

Fig. 1: amino acid (aa) alignment view of the N protein from the selected human respiratory syncytial virus (HRSV) sequences showing high conservation throughout the entire protein. The sequences are identified by their GenBank accession numbers.

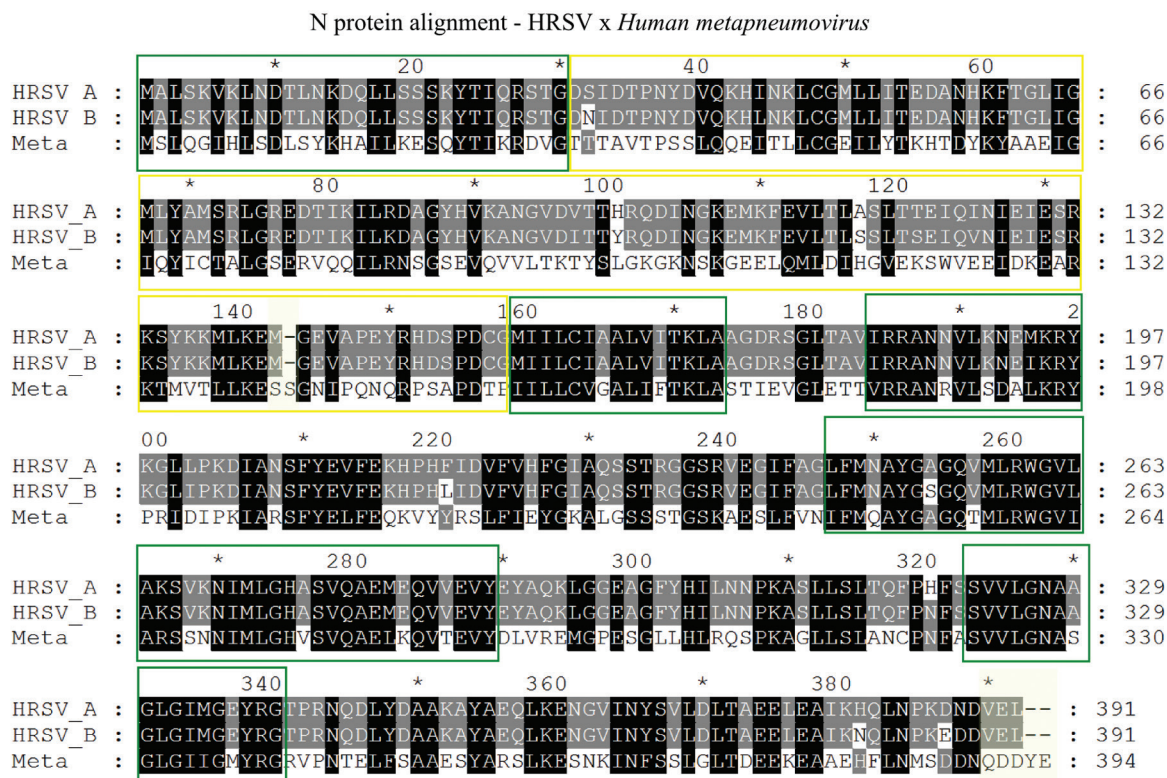
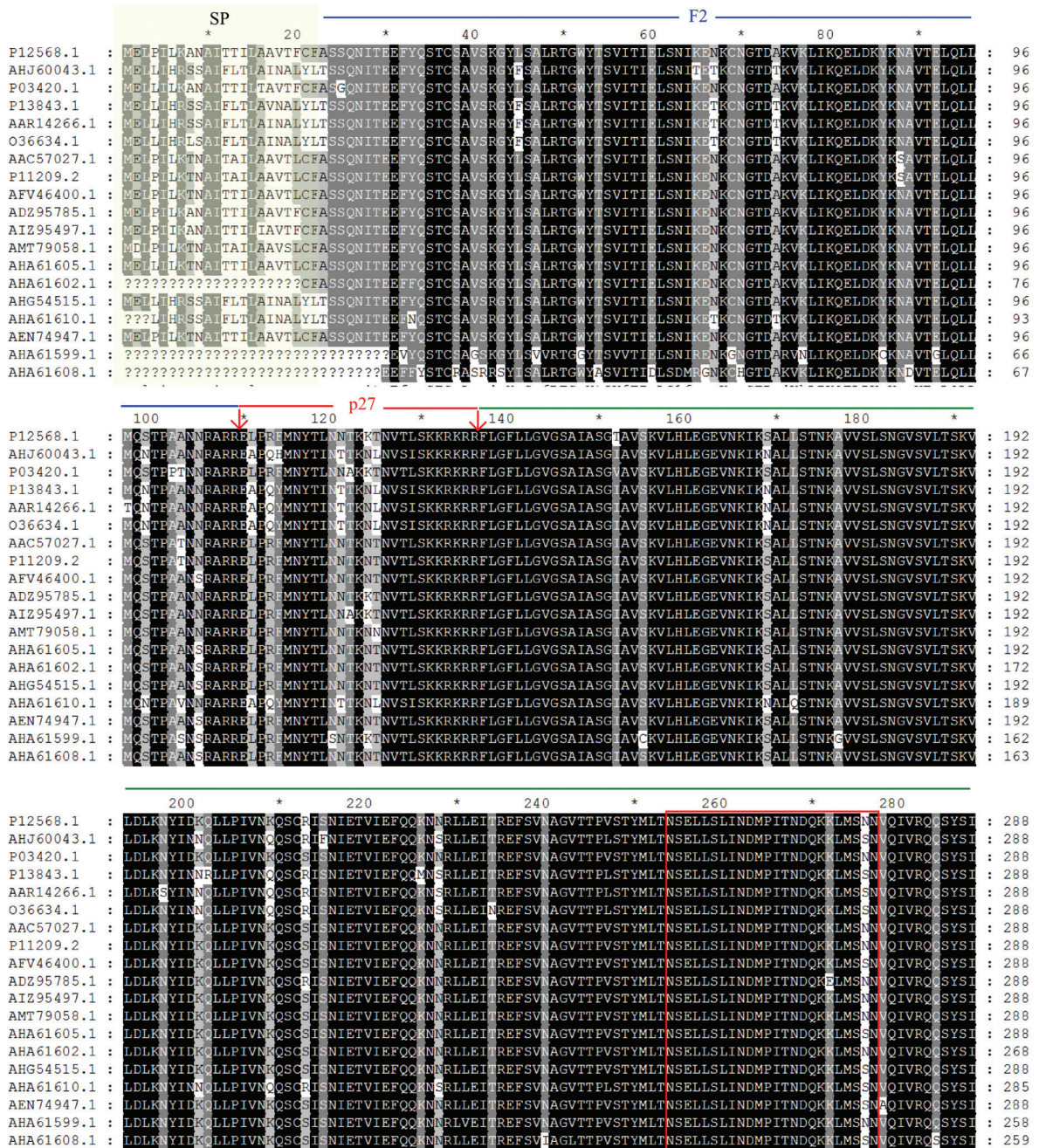


