```
AM936       1  M-------------SGEDEYKEIIRQCIGSVKEVFGEGRFDDVVASIMKMQEKVLASSM
APH_0248    1  MIPLAPWKSISVVYMSGSDEYKEIIKQCIGSVKEVFGEGRFDDVVASIMKMQEKVLASSM

                                                        _____
AM936      47  KDGDP--VGQI-AADGVGNELYDRIADRLEERVSQKISEDLRIIKKRLLRLERVVLGGGS
APH_0248   61  QQDDTGTVGQIESGEGSGARLSDEQVQQLMNSIREEFKDDLRAIKRRILKLERAVYGA--

               _____
AM936     104  VSGDAAAHQVSGNQPSQQNSSAAAEGG
APH_0248  121  ------------NTPKES---------
```

Figure S8. A global pairwise alignment of AM936 and APH_0248 (Asp14) using lalign. The line above the alignment (AM936 aa84-121) includes the binding domain of APH_0248 (aa113-124) and denotes the peptide used in the ELISAs. Amino acids that share identity are in white text with a black background. Conservative amino acid replacements are in white text with a gray background.