

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)
 - **Five** sites with significant evidence of **episodic** (or pervasive) diversifying selection.

More on site-level selection

- Three more methods in HyPhy
- Fixed Effects Likelihood (**FEL**)
 - A simpler alternative to MEME (looks for pervasive selection)
 - May be more suited for smaller datasets or datasets of low divergence
- Single Likelihood Ancestor Counting (**SLAC**)
- A counting-based approach
- Good for data exploration and visualization
- Fast Unrestricted Bayesian AppRoximation (**FUBAR**)
 - A novel statistical approach for detecting pervasive adaptive evolution on large datasets (scales to 10000s of sequences)