Fig. 2: amino acid (aa) alignment view of the N protein from the selected human respiratory syncytial virus-A (HRSV-A) (4BKK), HRSV-B (O42053.1) and human metapneumovirus (AEA02277.1) sequences. The green boxes show conserved regions. The yellow box shows the most divergent region. The ivory, filled boxes represent the unreliable alignment regions according to the PSI-Coffee result and should not be considered.

F protein alignment



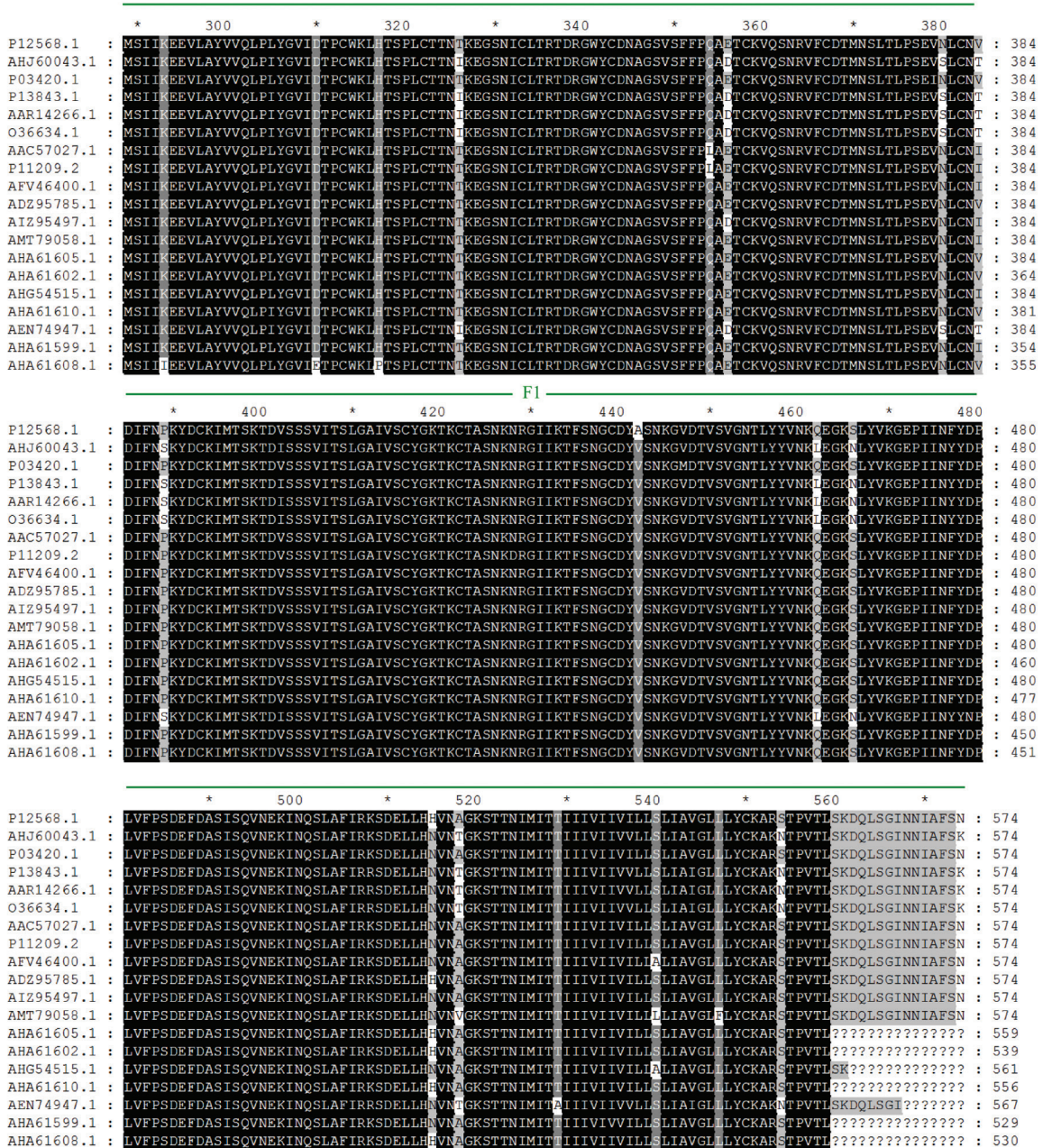


Fig. 3: amino acid (aa) alignment view of the F protein from the selected human respiratory syncytial virus (HRSV) sequences showing conservation throughout the entire protein. The sequences are identified by their GenBank accession numbers. Missing alignment data is represented as a question mark (?). The ivory, filled box on the N-terminal region represents the signal peptide (SP). The F2, p27 and F1 regions are indicated by blue, red and green lines, respectively. The palivizumab-specific antibody epitope sequence is represented by a red box.

