

Figure 1: Predicted Protein Sequence

1	ADPHHHHHH	HSSSDYSDLQ	RVKQELLEEV	KKELQKVKEE	IIEAFVQELR
51	KRGS LV PRGS	PSRSEFVTLA	GNSSLCSISG	WAIYTKD NSI	RIGSKGDV FV
101	IREF FIS CSH	LECR TFF L TQ	GALLNDKHSN	GTVKDRSPYR	ALMSCPLGEA
151	PSPYNSKFES	VAWSASACHD	GMGWLTIGIS	GPDNGAVAVL	KYNGIITETI
201	KSWKKRILRT	QESECVCVNG	SCFTIMTDGP	SNGAASYKIF	KIEKGKVTKS
251	IELNAPNFHY	EECSCYPDTG	TVMCVC R DNW	HGSNRPWVSF	NQNLDYQIGY
301	ICSGVFGDNP	RPKDGE G SCN	PVTVDGADGV	KGFSYKYGNG	VWIGRTKSNR
351	LRKGFEMIWD	PNGWTD T DSD	FSVKQDVVAI	TDWSGYSGSF	VQHP E L T GLD
401	CIRPCFWVEL	VRGLPRE N TT	IWTSGSSISF	CGVNSDTANW	SWPDGAELPF
451	TIDK				

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

Octa-histidine tag – Residues 4 to 11

Tetramerization domain – Residues 12 to 54

Thrombin cleavage sequence – Residues 55 to 60

NA protein – Residues 67 to 454 [represents amino acid residues 83 to 470 of the native NA protein (GenPept: [AFO65030](#))]