**Figure S3**

A

NUCDISC: discrimination of nuclear
localization signals
pat4: KPRK (4) at 56
pat4: PRKK (4) at 57
pat4: RKKK (5) at 58
pat7: PTFKKSK (3) at 46
pat7: PRKKKAR (5) at 57
bipartite: KKSKKNTKPRKKKARKK at 49
bipartite: KKNTKPRKKKARKKMGK at 52
content of basic residues: 17.1%
NLS Score: 2.18

B

CELLO Prediction:

Nuclear	2.075*
Mitochondria	1.334
Extracellular	0.559
Cytoplasmic	0.440
Chloroplast	0.283
PlasmaMembrane	0.158
Peroxisomal	0.037
Lysosomal	0.028
Vacuole	0.027
ER	0.025
Cytoskeletal	0.024
Golgi	0.011

C
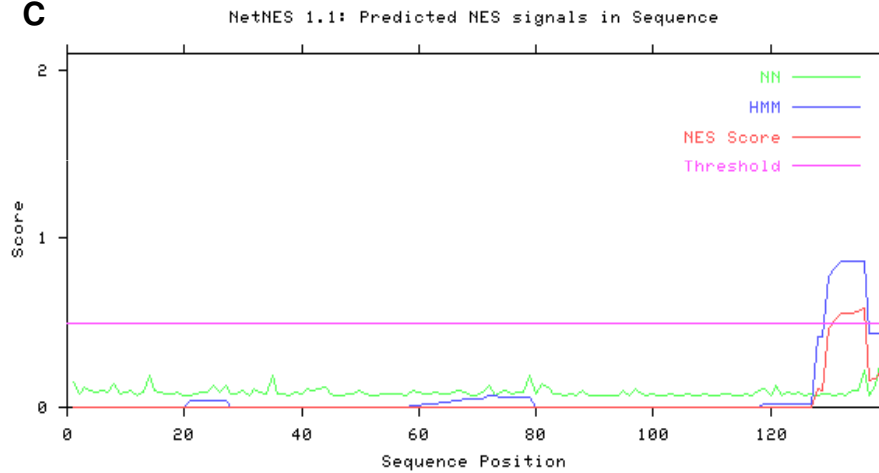
D

>Sequence - NetNES 1.1 prediction

Seq-Pos-Residue	ANN	HMM	NES	Predicted
Sequence-131-T	0.073	0.827	0.517	Yes
Sequence-132-K	0.080	0.862	0.553	Yes
Sequence-133-D	0.071	0.862	0.552	Yes
Sequence-134-L	0.095	0.862	0.557	Yes
Sequence-135-I	0.102	0.862	0.561	Yes
Sequence-136-L	0.214	0.861	0.588	Yes