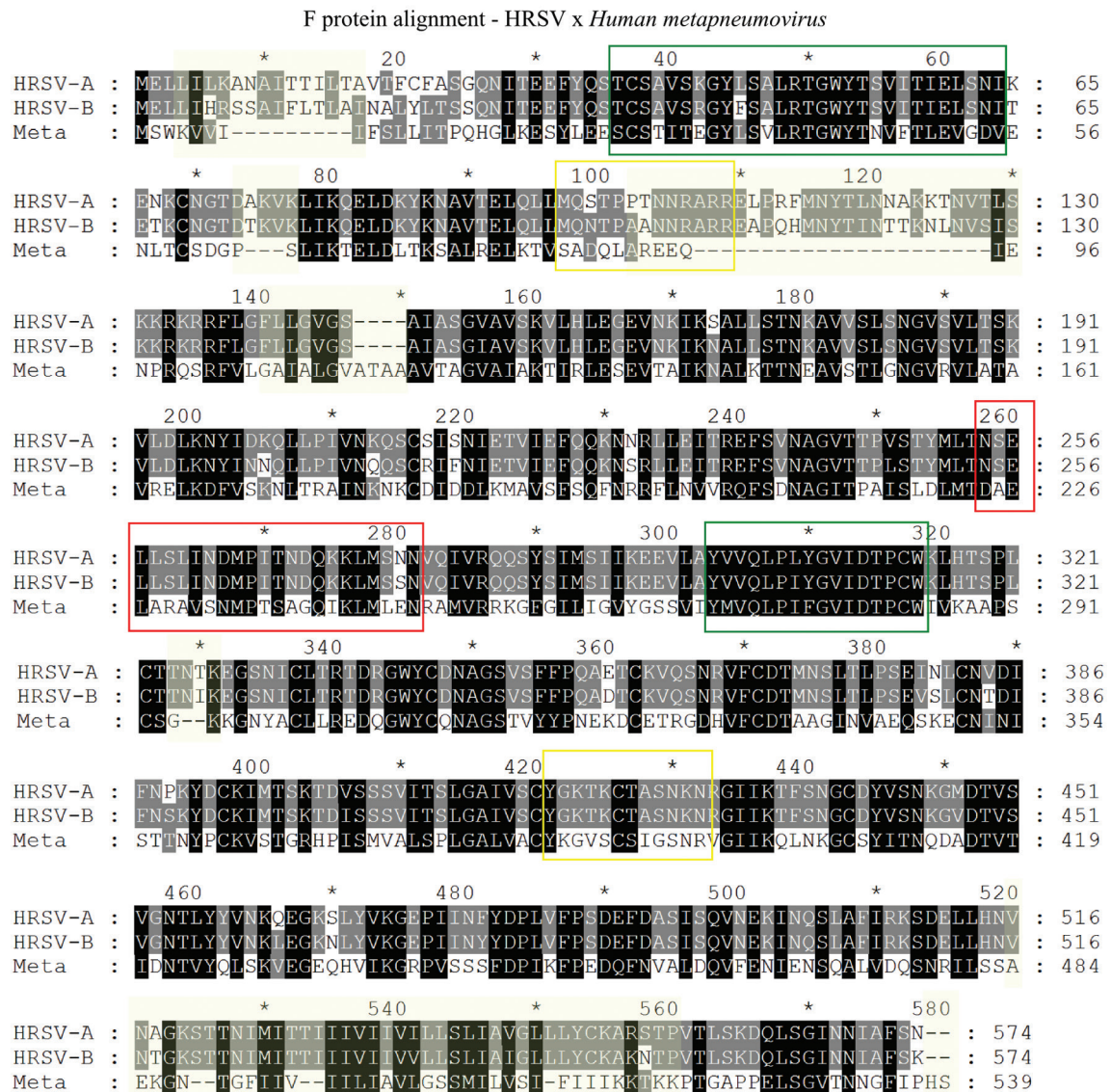


Fig. 4: amino acid (aa) alignment view of the F protein from the selected human respiratory syncytial virus-A (HRSV-A) (P03420.1), HRSV-B (AHJ60043.1) and human metapneumovirus (AAQ67695.1) sequences. The green boxes show conserved regions, and the yellow boxes show the possible targets (positions 97-109 and 417-428). The palivizumab-specific antibody epitope sequence is represented by a red box. The ivory, filled boxes represent the unreliable alignment regions according to the PSI-Coffee result and should not be considered.

