PERU_SP223X_GI_2_2018	0.31


Nucleotide GTR	12024.85	-5929.32	83			
				non-synonymous/synonymous rate ratio for *test*		
Global MG94xREV	11336.94	-5578.10	90	100%	@	0.118

This table reports a statistical summary of the models fit to the data. Here, **MG94** refers to the MG94xREV baseline model that infers a single  $\omega$  rate category per branch.

Datamonkey is funded jointly by [MIDAS](#) and [NIH award R01 GM093939](#)




Tweets by @hyphy\_software

 **HyPhy**  
@hyphy\_software

Datamonkey now been released with a new API!  
Submit jobs from your pipeline scripts or from  
anywhere you else you may find convenient.  
Documentation can be found here --  
[github.com/kjlevitz/datam...](#)

Aug 11, 2020

HyPhy Retweeted

 **Sergei Pond**  
@sergeilkp

As [@BallouxFrancois](#) also pointed out, S 614  
(talked about a lot) and RdRp 323 (not talked  
about much at all) are strongly linked (LD R2 >  
0.99), and both show about the same extent of  
evidence for selection: both arose early on and  
stayed "on"  
[https://twitter.com/OscarMacLean1/status/12891](#)

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