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.

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 Bayseian AppRoximation (**FUBAR**)

  - A novel statistical approach for detecting pervasive adaptive evolution on large datasets (scales to 10000s of sequences)