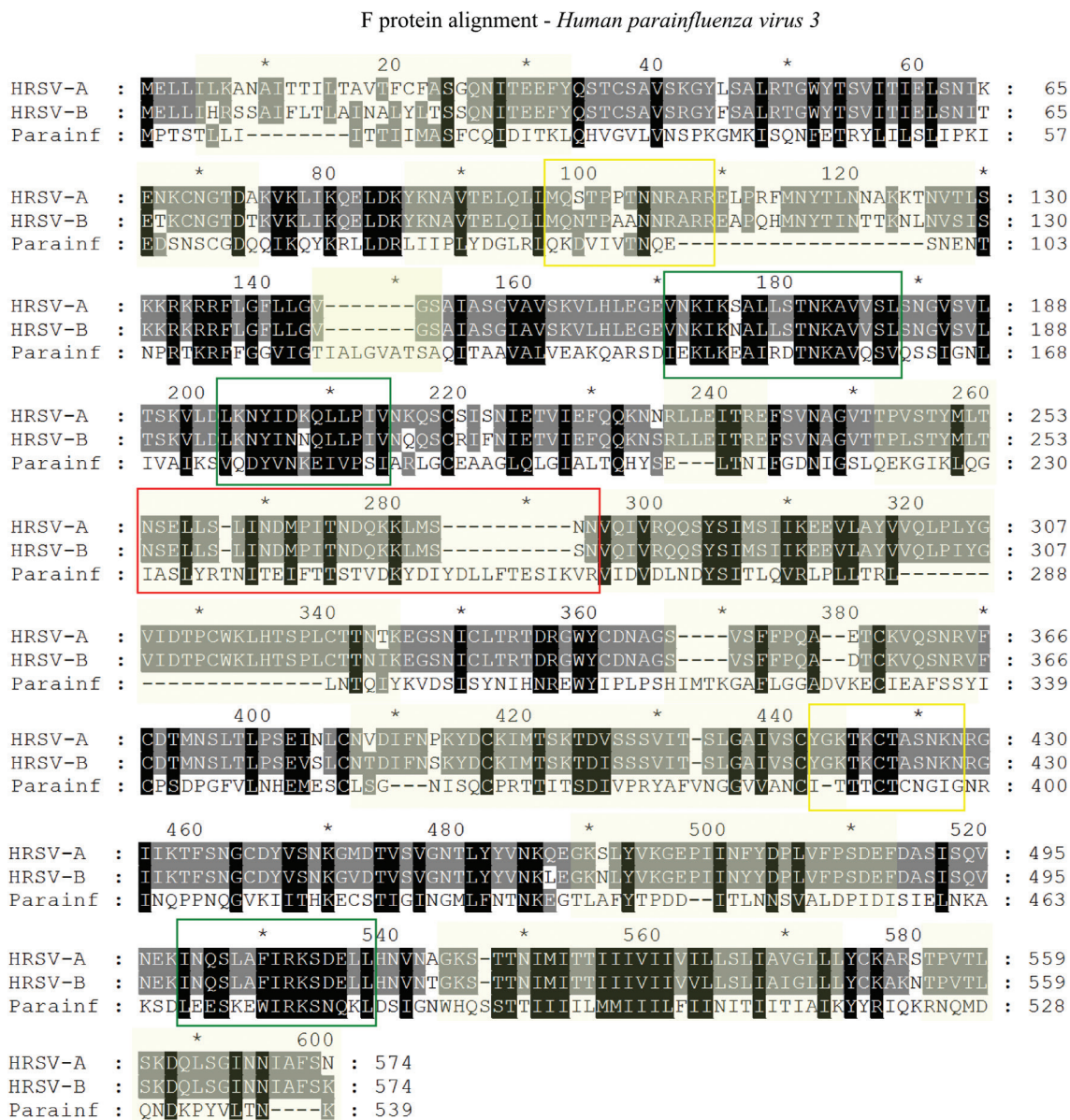


Fig. 5: amino acid (aa) alignment view of the F protein from the selected human respiratory syncytial virus-A (HRSV-A) (P03420.1), HRSV-B (AHJ60043.1) and human parainfluenza virus 3 (NP\_067151.1) sequences. The green boxes show conserved regions, and the yellow boxes show the possible targets (positions 97-109 and 417-428). The palivizumab-specific antibody epitope sequence is represented by a red box. The ivory, filled boxes represent the unreliable alignment regions according to the PSI-Coffee result and should not be considered.

