

Figure 1: Predicted Protein Sequence

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1      ADPHHHHHHH  HSSSDYSDLQ  RVKQELLEEV  KKELOQVKKEE  IIEAFVQELR
51     KRGSLVPRGS  PSRSEFYMYN  NTEPLCEAQG  FAPFSKDNGI  RIGSRGHVVF
101    IREPFVSCSP  SECRFFFLTQ  GSLLNDKHSN  GTVKDRSPYR  TLMSVKIGQS
151    PNVYQARFES  VAWSATACHD  GKKWMTVGVT  GPDNQAIADV  NYGGVPVDII
201    NSWAGDILRT  QESSCTCIKG  DCYWVMTDGP  ANRQAKYRIF  KAKDGRVIGQ
251    TDISFNGGHI  EECSCYPNEG  KVEICICRDNW  TGTNRPIILVI  SSDLSYTVGY
301    LCAGIPTDTP  RGEDGQFTGS  CTNPLGNKGY  GVKGFGFRQG  TDVWAGRTIS
351    RTSRSGFEII  KIRNGWTQNS  KDQIRRVQVII  DDPNWSGYSG  SFTLPVELTK
401    KECLVPCFWV  EMIRGKPEET  TIWTSSSSIV  MCGVDHKIAS  WSWHDGAILP
451    FDIDKM

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Plasmid-derived amino acids – Residues 1 to 3 and 61 to 66

His Tag – Residues 4 to 11

Tetramerization domain – Residues 12 to 54

Thrombin cleavage sequence – Residues 55 to 60

NA protein – Residues 67 to 456 [represents amino acid residues 74 to 463 of the native NA protein (GenPept: [BAI68051](#))]¹
¹Note: The predicted protein sequence for NR-13523 is identical to Influenza A virus, A/equine/Yokohama/aq19/2009 except for a serine to glycine change at position 322 of the neuraminidase precursor protein (position 315 of the recombinant protein).