

A

DKICIGYHANNSTTQVD TILEKNI TVTHSIELLETQKEERFCRVLNKA PLDLR **ECTIEGWMLGNPRCDILLEDQR**  
WSYIVERPSASNGICYPGPLNEIEELR **SLIGSERVERFEMFPKSTWNGVDTENGITRACSSSTGGSSFYR **NLLW****  
**I IKNKSASYPVIK**GTYNNTGNQPIIYFWGVHHPDADR **QNNLYGSGDRYIRMGTESMHFAKPEIAARPSVNGQR**  
**GRIDYYWSVLNPGETLNIESNGNFIAPRYAYR **FFSTNKK****GVIFKSNLPIENCDAQCQTTLGVLRTNK**TFQNVSPQ**  
**WTGECPKYVKSLSRLATGLRNVPQVETR**GIFGAIAGFIEGGWTGMIDGWYGYHHENSQGSgyAADR**DSTQKAID**  
**GITNKVNTIIDKMNTQFEAVGHEFSNLER****IDNLNKR**MEDGLLDVWTYNAELLVLENER**TLDLHDANVKNLIER**  
VKSQLR**DNANDLGNGCFEFWHK**CDNDCMESVK**NGTYDYPK**YQDESKLNR**QKIESVK**LDNLGVYQILAIYSTVSSS  
LVLVGLIIAMGLWMCSNGSMQCRVCI

B

MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIIGIVHLILWIIDR**LFSKSIYRIFKHGLK****RGPSTEGVPESMREE**  
**YREEQQNAVDADDGHFVSIELE**

**Figure S2. LC-MS/MS based peptide sequence analysis for SDS-PAGE bands of approximately 62 kDa (A) and 14 kDa (B), respectively.** For the 62 kDa band, peptide sequences are mapped against the hemagglutinin protein sequence of A/chicken/South Africa/N2826/2016 (H6N2) for reference. For the 14 kDa band, peptide sequences are mapped against the M2 ion channel protein sequence of A/New Caledonia/20/1999 (H1N1) for reference. Peptides identified with >95% confidence are highlighted in green and <50% confidence in red. No peptides were identified for the non-highlighted grey regions of the protein sequences.