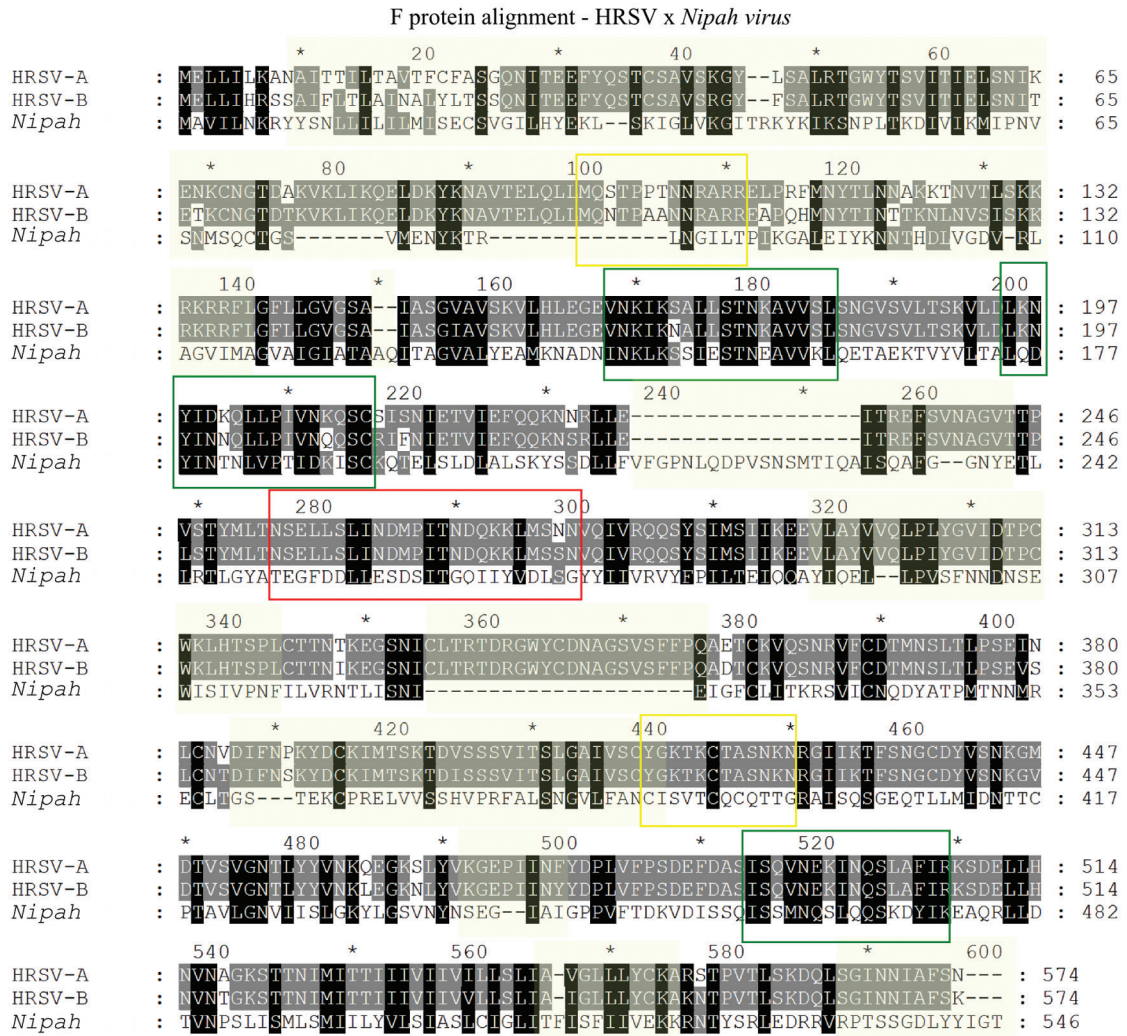


Fig. 6: amino acid (aa) alignment view of the F protein from the selected human respiratory syncytial virus-A (HRSV-A) (P03420.1), HRSV-B (AHJ60043.1) and *Nipah virus* (AAY43915.1) sequences. The green boxes show conserved regions, and the yellow boxes show the possible targets (positions 97-109 and 417-428). The palivizumab-specific antibody epitope sequence is represented by a red box. The ivory, filled boxes represent the unreliable alignment regions according to the PSI-Coffee result and should not be considered.

