

Supplementary material for Danecek et al., Analysis of Flavivirus variance

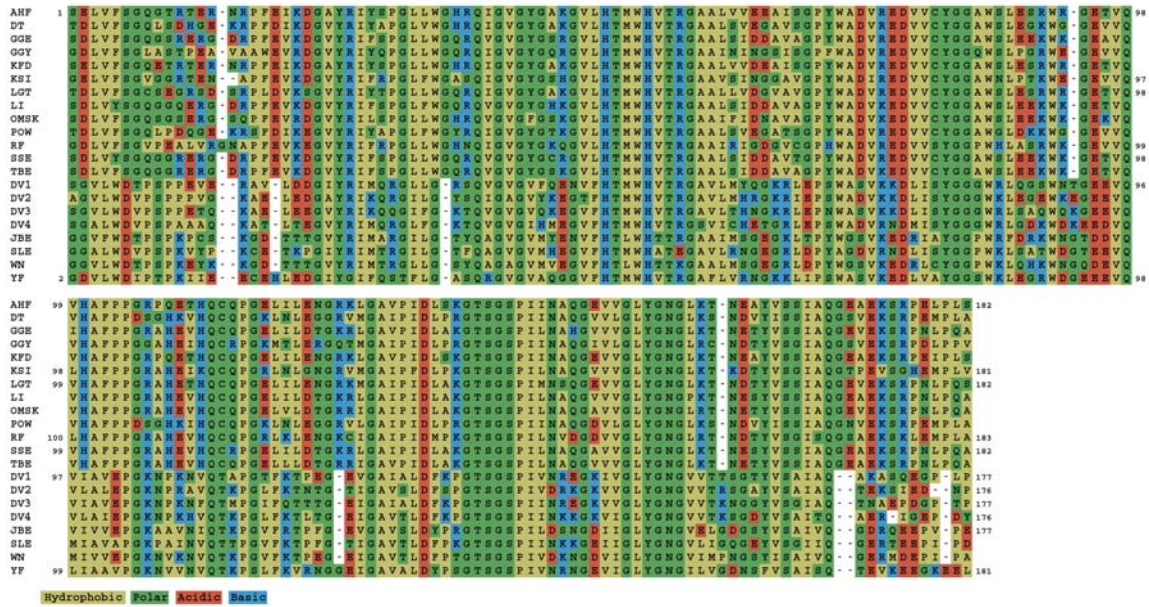
Note: The multiple sequence alignment of 928 flavivirus polyprotein sequences, prepared with Muscle, can be accessed at our Flavitrack website in a Java applet (<http://carnot.utmb.edu/flavitrack/align.php>).

S01-eprotein-cons.pdf

The multiple sequence alignment of 928 flavivirus envelope protein sequences simplified to the multiple sequence alignment of 27 consensus sequences. The residues are colored according to their type (hydrophobic, polar, acidic, basic). The boxes highlight the areas mentioned in the text or shown in the figures. The boxes are labeled according to TBE (black) or DENV2 (red).

S02-ns3protease-cons.pdf

The multiple sequence alignment of 928 flavivirus NS3 protease sequences simplified to the multiple sequence alignment of 27 consensus sequences. The residues are colored according to their type (hydrophobic, polar, acidic, basic).



S03-DENV2-tbe-cleavage-sites.png

The area around the four cleavage sites (NS2A-NS2B, NS2B-NS3, NS3-NS4A, NS4B-NS5) of the NS3 protease, in the mosquito borne DENV or tick (TBE) viruses.

