

SARS CoV-2 Spike  
Internal Branches Only

Codon	Partition	alpha	beta+	p+	LRT	Episodic selection detected?	# branches	Most common codon substitutions at this site
367	1	0.000	98.114	0.459	9.062	Yes, p = 0.0047	2	[2]Gtc>Ttc
439	1	0.000	35.271	1.000	4.990	Yes, p = 0.0379	1	[1]aaC>aaA
452	1	0.000	30.877	1.000	5.520	Yes, p = 0.0288	1	[4]cTg>cGg [1]Ctg>Atg
477	1	0.000	51.490	0.460	4.334	Yes, p = 0.0532	1	[1]aGc>aAc
501	1	0.000	271.405	0.145	3.460	Yes, p = 0.0839	1	[3]Aat>Tat [1]aAt>aCt,Tat>Aat
614	1	0.000	49.307	0.464	3.187	Yes, p = 0.0968	1	[1]Gat>Aat,gGt>gAt

# MEME results

- **West Nile Virus NS3 protein**
  - **Four** sites (incl. 249, **previously reported**) with significant evidence of **episodic** (or pervasive) diversifying selection.
- **HIV-1 transmission pair**
  - **Nine** sites with significant evidence of **episodic** (or pervasive) diversifying selection. HIV-1 transmission pair
- SARS-CoV-2 spike (all)
  - **Six** sites with significant evidence of **episodic** (or pervasive) diversifying selection.
- SARS-CoV-2 spike (internal)
  - **Six** sites with significant evidence of **episodic** (or pervasive) diversifying selection.