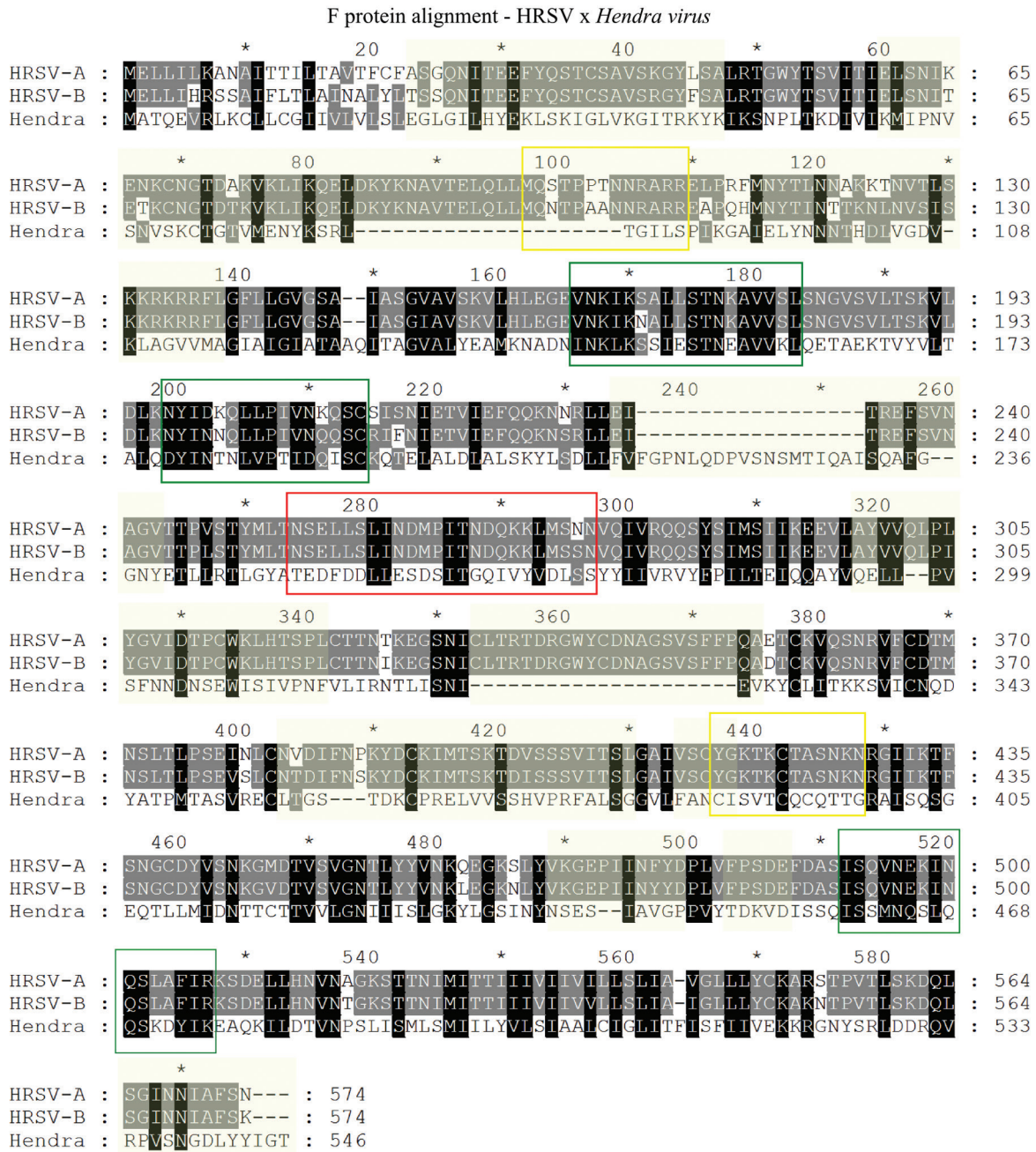


Fig. 7: amino acid (aa) alignment view of the F protein from the selected human respiratory syncytial virus-A (HRSV-A) (P03420.1), HRSV-B (AHJ60043.1) and *Hendra virus* (AEQ38114.1) sequences. The green boxes show conserved regions, and the yellow boxes show the possible targets (positions 97-109 and 417-428). The palivizumab-specific antibody epitope sequence is represented by a red box. The ivory, filled boxes represent the unreliable alignment regions according to the PSI-Coffee result and should not be considered.



