

adaptive Branch Site REL results summary

INPUT DATA | WestNileVirus_NS3.fas | 19 sequences | 619 sites

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aBSREL **found no evidence** of episodic diversifying selection in your phylogeny.

A total of **33** branches were formally tested for diversifying selection. Significance was assessed using the Likelihood Ratio Test at a threshold of $p \leq 0.05$, after correcting for multiple testing. Significance and number of rate categories inferred at each branch are provided in the [detailed results](#) table.

See [here](#) for more information about this method.
Please cite [PMID 25697341](#) if you use this result in a publication, presentation, or other scientific work.

Tree summary

ω rate classes	# of branches	% of branches	% of tree length	# under selection
1	30	91%	37%	0
2	3	9.1%	63%	0

This table contains a summary of the inferred aBSREL model complexity. Each row provides information about the branches that were best described by the given number of ω rate categories.

```
hyphy absrel --alignment data/WestNileVirus_NS3.fna
```

adaptive Branch Site REL

results summary

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

Download Export

aBSREL **found no evidence** of episodic diversifying selection in your phylogeny.

A total of **44** branches were formally tested for diversifying selection. Significance was assessed using the Likelihood Ratio Test at a threshold of $p \leq 0.05$, after correcting for multiple testing. Significance and number of rate categories inferred at each branch are provided in the [detailed results](#) table.

See [here](#) for more information about this method.
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Tree summary

ω rate classes	# of branches	% of branches	% of tree length	# under selection
1	161	99%	61%	0
2	1	0.62%	39%	0

This table contains a summary of the inferred aBSREL model complexity. Each row provides information about the branches that were best described by the given number of ω rate categories.

```
hyphy absrel --alignment data/spike.fas --tree data/spike.tree --branches Internal
```