Appendix I for NR-43784

Figure 1: Predicted Protein Sequence

1 ADPHHHHHHH HSSSDYSDLQ RVKQELLEEV KKELQKVKEE IIEAFVQELR
51 KRGSLVPRGS PSRSEF**EICP KLAEYRNWSK PQCDITGFAP FSKDNSIRLS**
101 **AGGDIWVTRE PYVSCDPDKC YQFALGQGTT LNNVHSNDTV RDRTPYRTLL**
151 **MNELGVPFHL GTKQVCIAWS SSSCHDGKAW LHVCITGDDK NATASFIYNG**
201 **RLVDSIVSWS KEILRTQESE CVCINGTCTV VMTDGSASGK ADTKILFIEE**
251 **GKIVHTSTLS GSAQHVEECS CYPRYPGVRC VCRDNWKGSN RPIVDINIKD**
301 **HSTVSSYVCS GLVGDTPRKN DSSSSSHCLD PNNEEGGHGV KGWAFDDGND**
351 **VWMGRTISEK SRLGYETFKV IEGWSNPKSK LQINRQVIVD RGNRSGYSGI**
401 **FSVEGKSCIN RCFYVELIRG RKEETEVLWT SNSIVVFCGT SGTYGTGSWP**
451 **DGADINLMPI**

Plasmid-derived amino acids – Residues 1 to 3, 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 460 [represents amino acid residues 76 to 469 of the native NA protein (GenPept: AFN11835)]