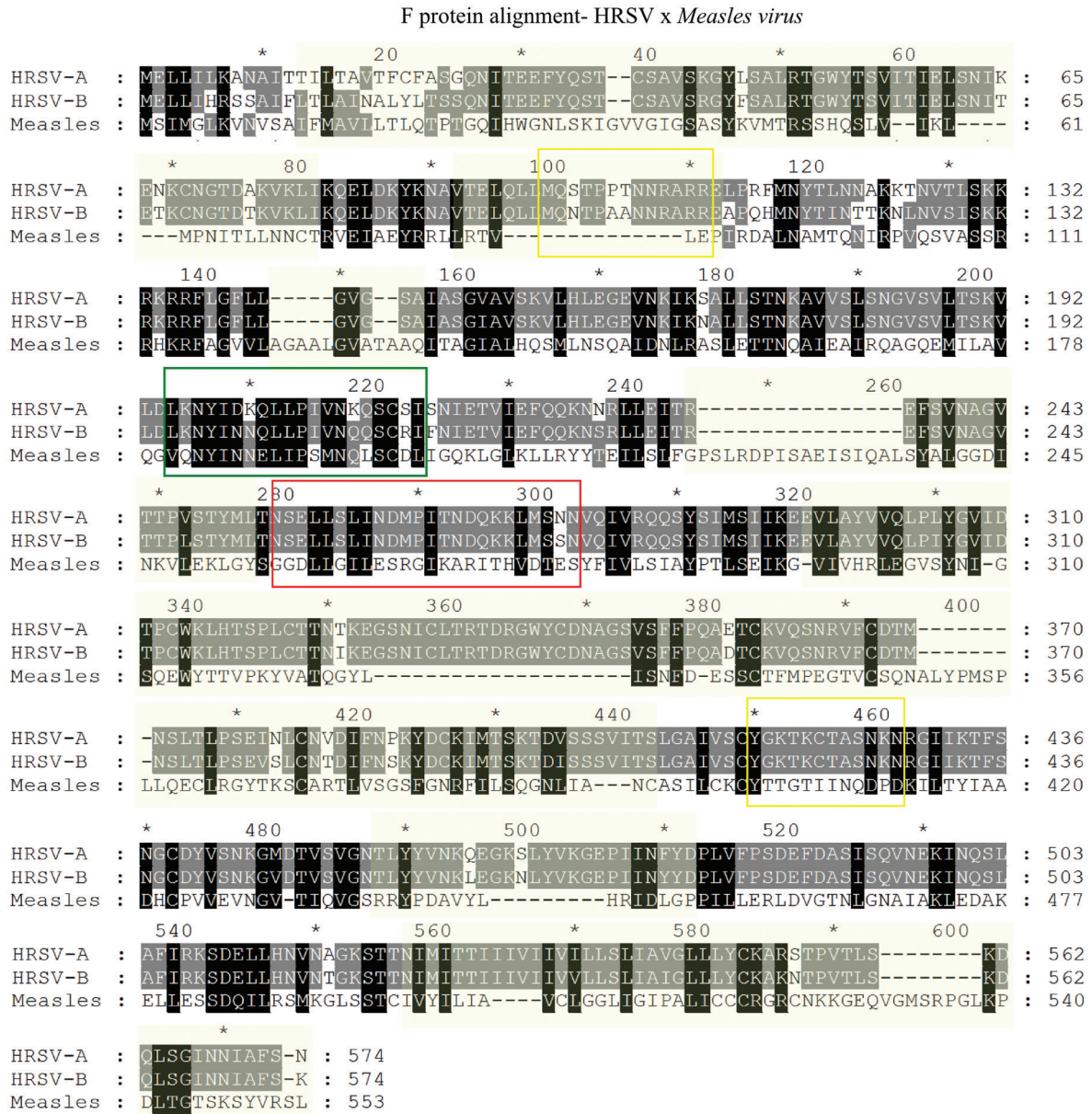


Fig. 8: amino acid (aa) alignment view of the F protein from the selected human respiratory syncytial virus-A (HRSV-A) (P03420.1), HRSV-B (AHJ60043.1) and measles virus (ABY58017.1). The green boxes show conserved regions, and the yellow boxes show the possible targets (positions 97-109 and 417-428). The palivizumab-specific antibody epitope sequence is represented by a red box. The ivory, filled boxes represent the unreliable alignment regions according to the PSI-Coffee result and should not be considered.